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DR InterPro: IPR000504; RNA_rec_mot.
DR Pfam: PF05383; la; 1.
DR Pfam: PF00076; trm; 1.
DR PRINTS: PR00302; LUPUSLA.
DR SMART: SM00715; LA; 1.
DR SMART: SM00360; RRM; 1.
DR PROSITE: PS50102; RRM; 1.
DR PROSITE: PS00030; RRM_RNP_1; 1.
DR PROSITE: PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 206 AA; 23992 MW; 965862F7DFPB90E9 CRC64;

Query Match
Best Local Similarity 57.1%; Score 47; DB 13; Length 206;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 ERAIIRQVEYFGD 15
DB 14 ESKICQIIEYFGN 27

RESULT 14
QEMTR3
ID Q8MYR3; PRELIMINARY; PRT; 269 AA.
AC Q8MYR3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE S018087P (Fragment).
GN LARP OR CG14066.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dreesnek D., Farfan D., Friese E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Pounanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celinker S.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY113653; AAM29658.1; -.
DR Flybase; FBgn0040108; larp.
DR InterPro; IPR006630; LUPUS_La_dom.
DR Pfam; PF05383; la; 1.
DR SMART; SM00715; LA; 1.
FT NON TER 269
SQ SEQUENCE 269 AA; 29223 MW; 5295D9EABF04922 CRC64;

Query Match
Best Local Similarity 56.0%; Score 47; DB 5; Length 269;
Matches 11; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 ERAIIRQVEYFGD-----GDF 16
DB 22 KEAIKQVEYFSDNLTGDF 42

RESULT 15
Q7XUK8
ID Q7XUK8; PRELIMINARY; PRT; 435 AA.
AC Q7XUK8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE OSJNB0067K08.21 protein.
GN OSJNB0067K08.21.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_Taxid=4530;

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RN [1]
RP SEQUENCE FROM N.A.
RA Fu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F.,
RA Jia J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y.,
RA Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W.,
RA Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Han B., Feng Q.,
RA Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z.,
RA Chen L., Fan D.L., Wang Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu X.H.,
RA Lu T.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y., Hu H., Jia P.X.,
RA Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M.,
RA Zhang R.Q., Guan J.P., Hong G.F.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL606627; CAD41244.1; -.
SQ SEQUENCE 435 AA; 48295 MW; 66BA0B471B0AE119 CRC64;

Query Match
Best Local Similarity 56.0%; Score 47; DB 10; Length 435;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 RAIIRQVEYFGD 15
DB 17 KEVLRQVEYFSD 29

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Search completed: September 10, 2004, 18:00:18
 Job time : 37.648 secs

SEQ	SEQUENCE	433 AA;	48095 MW;	E58EBAF51C35A8F7	CRC64;
QY	Query Match	57.1%;	Score 48;	DB 10;	Length 433;
	Best Local Similarity	53.8%;	Pred. No. 8.9;		
	Matches	7;	Conservative	4;	Mismatches 2;
					Indels 0;
					Gaps 0;
DB	12 KTVLRQVEYFPGD	24			
RESULT 11					
Q8L7E4	PRELIMINARY;	PRT;	433 AA.		
AC	Q8L7E4				
DT	01-OCT-2002 (TREMBLrel. 22, Created)				
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)				
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)				
DE	Hypothetical protein.				
GN	Atg632720.				
OS	Arabidopsis thaliana (Mouse-ear cress).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
CC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;				
CC	eucosids II; Brassicales; Brassicaceae; Arabidopsis.				
OX	NCBI_TaxID=3702;				
RP	[1]				
RA	SEQUENCE FROM N.A.				
RA	Southwick A., Nguyen M., Tripp M., Palm C.J., Jones T., Wu T.,				
RA	Carninci P., Chen H., Cheuk R., Chan M.M., Chang C.H., Dale J.M.,				
RA	Deng J.M., Hayashizaki Y., Heuan Y.W., Lee J.M., Ishida J., Kamiya A.,				
RA	Kawai J., Kim C.J., Narusaka M., Quach H.L., Sakurai T., Satou M.,				
RA	Seki M., Shim P., Tang C.C., Toroumi M., Wallender E.K., Wong C.,				
RA	Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Ecker J.,				
RA	Theologis A., Davis R.W.;				
RL	Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Nguyen M., Karlin-Neumann G., Southwick A., Tripp M., Miranda M.,				
RA	Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,				
RA	Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,				
RA	Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,				
RA	Sakurai T., Satou M., Seki M., Shim P., Yamada K., Shinozaki K.,				
RA	Ecker J., Theologis A., Davis R.W.;				
RL	Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AY136302; AAM96968.1; -				
DR	EMBL; BT000396; AAN15715.1; -				
DR	GO; GO:0005634; C:nucleus; IEA.				
DR	GO; GO:0003723; F:RNA binding; IEA.				
DR	InterPro; IPR0062344; Lupus_La.				
DR	InterPro; IPR006630; Lupus_La_dom.				
DR	InterPro; IPR005054; RNA_rec_mot.				
DR	Pfam; PF05383; La; 1.				
DR	Pfam; PF00076; rrm; 1.				
DR	PRINTS; PR00302; LUPUSLA.				
DR	SMART; SM00715; LA; 1.				
DR	SMART; SM00360; RRM; 1.				
DR	PROSITE; PS50102; RRM; 1.				
KW	Hypothetical protein.				
SEQ	SEQUENCE	433 AA;	48126 MW;	CPF6F11A29A0318	CRC64;
Query Match	57.1%;	Score 48;	DB 10;	Length 433;	
Best Local Similarity	53.8%;	Pred. No. 8.9;			
Matches	7;	Conservative	4;	Mismatches	2;
					Indels 0;
					Gaps 0;
QY	3 RAIIRQVEYFPGD	15			
	:::				
DB	12 KTVLRQVEYFPGD	24			
RESULT 12					
ID	065529	PRELIMINARY;	PRT;	483 AA.	
AC	065529;				

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DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN FAD11.80 OR AY632720.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Beyer M., Beyer V., Rechmann S., Borkova D., Ansgore W., Hohnseel J.,
RA Mewes H.W., Mayer K.F.X., Scheller C.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Beyer V., Rechmann S., Borkova D., Ansgore W., Mewes H.W., Lemcke K.,
RA Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN EMBL; AL022537; CAA18589.1; -.
DR EMBL; AL161582; CAB79989.1; -.
DR PIR; T04453; T04453.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR00504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF0076; Irm; 1.
DR PRINTS; PRO0302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS0102; RRM; 1.
KW Hypothetical protein.
SQ
SEQUENCE 483 AA; 54125 MW; 20840B34A0BC94E2 CRC64;

Query Match 57.1%; Score 48; DB 10; Length 483;
Best Local Similarity 53.8%; Pred. No. 9.9;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 RAIRQVEYFPGD 15
DB 12 KTVLRQVEYFPGD 24

RESULT 13
Q8QCH5 PRELIMINARY; PRT; 206 AA.
AC Q8QCH5;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Untranslated region binding-protein.
DE UBP.
GN Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA L'Ecuquer T.J., Fang H.-L.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN EMBL; AF467897; AAL76269.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.

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DR 01-JUN-2003 (TREMBlrel. 24, last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
DE Similar to lupus LA protein homolog B.
OS Xenopus laevis (African clawed frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Piplidae;
OC Xenopodinae; Xenopus.
OK NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Straubeberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046654; AAA46654.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR Pfam; PF00706; rtm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR PROSITE; PS50102; RRM; 2.
SQ SEQUENCE 427 AA; 48996 MW; 1E7CD82D8AB9C69A CRC64;
Query Match 57.1%; Score 48; DB 13; Length 427;
Best Local Similarity 72.7%; Pred. No. 8.7;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 5 IIRGVYFFGD 15
Db 16 ICEQIEYVFGD 26
RESULT 10
O93ZV7 PRELIMINARY; PRT; 433 AA.
AC O93ZV7
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
DE Putative RNA-binding protein LAH1.
GN ATG32720.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eustroids II; Brassicales; Brassicaceae; Arabidopsids.
OK NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Banb J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M.,
RA Onodera C.S., Quach H.U., Tang C., Toriumi M., Yamamura Y., Yu G.,
RA Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C.,
RA Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shimizu P.,
RA Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,
RA Thellogis A.;
RT "Full length cDNA of gene ATG32720 (GI:7270219).";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY056237; AL070986.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR005044; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; rtm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.

Best Local Similarity 57.1%; Pred. No. 1.1;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 ERLIROYEYFGD 15
| : : |||||

Db 11 EKRVAEIQEYFGD 24

RESULT 5

ID Q9FL36 PRELIMINARY; PRT; 411 AA.

AC Q9FL36; 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

OS Arabidopsis thaliana (Mouse-ear cress)

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;

SEQUENCE FROM N.A.

RC STRAIN=Columbia;

RX MEDLINE=98344145; PubMed=9679202;

RA Kaneko T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,

Tabata S.;

RT "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence

features of the regions of 1,381,565 bp covered by twenty one

physically assigned P1 and TAC clones.";

RL DNA Res. 5:131-145(1998).

DR EMBL: AB010698; BAB1080.1; -

DR GO: GO:0005634; C:nucleus; IEA.

DR GO: GO:0003723; F:RNA binding; IEA.

DR InterPro: IPR002344; Lupus_La.

DR InterPro: IPR006630; Lupus_La_dom.

DR InterPro: IPR005054; RNA_rec_mot.

DR Pfam: PF05383; La; 1.

DR Pfam: PF00076; rtm; 1.

DR PRINTS: PR00302; LUPUSLA.

DR SMART: SM00715; La; 1.

DR SMART: SM00360; RRM; 1.

DR PROSITE: PSS0102; RRM; 1.

SEQUENCE 411 AA; 45655 MW; A2EF62B5B98099 CRC64;

QY 5 IIRQVEYFGD 15
| |||||

Db 96 IIRQVEYFGD 106

RESULT 6

ID Q94A38 PRELIMINARY; PRT; 422 AA.

AC Q94A38; 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

OS Arabidopsis thaliana (Mouse-ear cress)

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;

SEQUENCE FROM N.A.

RA Shih P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,

Banh J., Bowser L., Carrinci P., Dale J.M., Goldsmith A.D.,

Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,

Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,

hiranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
Pam P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

RT "Arabidopsis cDNA clones.";

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

SEQUENCE FROM N.A.

RA Cheuk R., Chen H., Kim C.J., Shih P., Bowser L., Carrinci P.,

Chen M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,

Huan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,

Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,

Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,

Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C.,

Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A.,

Ecker J.R.;

RT "Arabidopsis ORF clones.";

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY050403; AAK91419.1; -

DR EMBL: BT000588; AAN18157.1; -

DR GO: GO:0005634; C:nucleus; IEA.

DR GO: GO:0003723; F:RNA binding; IEA.

DR InterPro: IPR002344; Lupus_La.

DR InterPro: IPR006630; Lupus_La_dom.

DR InterPro: IPR005054; RNA_rec_mot.

DR Pfam: PF05383; La; 1.

DR Pfam: PF00076; rtm; 1.

DR PRINTS: PR00302; LUPUSLA.

DR SMART: SM00715; La; 1.

DR SMART: SM00360; RRM; 1.

DR PROSITE: PSS0102; RRM; 1.

SEQUENCE 422 AA; 46842 MW; 4EC4BBE1E068F0E CRC64;

QY 5 IIRQVEYFGD 15
| |||||

Db 107 IIRQVEYFGD 117

RESULT 7

ID O01806 PRELIMINARY; PRT; 396 AA.

AC O01806; 01-JUL-1997 (TREMBlrel. 04, Created)

DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)

DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

OS Caenorhabditis elegans

OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Pelodermidae; Caenorhabditis.

NCBI_TaxID=6239;

SEQUENCE FROM N.A.

RA STRAIN=Bristol N2;

RE MEDLINE=99069613; PubMed=9851916;

None;

RT "Genome sequence of the nematode C. elegans: a platform for

investigating biology. The C. elegans Sequencing Consortium.";

RL Science 282:2012-2018(1998).

SEQUENCE FROM N.A.

RA STRAIN=Bristol N2;

RC Sammons L., Wohldmann P., Gillam B.;

RT "The sequence of C. elegans cosmid C44B4.";

Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.

SEQUENCE FROM N.A.

RA STRAIN=Bristol N2;

RC Waterston R.;

Query Match	Similarity	92.9%	Score 78:	DB 5:	Length 390:
Best Local	Similarity	100.0%	Pred. NO. 5.9e-05:		
Matches	15:	Conservative	0:	Mismatches	0:
				Indels	0:
				Gaps	0:
Qy	1 QERAIRQVEYYFGD 15				
Db	50 QERAIRQVEYYFGD 64				
RESULT 2					
Q9CYB9	PRELIMINARY:		PRT:	381 AA.	
AC	O9CYB9:				
DT	01-JUN-2001 (TREMBlrel. 17, Created)				
DT	01-JUN-2001 (TREMBlrel. 17, Last sequence update)				
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)				
DE	Sjogren syndrome antigen B.				
GN	SSB.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Euteleia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
NCBI_Taxid	10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-C57BL/6J; TISSUE=Embryo;				
RA	MEDLINE=21085660; PubMed=11217851;				
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,				
RA	Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,				
RA	Aizawa K., Izawa M., Niehi K., Kiyosawa H., Kondo S., Yamana K.,				
RA	Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,				
RA	Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,				
RA	Fleischmann W., Gasteierland T., Gissi C., King B., Kochwa H.,				
RA	Kuehl P., Lewis S., Matuo Y., Nikaido I., Pesole G., Quackenbush J.,				
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,				
RA	Blake J., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,				
RA	Sakai K., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,				
RA	Brownstein M.J., Bulc C., Fletcher C., Fujita M., Gariboldi M.,				
RA	Guertinich S., Hill D., Hofmann M., Hume D.A., Kamuya W., Lee N.H.,				
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,				
RA	Notione P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,				
RA	Saeki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,				
RA	Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilming L.,				
RA	Wynshaw-Borzi Y., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,				
RA	Hayashizaki Y.;				
RT	"Functional annotation of a full-length mouse cDNA collection.";				
RL	Nature 409:685-690(2001).				
EMB	AK017823; BAB30957.1; -				
DR	MGD; MGI:98423; Ssb				
DR	GO; GO:0005634; C:nucleus; IDA.				
DR	InterPro; IPR002344; Lupus_La.				
DR	InterPro; IPR006630; Lupus_La.dom.				
DR	InterPro; IPR000504; RNA_rec_mot.				
DR	Pfam; PF05383; La; 1.				
DR	Pfam; PF00076; trm; 1.				
DR	PRINTS; PR00302; LUPUSLA.				
DR	SMART; SM00715; La; 1.				
SEQ	SEQUENCE 381 AA; 43891 MW; 282DEF1452C0F0E9 CRC64;				
Query Match	67.9%	Score 57:	DB 11:	Length 381;	
Best Local Similarity	66.7%	Pred. NO. 0.22;			
Matches	10:	Conservative	1:	Mismatches	4:
				Indels	0:
				Gaps	0:
Qy	2 ERAIRQVEYYFGD 16				
Db	14 EAKICHQIEYYRGDF 28				
RESULT 3					
Q8BTU4	PRELIMINARY:		PRT:	415 AA.	
AC	O8BTU4:				
DT	01-MAR-2003 (TREMBlrel. 23, Created)				
DT	01-MAR-2003 (TREMBlrel. 23, Last sequence update)				

```

DE 01-OCR-2003 (TREMBLrel. 25, last annotation update)
DE Stogren syndrome antigen B.
CN SSB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium,
RA the RIKEN Genome Mouse Transcription Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
RL EMBL; AK088677; BAC0498.1; -.
DR MGD; MGI:98423; Ssd.
DR GO; GO:0005634; C:nucleus; IDA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR00630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; Ia; 1.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 401 AA; 46138 MW; 2EF032FDD3916291 CRC64;

Query Match 63.1%; Score 53; DB 13; Length 401;

0Y 2 ERATIRQVEYYFGDF 16
Db 14 EAKIChQIEYYFGDF 28

RESULT 4
Q7ZTIO PRELIMINARY; PRT; 401 AA.
ID Q7ZTIO.
AC Q7ZTIO.
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCR-2003 (TREMBLrel. 25, Last annotation update)
DE Similar to stogren syndrome antigen B (Autoantigen Ia) .
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Body;
RL Strausberg R.;
RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DE EMBL; BC045392; AAH45392.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR00630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 401 AA; 46138 MW; 2EF032FDD3916291 CRC64;

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:29:01 / Search time 36.648 Seconds
(without alignments)
137.751 Million cell updates/sec

Title: US-09-836-073-19

Sequence: 1 QERAIIRQVEYRFGDF 16

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78	92.9	390	5 Q8T8V5	Q8T8V5 drosophila
2	57	67.9	381	11 Q9CYB9	Q9CYB9 mus musculus
3	57	67.9	415	11 Q8BTU4	Q8BTU4 mus musculus
4	53	63.1	401	13 Q7ZTU0	Q7ZTU0 brachydanio
5	53	63.1	411	10 Q9FL36	Q9FL36 arabidopsis
6	53	63.1	422	10 Q94A38	Q94A38 arabidopsis
7	50	59.5	396	5 Q01806	Q01806 caenorhabdi
8	49	58.3	389	10 Q8S0T8	Q8S0T8 oryza sativ
9	48	57.1	427	13 Q7ZTK2	Q7ZTK2 xenopus lae
10	48	57.1	433	10 Q93ZV7	Q93ZV7 arabidopsis
11	48	57.1	433	10 Q8L7B4	Q8L7B4 arabidopsis
12	48	57.1	433	10 Q6S5Z9	Q6S5Z9 arabidopsis
13	47	56.0	206	13 Q8Q4H5	Q8Q4H5 gallus gall
14	47	56.0	269	5 Q8MYR3	Q8MYR3 drosophila
15	47	56.0	435	10 Q7XU88	Q7XU88 oryza sativ
16	47	56.0	545	10 Q80567	Q80567 arabidopsis

17	47	56.0	826	10 Q940X9	Q940X9 arabidopsis
18	47	56.0	965	5 Q9VAM5	Q9VAM5 drosophila
19	47	56.0	1403	5 Q9NHM6	Q9NHM6 drosophila
20	47	56.0	1403	5 Q8IMM4	Q8IMM4 drosophila
21	47	56.0	1442	5 Q86B76	Q86B76 drosophila
22	45.5	54.2	642	16 Q9KEU7	Q9KEU7 bacillus ba
23	45	53.6	481	10 Q8LMP9	Q8LMP9 oryza sativ
24	45	53.6	914	12 Q854Z7	Q854Z7 rat cytochrome
25	43	51.2	343	2 Q9XB17	Q9XB17 bacillus ce
26	43	51.2	373	16 Q8CU33	Q8CU33 staphylococ
27	43	51.2	469	16 Q66887	Q66887 aquifex aeo
28	43	51.2	669	16 Q8XRQ1	Q8XRQ1 ralatonia s
29	43	51.2	846	16 Q8LUP0	Q8LUP0 bacillus an
30	43	51.2	846	16 Q9RT05	Q9RT05 delnocooc
31	42.5	50.6	175	5 Q81979	Q81979 plasmodium
32	42	50.0	166	16 Q87NT5	Q87NT5 vibrio para
33	42	50.0	181	16 Q82Z79	Q82Z79 enterococu
34	42	50.0	213	12 Q9YFX1	Q9YFX1 focc-and-mo
35	42	50.0	236	11 Q9CTN3	Q9CTN3 mus musculu
36	42	50.0	343	10 Q94LDO	Q94LDO oryza sativ
37	42	50.0	395	5 Q819V8	Q819V8 manduca sex
38	42	50.0	398	2 Q7X4V8	Q7X4V8 escherichia
39	42	50.0	398	16 Q7UAP6	Q7UAP6 shigella fl
40	42	50.0	407	16 Q83IM4	Q83IM4 mus musculu
41	42	50.0	492	11 Q9D3J0	Q9D3J0 mus musculu
42	42	50.0	492	11 Q8CA51	Q8CA51 mus musculu
43	42	50.0	492	11 Q8C9A3	Q8C9A3 mus musculu
44	42	50.0	492	11 Q8BN59	Q8BN59 mus musculu
45	42	50.0	788	17 Q58603	Q58603 pyrococcus

ALIGNMENTS

RESULT 1

ID Q8T8V5 PRELIMINARY; PRT; 390 AA.

AC Q8T8V5; 08T8V5; 21, Created)

DT 01-JUN-2002 (TREMREL_21, Last sequence update)

DT 01-JUN-2002 (TREMREL_21, Last sequence update)

DT 01-OCT-2003 (TREMREL_25, Last annotation update)

DE AT22034P.

GN LA OR CG10922.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

CC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RA Stapleton M., Brokerlein P., Hong L., Agbayani A., Carlson J.,

RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Friae E.,

RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,

RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,

RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,

RA Cejnkner S.

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

EMBL: AY075257; AA068124.1; -.

DR FLYBase; FBgn0011638; La.

DR GO; GO:0008098; F:5S rRNA primary transcript binding; IDA.

DR GO; GO:0003723; F:rRNA binding; NAS.

DR InterPro; IPR002344; Lupus La.

DR InterPro; IPR006630; Lupus La dom.

DR InterPro; IPR000504; RNA_rec_mot.

DR Pfam; PF05383; La; 1.

DR Pfam; PF00076; xtm; 1.

DR PRINTS; PR00302; LUPUSLA.

DR SMART; SM00715; LA; 1.

DR SMART; SM00360; RRM; 1.

DR PROSITE; PS01021; RRM; 1.

DR PROSITE; PS00303; RRM_RNP_1; 1.

SQ SEQUENCE 390 AA; 44869 MW; 797FDE26B903C909 CRC64;

```

RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Manthariman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blatter F.R.;
RA "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
RA Nature 409:529-533 (2001).
RL
RN
RP
SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shingawa H.;
RA "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RT DNA Res. 8:11-22 (2001).
CC
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC
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CC
CC EMBL; AE005657; AAG59456.1; ALT_INTT.
DR EMBL; AF002569; BAB38657.1; -.
DR PIR; B91283; B91283.
KW Hypothetical protein; Transmembrane; Complete proteome.
KM
FT TRANSMEM 25 45
FT TRANSMEM 74 94
FT TRANSMEM 96 116
FT TRANSMEM 143 163
FT TRANSMEM 176 196
FT TRANSMEM 229 249
FT TRANSMEM 279 299
FT TRANSMEM 334 354
SQ SEQUENCE 398 AA; 44817 MW; C43710A463D289C9 CRC64;

Query Match 50.0%; Score 42; DB 1; Length 398;
Best Local Similarity 57.1%; Pred. No. 8.5;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 QERRAIRQVEYVYFG 14
DB 276 QRRMTIAQLIYVYFG 289

RESULT 15
YJGN_ECOLI STANDARD; PRT; 398 AA.
AC P39338; P39339; P76811;
DT 01-FEB-1995 (Rel. 31, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein yjgn.
DE YJGN OR B4257.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN
RP
SEQUENCE FROM N.A.
RC STRAIN=X12 / MG1655;
RX MEDLINE=95334362; PubMed=7610040;
RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RA Blatter F.R.;
RA "Analysis of the Escherichia coli genome VI: DNA sequence of the
RT region from 92.8 through 100 minutes.";
RT Nucleic Acids Res. 23:2105-2119 (1995).
RN
RP
REVISIONS.

```

```

RC STRAIN=X12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden W.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RT Science 277:1453-1474 (1997).
RL
RN
RP
CONCEPTUAL TRANSLATION.
RA
RA Rudd K.E.;
RL Unpublished observations (JAN-2000).
CC
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESHIFT HAD TO
CC BE INTRODUCED IN POSITION 12 TO PRODUCE THIS ORF.
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CC
CC EMBL; U14003; AAA97153.1; ALT_FRAME.
DR EMBL; U14003; AAA97154.1; ALT_FRAME.
DR Ecogene; EG12533; YJGN.
KW Hypothetical protein; Transmembrane; Complete proteome.
KM
FT TRANSMEM 25 45
FT TRANSMEM 74 94
FT TRANSMEM 96 116
FT TRANSMEM 143 163
FT TRANSMEM 176 196
FT TRANSMEM 229 249
FT TRANSMEM 279 299
FT TRANSMEM 334 354
SQ SEQUENCE 398 AA; 44877 MW; 814BFD98E816A63 CRC64;

Query Match 50.0%; Score 42; DB 1; Length 398;
Best Local Similarity 57.1%; Pred. No. 8.5;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 QERRAIRQVEYVYFG 14
DB 276 QRRMTIAQLIYVYFG 289

Search completed: September 10, 2004, 17:53:13
Job time : 7.43575 secs

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LAH1 YEAST
 ID LAH1 YEAST STANDARD; PRT; 275 AA.
 AC P3339;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 10-OCT-1994 (Rel. 30, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE LA PROTEIN HOMOLOG (La ribonucleoprotein) (La autoantigen homolog).
 GN LAH1 OR LHP1 OR YLAI OR YDL051W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=YH501;
 RX MEDLINE=94309661; PubMed=8035818;
 RA Yoo C.J., Molin S.L.;
 RT "La proteins from *Drosophila melanogaster* and *Saccharomyces cerevisiae*: a yeast homolog of the La autoantigen is dispensable for growth."
 RL Mol. Cell. Biol. 14:5412-5424(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / FY1678;
 RX MEDLINE=97313263; PubMed=9169867;
 RA Jacq C., Alt-Moerbe J., Andre B., Arnold W., Bahr A., Ballesta J.P.G., Barques M., Baron L., Becker A., Bileau N., Blocher H., Blugeon C., Boskovic J., Brandt P., Bruckner M., Buitrago M.J., Coster F., Delavaud T., del Rey F., Dujon B., Eide L.G., Garcia-Cantalejo J.M., Goffeau A., Gomez-Peris A., Granotier C., Hanemann V., Hankeln T., Hoelsel J.D., Jaeger W., Jimenez A., Joniaux J.-L., Kraemer C., Kuester H., Laanman P., Legros Y., Louis E.J., Moeller-Rieker S., Monnet A., Moro M., Mueller-Auer S., Nussbaumer B., Paricio N., Paulin L., Perera J., Perez-Alonso M., Perez-Ortin J.E., Pohl T.M., Prydz H., Purnelle B., Rasmussen S.W., Remacha M., Revuelta J.L., Rieger M., Salom D., Saluz H.P., Salz J.E., Saren A.-M., Schaefer M., Scharte M., Schmidt E.R., Schneider C., Scholler P., Schwarz S., Urrasazazu L.A., Verhasselt P., Vissers S., Voet M., Volckaert G., Wagner G., Wambuit R., Wedler E., Wedler H., Woelfl S., Harris D.E., Bowman S., Brown D., Churcher C.M., Connor R., Dedman K., Gentles S., Hamlin N., Hunt S., Jones L., McDonald S., Murphy L., Niblett D., Odell C., Oliver K., Rajandream M.A., Richards C., Shore L., Walsh S.V., Barrett B.G., Dietrich F.S., Milligan J.T., Allen E., Arujo R., Aviles E., Bero A., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Hunnicke-Smith S., Hyman R.W., Komp C., Laekhat D., Lew H., Lin D., Moseedale D., Nakamura K., Namach A., Oehner P., Oh C., Petem F.X., Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N., Winant A., Yelton M.A., Botstein D., Davis R.W., Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z., Favello A., Fulton L., Gattung S., Greco T., Hallsworth K., Hawkins J., Hillier L.W., Jier M., Johnson D., Johnston L., Kirsten J., Kucaba T., Langston Y., Latreille P., Le T., Mardis E., Meneses S., Miller N., Nhan M., Pauley A., Peluso D., Rifkin L., Riles L., Tach A., Trevasis E., Vignati D., Wilcox L., Wohlman P., Vaudin M., Wilson R., Waterston R., Albertmann K., Hani J., Heumann K., Kleine K., Mewes H.-W., Zollner A., Zaccaria P.;
 RT "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome IV."
 RL Nature 387:75-78(1997).
 RN [3]
 RP SEQUENCE OF 101-275 FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=95097387; PubMed=7799435;
 RA Lin-Marg N., Clarkson S.G.;
 RT "A yeast RNA binding protein that resembles the human autoantigen La."
 RL J. Mol. Biol. 245:81-85(1995).
 RN [4]
 RP SEQUENCE OF 1-252 FROM N.A.
 RX MEDLINE=94012814; PubMed=8408076;
 RA Naele M.W., Wells G.B., Lester R.L., Dickson R.C.;
 RT "A suppressor gene that enables *Saccharomyces cerevisiae* to grow without making sphingolipids encodes a protein that resembles an *Escherichia coli* fatty acyltransferase."
 RL J. Biol. Chem. 268:22156-22163(1993).

RN [5]
 RP SIMILARITY TO PROTEIN LA.
 RA Baum B.;
 RL Unpublished observations (NOV-1993).
 CC -1- FUNCTION: Binds to the precursors of polymerase III RNAs. Binds preferentially to precursors ending in U residues.
 CC -1- SUBCELLULAR LOCATION: Nuclear (probable).
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
 CC -1- SIMILARITY: TO VERTEBRATE PROTEIN LA.
 CC -----
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 CC -----
 DR EMBL; L33023; AAA21777.1; -
 DR EMBL; Z74099; CAA98612.1; -
 DR EMBL; L13282; AAA16515.1; -
 DR EMBL; X80801; CAA56782.1; -
 DR PIR; B48600; B48600.
 DR GERMOnline; 140293; -
 DR SGD; S0002209; LHP1.
 DR GO; GO:0005730; C:nucleolus; IDA.
 DR GO; GO:0005654; C:nucleoplasm; IDA.
 DR GO; GO:0003723; F:RNA binding; IDA.
 DR GO; GO:0008033; P:RNA processing; IMP.
 DR InterPro; IPR002344; Lupus_La.
 DR InterPro; IPR006630; Lupus_La_dom.
 DR InterPro; IPR005004; RNA_rec_mot.
 DR Pfam; PF05383; La; 1.
 DR Pfam; PF00076; rrm; 1.
 DR PRINTS; PR0302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PS50102; RRM; 1.
 DR PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
 KM RNA-binding; Nuclear Protein.
 FT DOMAIN 123 216
 FT FT 240 256
 SQ SEQUENCE 275 AA; 32104 MW; 43CDB2EC740978D CRC64;
 Query Match 50.0%; Score 42; DB 1; Length 275;
 Best Local Similarity 54.5%; Pred. No. 5.8;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Oy 6 IRQVEYFSGDF 16
 Db 34 LKQVEYFSEF 44
 RESULT 14
 YIGN_ECO57
 ID YIGN_ECO57 STANDARD; PRT; 398 AA.
 AC P58213;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein yign.
 GN YIGN OR Y5869 OR EGS5234.
 OS *Escherichia coli* O157:H7.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; *Escherichia*.
 OX NCBI_TaxID=83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glaesner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

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CC -----
 CC EMBL; X59720; CAA42379.1; -
 CC DR PIR; S19365; S19365.
 CC DR GenOnline; 138873; -
 CC DR SGD; S0000542; SRO9.
 CC DR GO; GO:0005844; C:polysome; IDA.
 CC DR GO; GO:0003723; F:RNA binding; IDA.
 CC DR GO; GO:0006412; P:protein biosynthesis; IPT.
 CC DR InterPro; IPR006630; Lupus_la_dom.
 CC DR Pfam; PF05383; La; 1.
 CC DR SMART; SM00715; La; 1.
 CC FT DOMAIN 200 POLY-GUN.
 CC FT 254 POLY-ASN.
 CC SQ SEQUENCE 466 AA; 51789 MW; AD8B089545117C CRC64;

Query Match 51.2%; Score 43; DB 1; Length 466;
 Best Local Similarity 63.6%; Pred. No. 6.7;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 5 IIRQVEYFGD 15
 Db 297 IARQIEYFSE 307

RESULT 12
 ID VP45 ARATH STANDARD; PRT; 569 AA.
 AC 049068; 080650;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DN VACUOLAR PROTEIN-SORTING PROTEIN 45 homolog (AtVP54S).
 OS VPS4S OR AT1G7140 OR T14N5.2.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Eurosid 1; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=98289086; PubMed=9625693;
 RA Bassham D.C., Raikhel N.V.;
 RT "An Arabidopsis VPS45p homolog implicated in protein transport to the
 RL vacuole.";
 RL Plant Physiol. 117:407-415 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
 RA Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gail J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kvan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
 RA Miliutecner J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Uterback T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,
 RA Wu D., Yu G., Frazer C.M., Venter J.C., Davis R.W.,

RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 RT thaliana.";
 RT Nature 408:816-820 (2000).
 RL Nature 408:816-820 (2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=22954850; PubMed=14593172;
 RA Yamada K., Lim J., Dale J.M., Chen H., Shim P., Palm C.J.,
 RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
 RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
 RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
 RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
 RA Arakawa T., Banh J., Banno F., Bowser L., Brooke S.Y., Carninci P.,
 RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
 RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,
 RA Khan S., Koeseema B., Ishida J., Jiang P.X., Jones T., Kawai J.,
 RA Kamita A., Meyers C., Nakajima M., Natusaka M., Seki M., Sakurai T.,
 RA Satou M., Tames R., Vayberg M., Wallender E.K., Wong C., Yamamura Y.,
 RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RT "Empirical analysis of transcriptional activity in the Arabidopsis
 RT genome.";
 RL Science 302:842-846 (2003).
 RN [4]
 RP INTERACTIONS WITH SYP21, SYP22, SYP31, SYP41, SYP42, SYP61, VT111 AND
 RP VT112.
 RX MEDLINE=20346955; PubMed=10886666;
 RA Bassham D.C., Sanderfoot A.A., Kovaleva V., Zheng H., Raikhel N.V.;
 RT "AtVP54S complex formation on the trans-Golgi network.";
 RL Mol. Biol. Cell 11:2251-2265 (2000).
 CC -1- FUNCTION: Involved in the protein transport to the vacuole,
 CC probably at the level of vesicle fusion at the prevacuolar
 CC (TGN) and not in transport from the TGN to the prevacuolar
 CC compartment. Binds syntaxins.
 CC -1- SUBUNIT: Interacts with both SYP41 or SYP42 and VT112, but in
 CC different domains of the trans-Golgi network. Does not interact on
 CC the prevacuolar compartment with VT111, SYP21 or SYP22, or on the
 CC cis-Golgi with SYP31.
 CC -1- SUBCELLULAR LOCATION: Peripheral membrane protein. Binds to trans-
 CC Golgi network membranes through interaction with other proteins.
 CC -1- TISSUE SPECIFICITY: Highly expressed in roots, lower expression in
 CC leaves, stems and flowers.
 CC -1- SIMILARITY: Belongs to the STXBP/UNC-18/SEC1 family.
 CC -----
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CC -----
 CC EMBL; AF036234; AAC39472.1; -
 CC DR EMBL; AC004260; AAC34344.1; -
 CC DR EMBL; AY050370; AAK91388.1; -
 CC DR EMBL; AY101517; AAM26638.1; -
 CC DR PIR; T00445; T00445.
 CC DR PIR; T52056; T52056.
 CC DR InterPro; IPR001619; Sec1-like.
 CC DR Pfam; PF00995; Sec1; 1.
 CC TRANSFAC: Protein transport; Golgi stack; Multigene family.
 CC FT CONFLICT 362 362 T -> I (IN REF. 1).
 CC SQ SEQUENCE 569 AA; 64942 MW; 844F24C9A21E9D1D CRC64;

Query Match 51.2%; Score 43; DB 1; Length 569;
 Best Local Similarity 40.0%; Pred. No. 8.2;
 Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

OY 2 ERATIRQVEYFGDF 16
 Db 116 EDRVQVQVEYVADF 130

RESULT 13

DR PIR: T43542; T43542.
 DR Genedb Spombe: SPACS7A10.10c; --
 DR InterPro: IPR002344; Lupus_La.
 DR InterPro: IPR006300; Lupus_La.dom.
 DR InterPro: IPR005054; RNA_rec_mot.
 DR Pfam: PF05383; La; 1.
 DR Pfam: PF00076; rrm; 1.
 DR PRINTS: PR00302; LUPUSLA.
 DR SMART: SM00715; LA; 1.
 DR SMART: SM00360; RRM; 1.
 DR PROSITE: PS50102; RRM; 1.
 DR PROSITE: PS00030; RRM_RNP_1; FALSE_NEG.
 DR RNA-binding; Nuclear protein.
 FT DOMAIN 154 236 RNA-BINDING (RRM).
 FT CONFLICT 188 188 M -> I (IN REF. 1 AND 2).
 SQ SEQUENCE 298 AA; 34616 MW; 64E6AB99340B87F4 CRC64;

Query Match 54.8%; Score 46; DB 1; Length 298;
 Best Local Similarity 50.0%; Pred. No. 1.2;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 2 ERAIRQVEYFGD 15
 DB 64 EAEVTKQVEFYFSD 77

RESULT 10
 ID_HO2_RAT STANDARD; PRT; 315 AA.
 AC P23711;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Heme oxygenase 2 (EC 1.14.99.3) (HO-2).
 GN HMOX2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=90237051; PubMed=2185251;
 RA Rosenberg M.O., Maines M.D.;
 RT "Isolation, characterization, and expression in Escherichia coli of a
 RT cDNA encoding rat heme oxygenase-2.";
 RL J. Biol. Chem. 265:7501-7506(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=94156193; PubMed=8112599;
 RA McCoubrey W.K., Jr., Maines M.D.;
 RT "The structure, organization and differential expression of the gene
 RT encoding rat heme oxygenase-2.";
 RL Gene 139:155-161(1994).
 RN [3]
 RP SEQUENCE OF 142-232 FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Liver, and Testis;
 RX MEDLINE=88139412; PubMed=3343248;
 RA Cruse I., Maines M.D.;
 RT "Evidence suggesting that the two forms of heme oxygenase are
 RT products of different genes";
 RL J. Biol. Chem. 263:3348-3353(1988).
 CC -1- FUNCTION: Heme oxygenase cleaves the heme ring at the alpha
 CC mebrane bridge to form biliverdin. Biliverdin is subsequently
 CC converted to bilirubin by biliverdin reductase. Under
 CC physiological conditions, the activity of heme oxygenase is
 CC highest in the spleen, where senescent erythrocytes are
 CC sequestered and destroyed.
 CC -1- FUNCTION: Heme oxygenase 2 could be implicated in the production
 CC of carbon monoxide in brain where it could act as a
 CC neurotransmitter.
 CC -1- CATALYTIC ACTIVITY: Heme + 3 AH(2) + O(2) = biliverdin + Fe(2+) +

CC CO + 3 A + 3 H(2)O.
 CC -1- SUBCELLULAR LOCATION: Microsomal.
 CC -1- TISSUE SPECIFICITY: Widely distributed in body with a high
 CC concentration in the brain.
 CC -1- INDUCTION: Heme oxygenase 2 activity is non-inducible.
 CC -1- SIMILARITY: Belongs to the heme oxygenase family.
 CC -1- SIMILARITY: Contains 2 heme regulatory motif (HRM) repeats.
 CC -----
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 CC -----

DR EMBL: J05405; AAA41340.1; --
 DR EMBL: U05013; AAA19130.1; --
 DR EMBL: M1918; AAA41347.1; --
 DR PIR: A35199; A35199.
 DR HSSP: P06762; IDVG.
 DR InterPro: IPR002051; Heme oxygenase.
 DR Pfam: PF01126; Heme oxygenase.
 DR PRINTS: PR00088; HHEMOXYGNASE.
 DR PROSITE: PS00593; HEME_OXYGENASE; 1.
 DR Heme; Oxidoreductase; Microsome; Multigene family; Repeat.
 KM METAL 44 44 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT REPEAT 263 268 HRM 1.
 FT REPEAT 280 285 HRM 2.
 FT CONFLICT 142 146 ONEPE -> EFRNK (IN REF. 3).
 FT CONFLICT 230 232 MQI -> TER (IN REF. 3).
 SQ SEQUENCE 315 AA; 35762 MW; 981ADE01DE1AFCF CRC64;

Query Match 52.4%; Score 44; DB 1; Length 315;
 Best Local Similarity 40.0%; Pred. No. 3;
 Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

OY 1 QERAIRQVEYFGD 15
 DB 104 RKEALIKQMEYFGE 118

RESULT 11
 ID_SRO9_YEAST STANDARD; PRT; 466 AA.
 AC ?25567;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE SRO9 protein.
 GN SRO9 OR YCL037C OR YCL37C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Delgado M., Esteban M., Navas L.;
 RL Submitted (MAR-1992) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=98043396; PubMed=9383048;
 RA Kagami M., Tob-E A., Matsui Y.;
 RT "SRO9, a multicopy suppressor of the bud growth defect in the
 RT Saccharomyces cerevisiae RHO3-deficient cells, shows strong genetic
 RT interactions with tropomyosin genes, suggesting its role in
 RT organization of the actin cytoskeleton.";
 RL Genetics 147:1003-1016(1997).
 CC -1- FUNCTION: May overlap in function with tropomyosin and may be
 CC involved in organization of actin filaments. Acts as a multicopy
 CC suppressor of RHO3.
 CC -1- SIMILARITY: Some, to yeast Slp1.
 CC -----

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RESULT 8
LAA_XENIA STANDARD; PRT; 428 AA.
ID LAA_XENIA
AC P28048;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Lupa La protein homolog A (La ribonucleoprotein A) (La autoantigen
homolog A).
GN LAA1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE=Oocyte;
RX MEDLINE=93287095; PubMed=8510143;
RA Scherly D., Stutz F., Lin-Marg N., Clarkson S.G.;
RT "La proteins from Xenopus laevis. cDNA cloning and developmental
expression."
RL J. Mol. Biol. 231:196-204(1993).
CC -1- FUNCTION: La protein plays a role in the transcription of RNA
polymerase III. It is most probably a transcription termination
factor. Binds to the 3' terminus of virtually all nascent
polymerase III transcripts (by similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- DEVELOPMENTAL STAGE: Barely detectable in stage I/II oocytes,
accumulate in stage III/IV oocytes, then exhibit a roughly
constant steady state level in mature oocytes, eggs, and early
embryos.
CC -1- PTM: Phosphorylated (Probable).
CC -1- MISCELLANEOUS: There are two forms of La, Laa and Lab, in xenopus.
CC -1- SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN.
CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
CC -----
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CC -----
CC EMBL; X68817; CAA48715.1; -.
CC PIR; S33818; S33818.
CC InterPro: IPR002344; Lupa La.
CC InterPro: IPR006630; Lupa La_dom.
CC InterPro: IPR000504; RNA_rec_mot.
CC Pfam; PF00363; La; 1.
CC Pfam; PF00076; rrm; 1.
CC PRINTS; PR00302; LUPUSLA.
CC SMART; SM00715; LA; 1.
CC SMART; SM00360; RRM; 1.
CC PROSITE; PS50102; RRM; 1.
CC PROSITE; PS00030; RRM_RNP_1; 1.
CC KMW; KMW00000; Nuclear protein, Phosphorylation.
CC FT DOMAIN 111 203 RNA-BINDING (RRM).
CC FT DOMAIN 196 212 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
CC FT DOMAIN 316 332 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
CC SQ SEQUENCE 428 AA; 48864 MW; AEB3A38B7DE3EC3 CRC64;
Query Match 57.1%; Score 48; DB 1; Length 428;
Best Local Similarity 72.7%; Pred. No. 0.81;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 5 IIRVEYFGD 15
DB 17 ICEIIEYFGD 27

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RESULT 9
LAA1_SCHPO STANDARD; PRT; 298 AA.
ID LAA1_SCHPO
AC P87058; O13362; Q10458;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE La protein homolog (La ribonucleoprotein) (La autoantigen homolog).
GN SLAI OR SPAC57A10.10C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=98067398; PubMed=9404894;
RA van Horn D.J., Yoo C.J., Xue D., Shi H., Wolin S.L.;
RT "The La protein in Schizosaccharomyces pombe: a conserved yet
dispensable phosphoprotein that functions in tRNA maturation."
RL RNA 3:1434-1443(1997).
RN 12
RP SEQUENCE FROM N.A.
RA Utsunomiya R.R.U.;
RT Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN 13
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgourou J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentles S., Godle R., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsle J.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsle J.,
RA James K., Jones L., Jones M., Leathers S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares K., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymover B.,
RA Welfens I., Vansireels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wandt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garçon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Peltashkin J.,
RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe."
RL Nature 415:871-880(2002).
CC -1- FUNCTION: Binds to the precursors of polymerase III RNAs.
CC -1- FUNCTIONS: In tRNA maturation.
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
CC -1- SIMILARITY: TO VERTEBRATE PROTEIN LA.
CC -----
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CC -----
CC EMBL; AF022949; AAB82145.1; -.
CC DR EMBL; AB011371; BAA24981.1; -.
CC DR EMBL; Z94864; CAB08173.1; -.
CC PIR; T38937; T38937.

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DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PSS0102; RRM; 1.
 DR PROSITE; PS00030; RRM_RNP_1; 1.
 KW RNA-binding; Nuclear protein; Phosphorylation.
 FT DOMAIN 111 187 RNA-BINDING (RRM).
 SQ SEQUENCE 415 AA; 47777 MW; 033FD9CC1E475F98 CRC64;

Query Match 67.9%; Score 57; DB 1; Length 415;
 Best Local Similarity 66.7%; Pred. No. 0.021;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 ERAIRROVEYYFGDF 16
 DB 14 EAKICHOIEYYFGDF 28

RESULT 6
 LA_AEDAL STANDARD; PRT; 383 AA.
 ID LA_AEDAL
 AC Q26457;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE La protein homolog (La ribonucleoprotein) (La autoantigen homolog).
 OS Aedes albopictus (Forest day mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preyigota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes.
 OX NCBI_TaxID=7160;
 RN [1]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RX MEDLINE=96135233; PubMed=8551578;
 RA Pardigon N., Straus J.H.;
 RT "Mosquito homolog of the La autoantigen binds to Sindbis virus RNA.";
 RL J. Virol. 70:1173-1181(1996).
 CC -1- FUNCTION: May be involved in transcription termination by RNA
 polymerase III. Binds RNA and DNA. Binds to the 3' end of the
 minus strand of Sindbis virus RNA. This may be significant for
 Sindbis virus RNA replication.
 CC -1- SUBCELLULAR LOCATION: Nuclear. Primarily nuclear, but significant
 amounts are present in the cytoplasm.
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
 CC -1- SIMILARITY: TO VERTEBRATE PROTEIN LA.

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DR EMBL; S80954; AAB53931.1; -
 DR InterPro; IPR002344; Lupus_La.
 DR InterPro; IPR006630; Lupus_La_dom.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF05383; La; 1.
 DR Pfam; PF00076; rtm; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PSS0102; RRM; 1.
 DR PROSITE; PS00030; RRM_RNP_1; FALSE NEG.
 KW RNA-binding; Nuclear protein; DNA-binding.
 FT DOMAIN 141 228 RNA-BINDING (RRM).
 SQ SEQUENCE 383 AA; 44430 MW; 4B5CC8F21C40F452 CRC64;

Query Match 66.7%; Score 56; DB 1; Length 383;
 Best Local Similarity 71.4%; Pred. No. 0.028;
 Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 ERAIRROVEYYFGD 15
 | : ||| : ||| |

DB 44 EASTIROLEYFGD 57

RESULT 7
 LAB_XENLA STANDARD; PRT; 427 AA.
 ID LAB_XENLA
 AC P28049;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Lupus La protein homolog B (La ribonucleoprotein B) (La autoantigen
 homolog B).
 GN LAB1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8335;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Oocyte;
 RX MEDLINE=93287095; PubMed=8510143;
 RA Scherly D., Stutz F., Lin-Marg N., Clarkson S.G.;
 RT "A protein from Xenopus laevis. cDNA cloning and developmental
 expression.";
 RL J. Mol. Biol. 231:196-204(1993).
 CC -1- FUNCTION: La protein plays a role in the transcription of RNA
 polymerase III. It is most probably a transcription termination
 factor. Binds to the 3' terminus of virtually all nascent
 polymerase III transcripts (by similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear (probable).
 CC -1- DEVELOPMENTAL STAGE: Barely detectable in stage I/II oocytes,
 accumulate in stage III/IV oocytes, then exhibit a roughly
 constant steady state level in mature oocytes, eggs, and early
 embryos.

CC -1- PTM: Phosphorylated (probable).
 CC -1- MISCELLANEOUS: There are two forms of La, LaA and LaB, in xenopus.
 CC -1- SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN.
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
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 or send an email to license@isb-sib.ch).

DR EMBL; X68818; CAA48716.1; -
 DR PIR; S33817;
 DR InterPro; IPR002344; Lupus_La.
 DR InterPro; IPR006630; Lupus_La_dom.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF05383; La; 1.
 DR Pfam; PF00076; rtm; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PSS0102; RRM; 1.
 DR PROSITE; PS00030; RRM_RNP_1; FALSE NEG.
 KW RNA-binding; Nuclear protein; Phosphorylation.
 FT DOMAIN 110 202 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 SQ SEQUENCE 427 AA; 48995 MW; 4F3146F934A355 CRC64;

Query Match 57.1%; Score 48; DB 1; Length 427;
 Best Local Similarity 72.7%; Pred. No. 0.81;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 IIRROYEYFGD 15
 | : ||| : ||| |
 DB 16 ICEOIEYFGD 26

LA_MOUSE STANDARD; PRT; 415 AA.
 ID LA_MOUSE
 AC P32067;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Lupus La protein homolog (La ribonucleoprotein) (La autoantigen homolog)
 GN SSB OR SS-B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93203630; PubMed=8454877;
 RA Topfer F., Gordon T., McCluskey J.;
 RT "Characterization of the mouse autoantigen La (SS-B). Identification of conserved RNA-binding motifs, a putative ATP binding site and reactivity of recombinant protein with poly(U) and human autoantibodies.";
 RT J. Immunol. 150:3091-3100 (1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=FVB/N; Tissue=Mammary gland;
 MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F., Diatchenko L., Mausina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pange C., Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Millar S.J., Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Villalón D.K., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Faley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalms D.E., Scherach A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [3]
 RP SEQUENCE OF 1-11 FROM N.A.
 RA Groetz D., Bachmann M.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' terminus of virtually all nascent polymerase III transcripts. It is associated with precursor forms of RNA polymerase III transcripts including crRNA and 4.5S, 5S, 7S, and 7-2 RNAs.
 CC -1- SUBUNIT: Interacts with DDX15 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- PTM: Phosphorylated (By similarity).
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
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 CC EMBL; L00993; AAA39415.1; -
 DR EMBL; BC003820; AAA39415.1; -
 DR EMBL; Y07951; CAA69249.1; -
 DR MGI; 98423; Ssb.

DR GO; 0005634; C:nucleus; IDA.
 DR InterPro; IPR002344; Lupus_La.
 DR InterPro; IPR006630; Lupus_La_dom.
 DR InterPro; IPR005054; RNA_rec_mot.
 DR Pfam; PF05383; La; 1.
 DR Pfam; PF00076; rrm; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PS50102; RRM; 1.
 DR PROSITE; PS00030; RRM_RNP_1; 1.
 DR RNA-binding; Nuclear protein; Phosphorylation.
 FT DOMAIN 111 187
 FT BINDING (RRM).
 SQ SEQUENCE 415 AA; 47756 MW; 2D75197692FDC933 CRC64;
 Query Match 67.9%; Score 57; DB 1; Length 415;
 Best Local Similarity 66.7%; Pred. No. 0.021;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 2 EBAIRQVYRGRDF 16
 DB 14 EAKICHQIEYRGDF 28
 LA_RAT STANDARD; PRT; 415 AA.
 ID LA_RAT
 AC P38656;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lupus La protein homolog (La ribonucleoprotein) (La autoantigen homolog).
 GN SSB OR SS-B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_Taxid:10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93246255; PubMed=7916708;
 RA Semsei I., Troester H., Bartsch H., Schwemmler M., Igloi G.L., Bachmann M.;
 RT "Isolation of rat cDNA clones coding for the autoantigen SS-B/La: detection of species-specific variations.";
 RT Gene 126:265-268 (1993).
 RL -1- FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' terminus of virtually all nascent polymerase III transcripts. It is associated with precursor forms of RNA polymerase III transcripts including crRNA and 4.5S, 5S, 7S, and 7-2 RNAs.
 CC -1- SUBUNIT: Interacts with DDX15 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- PTM: Phosphorylated (By similarity).
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
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 CC EMBL; X67859; CAA48043.1; -
 DR PIR; JCI494; JCI494.
 DR InterPro; IPR002344; Lupus_La.
 DR InterPro; IPR006630; Lupus_La_dom.
 DR InterPro; IPR005054; RNA_rec_mot.
 DR Pfam; PF05383; La; 1.
 DR Pfam; PF00076; rrm; 1.
 DR PRINTS; PR00302; LUPUSLA.

DT 01-JUL-1989 (Rel. 11, last sequence update)
 DT 15-MAR-2004 (Rel. 43, last annotation update)
 DE lupus la protein (Sjogren syndrome type B antigen) (SS-B) (La
 DE ribonucleoprotein) (La autoantigen).
 GN SSB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 NC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89202037; PubMed=2468131;
 RA Chan E.K.L., Sullivan K.F., Tan E.M.;
 RT "ribonucleoprotein SS-B/La belongs to a protein family with consensus
 RT sequences for RNA-binding.";
 RL Nucleic Acids Res. 17:2235-2244(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89053970; PubMed=3192525;
 RA Chambers J.C., Kennan D., Martin B.J., Keene J.D.;
 RT "Genomic structure and amino acid sequence domains of the human La
 RT autoantigen.";
 RL J. Biol. Chem. 263:18043-18051(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta; PubMed=12477932;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedlin T.B., Tomihyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Woxley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Boulford G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallie D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE OF 54-408 FROM N.A.
 RX MEDLINE=88199081; PubMed=2452201;
 RA Sturges A.D., Peterson M.G., McNeillage L.J., Whittingham S.,
 RA Coppel R.S.;
 RT "Characteristics and epitope mapping of a cloned human autoantigen
 RT La.";
 RL J. Immunol. 140:3212-3218(1988).
 RN [5]
 RP SEQUENCE OF 54-97 FROM N.A.
 RX MEDLINE=85166283; PubMed=3856688;
 RA Chambers J.C., Keene J.D.;
 RT "Isolation and analysis of cDNA clones expressing human lupus La
 RT antigen.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:2115-2119(1985).
 RN [6]
 RP FUNCTION.
 RX MEDLINE=89251617; PubMed=2470590;
 RA Gottlieb E., Steltz J.A.;
 RT "Function of the mammalian La protein: evidence for its action in
 RT transcription termination by RNA polymerase III.";
 RL EMBO J. 8:851-861(1989).
 RN [7]
 RP PHOSPHORYLATION.
 RX MEDLINE=97207017; PubMed=9054510;
 RA Fan H., Sakulich A.L., Goodier J.L., Zhang X., Qin J., Marate R.J.;

RT "Phosphorylation of the human La antigen on serine 366 can regulate
 RT recycling of RNA polymerase III transcription complexes.";
 RL Cell 88:707-715(1997).
 RN [8]
 RP INTERACTION WITH DDX15.
 RX MEDLINE=22346609; PubMed=12458796;
 RA Fournoux M.A., Kolkmann M.J.M., Van der Heijden A., De Jong A.S.,
 RA Van Veenrooij W.J., Pijnij G.J.M.;
 RT "The human La (SS-B) autoantigen interacts with DDX15/hPrp43, a
 RT putative DEAD-box RNA helicase.";
 RL RNA 8:1428-1443(2002).
 CC -1- FUNCTION: La protein plays a role in the transcription of RNA
 CC polymerase III. It is most probably a transcription termination
 CC factor. Binds to the 3' termin of virtually all nascent
 CC polymerase III transcripts. It is associated with precursor forms
 CC of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S,
 CC and 7-2 RNAs.
 CC -1- SUBUNIT: Interacts with DDX15.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- PTM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES ARE AT THE
 CC C-TERMINAL PART OF THE PROTEIN.
 CC -1- PPM: The N-terminus is blocked.
 CC -1- DISEASE: Sera from patients with systemic lupus erythematosus
 CC often contain antibodies that react with the normal cellular
 CC La protein as if this antigen was foreign.
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
 CC -----
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 CC -----
 CC EMBL; X13697; CA31985.1; -;
 CC EMBL; J04205; AAA51885.1; -;
 CC EMBL; BC001289; AAH01289.1; -;
 CC EMBL; BC020818; AAH20818.1; -;
 CC PIR; A31888; A31888.
 CC Genew; HGNC:11316; SSB.
 CC MIM; 109090; -;
 CC DR GO; GO:0030529; C:ribonucleoprotein complex; TAS.
 CC DR GO; GO:0003729; F:mRNA binding; TAS.
 CC DR GO; GO:0000049; F:RNA binding; TAS.
 CC DR GO; GO:0008334; F:histone mRNA metabolism; TAS.
 CC DR GO; GO:0006400; P:RNA modification; TAS.
 CC DR InterPro; IPR002344; Lupus_La.
 CC DR InterPro; IPR006630; Lupus_La_dom.
 CC DR InterPro; IPR00504; RNA_rec_mot.
 CC DR Pfam; PF05383; La; 1.
 CC DR Pfam; PF00076; rrm; 1.
 CC DR PRINTS; PR00302; LUPUSLA.
 CC DR SMART; SM00715; LA; 1.
 CC DR SMART; SM00360; RRM; 1.
 CC DR PROSITE; PS0102; RRM; 1.
 CC DR PROSITE; PS00030; RRM_RNP_1; 1.
 CC DR Systemic lupus erythematosus; RNA-binding; Phosphorylation;
 CC Nucleic protein.
 CC KW DOMAIN 111 187 RNA-BINDING (RRM).
 CC FT MOD_RES 366 366 PHOSPHORYLATION (BY CK2).
 CC SQ SEQUENCE 408 AA; 46837 MW; EC153C15F9187FC4 CRC64;
 Query Match 67.9%; Score 57; DB 1; Length 408;
 Best Local Similarity 66.7%; Pred. No. 0.02;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 2 ERATIRQVEYFGDF 16
 DB 14 EAKIQHRIYFGDF 28
 RESULT 4

RA Laslo P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mated B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Mostrelet A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Munzy D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman K.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spiter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitakae R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Maassman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of *Drosophila melanogaster*.";
 RA Science 287:2185-2195(2000).
 CC -1- FUNCTION: May be involved in transcription termination by RNA
 CC polymerase III. Binds RNA and DNA. Binds to precursors of RNA
 CC polymerase III transcripts. May play a specialized role during fly
 CC development.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- DEVELOPMENTAL STAGE: Expressed throughout embryonic, larval,
 CC pupal, and adult development. Expression throughout the embryo is
 CC followed by a restricted pattern of mesodermal expression that is
 CC later confined to the visceral mesoderm, gonads, gut, and salivary
 CC glands.
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
 CC -1- SIMILARITY: TO VERTERATE PROTEIN LA.
 CC -----
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 CC -----
 CC EMBL, U07652; AAA20518.1; -
 CC EMBL, L32988; AAA21776.1; -
 CC EMBL, AE003666; AAF53885.1; -
 CC PIR, A53773; A53773.
 CC PIR, A53781; A53781.
 CC FlyBase, FBgn0011638; La.
 CC GO, GO:0008098; F:5S rRNA primary transcript binding; IDA.
 CC GO, GO:0003723; F:RNA binding; NAS.
 CC InterPro, IPR002344; Lupus La.
 CC InterPro, IPR006630; Lupus La dom.
 CC InterPro, IPR000504; RNA_rec_mot.
 CC Pfam, PF05383; La; 1.
 CC Pfam, PF00076; rrm; 1.
 CC PRINTS, PR00302; LUPUSLA.
 CC SMART, SMO0715; LA; 1.
 CC SMART, SMO0360; RRM; 1.
 CC SMART, SMO0102; RRM; 1.
 CC PROSITE, PS00030; RRM_RNP_1; 1.
 CC PROSITE, PS00030; RRM_RNP_1; 1.
 CC RNA-binding; Nuclear protein; DNA-binding.
 CC KW DOMAIN 149 234 RNA-BINDING (RRM).
 CC CONFLICT 169 169 A -> T (IN REF. 1).
 CC CONFLICT 182 183 KH -> NS (IN REF. 1).
 CC CONFLICT 283 283 A -> R (IN REF. 1).
 CC CONFLICT 329 329 K -> N (IN REF. 1).
 CC SEQUENCE 390 AA; 44884 MW; A8099288B90446A5 CRC64;

Query Match 92.9%; Score 78; DB 1; Length 390;
 Best Local Similarity 100.0%; Pred. No. 3; 9e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QERAIRQVEYFGD 15
 DB 50 QERAIRQVEYFGD 64

RESULT 2
 ID LA BOVIN STANDARD; PRT; 404 AA.
 AC ID LA BOVIN
 ID P10881;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lupus la protein homolog (La ribonucleoprotein) (La autoantigen
 DE homolog).
 GN SSB.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Plutary;
 RX MEDLINE=69202037; PubMed=2468111;
 RA Chan E.K.L., Sullivan K.F., Tan E.M.;
 RT "Ribonucleoprotein SS-B/La belongs to a protein family with consensus
 RT sequences for RNA-binding.";
 RL Nucleic Acids Res. 17:2233-2244(1989).
 CC -1- FUNCTION: La protein plays a role in the transcription of RNA
 CC polymerase III. It is most probably a transcription termination
 CC factor. Binds to the 3' termini of virtually all nascent
 CC of RNA polymerase III transcripts. It is associated with precursor forms
 CC of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S,
 CC and 7-2 RNAs.
 CC -1- SUBUNIT: Interacts with DDX15 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- PTM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES ARE AT THE
 CC C-TERMINAL PART OF THE PROTEIN.
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL, X13698; CAA1986.1; -
 CC PIR, S03849; S03849.
 CC InterPro, IPR002344; Lupus La.
 CC InterPro, IPR006630; Lupus La dom.
 CC InterPro, IPR000504; RNA_rec_mot.
 CC Pfam, PF05383; La; 1.
 CC Pfam, PF00076; rrm; 1.
 CC PRINTS, PR00302; LUPUSLA.
 CC SMART, SMO0715; LA; 1.
 CC SMART, SMO0360; RRM; 1.
 CC PROSITE, PS00102; RRM; 1.
 CC PROSITE, PS00030; RRM_RNP_1; 1.
 CC RNA-binding; Nuclear protein; Phosphorylation.
 CC KW DOMAIN 111 187 RNA-BINDING (RRM).
 CC SEQUENCE 404 AA; 46534 MW; 4EB30B5C262AD6A1 CRC64;

Query Match 67.9%; Score 57; DB 1; Length 404;
 Best Local Similarity 66.7%; Pred. No. 0.02;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 ERAIRQVEYFGD 16
 DB 14 EAKIRQVEYFGD 28
 RESULT 3
 ID LA HUMAN STANDARD; PRT; 408 AA.
 ID AC P05455;
 DT 01-NOV-1988 (Rel. 09, Created)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:01:41 ; Search time 6.43575 Seconds
(without alignments)
129,452 Million cell updates/sec

Title: US-09-836-073-19

Perfect score: 84
Sequence: 1 QERAIRQVEYFGDF 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	78	92.9	390	1 LA_DROME	P40796 drosophila
2	57	67.9	404	1 LA_BOVIN	P10881 bos taurus
3	57	67.9	408	1 LA_HUMAN	P05455 homo sapien
4	57	67.9	415	1 LA_MOUSE	P32067 mus musculu
5	57	67.9	415	1 LA_RAT	P38656 rattus norv
6	56	66.7	383	1 LA_AEDLA	Q26457 aedes albop
7	48	57.1	427	1 LAB_XENLA	P28049 xenopus lae
8	46	54.8	298	1 LAH1_SCHPO	P87058 schizosacch
9	45	52.4	315	1 HO2_RAT	P33711 rattus norv
10	44	51.2	466	1 SRO9_YEAST	P25567 saccharomyc
11	43	51.2	569	1 VP45_ARATH	Q49048 arabidopsis
12	43	50.0	275	1 LAH1_YEAST	P33399 saccharomyc
13	42	50.0	398	1 YXGN_ECOS7	P58219 escherichia
14	42	50.0	398	1 YXGN_ECOLI	P39338 escherichia
15	41	48.8	500	1 SYH_EHILLO	Q98702 rhizobium l
16	41	48.2	506	1 TWMO_PETOR	Q43033 petroselinu
17	40.5	47.6	304	1 Y687_HAEIN	P71356 haemophilus
18	40	47.6	373	1 TYRA_ECOLI	P07023 escherichia
19	40	47.6	634	1 IDUA_MOUSE	P48441 mus musculu
20	40	46.4	206	1 VADI_TREPA	O84441 treponema p
21	39	46.4	253	1 SOJ_TREPA	O83296 treponema p
22	39	46.4	267	1 PSTB_XYLFA	Q9PBD0 xyloella fas
23	39	46.4	312	1 HO2_RABIT	P43242 oryctolagus
24	39	46.4	315	1 HO2_MOUSE	O70252 mus musculu
25	39	46.4	315	1 HO2_HUMAN	O96541 homo sapien
26	39	46.4	368	1 PERQ_LACDE	P46545 lactobacilli
27	39	46.4	368	1 PERQ_LACDE	P46545 lactobacilli
28	39	46.4	368	1 PERQ_LACDE	P46545 lactobacilli
29	39	46.4	532	1 IPAT_SHIFL	P18014 shigella fl
30	39	46.4	602	1 EXSA_BUCAL	P57530 buchnera ap
31	38	45.2	625	1 BGAL_LACSK	Q48846 lactobacilli
32	37	44.0	216	1 POLG_PMDVC	P03309 foot-and-mo
33	37	44.0	230	1 POLG_PMDVC	P03307 foot-and-mo

34	37	44.0	234	1 POLG_FMDVI	P03310 foot-and-mo
35	37	44.0	281	1 Y818_PYPAB	Q8ZVE1 pyrobaculum
36	37	44.0	363	1 YCDM_ECOS7	Q8XU1 escherichia
37	37	44.0	363	1 YCDM_ECOLI	P75898 escherichia
38	37	44.0	550	1 SYR_MYCLE	P45840 mycobacteri
39	37	44.0	570	1 VP45_HUMAN	O9N977 homo sapien
40	37	44.0	570	1 VP45_MOUSE	P97390 mus musculu
41	37	44.0	570	1 VP45_RAT	O08700 rattus norv
42	37	44.0	611	1 VAPR_PLAFA	Q03498 plasmodium
43	37	44.0	781	1 APEZ_SULTO	Q97406 sulfolobus
44	37	44.0	900	1 GDNH_CLOTM	P16218 clostridium
45	37	44.0	905	1 CHD2_SCHPO	Q74787 schizosacch

ALIGNMENTS

RESULT 1
LA_DROME STANDARD; PRT; 390 AA.
ID LA_DROME
AC P40796; Q24375; Q9V1N2;
DT 01-FEB-1995 (Rel. 31, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE La protein homolog (La ribonucleoprotein) (La autoantigen homolog).
GN LA OR CG10922.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Canton-S; TISSUE=Ovary;
RX MEDLINE=94309632; PubMed=8035794;
RA Bai C., Li Z., Tollas P.P.;
RT "Developmental characterization of a Drosophila RNA-binding protein homologous to the human systemic lupus erythematosus-associated La/SS-B autoantigen."
RT La/SS-B autoantigen."
RL Mol. Cell. Biol. 14:5123-5129 (1994).
RU [2]
RN SEQUENCE FROM N.A.
RP STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayan A., An H.-U., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Baer A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolintsov S.,
RA Borkova K., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Paulis B., Dichter A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Fiertera S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harria M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

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A;Title: Isolation, characterization, and expression in *Escherichia coli* of a cDNA encoding
 A;Reference number: A35199; MUID:90237051; PMID:2185251
 A;Accession: A35199
 A;Molecule type: mRNA
 A;Residues: 1-315 <ROT>
 A;Cross-references: GB:J05405; NID:g204626; PIDN:AAA41340.1; PID:g204627
 R;Cruse, I.; Maines, M.D.
 J. Biol. Chem. 263, 3348-3353, 1988
 A;Title: Evidence suggesting that the two forms of heme oxygenase are products of different
 A;Reference number: A29922; MUID:8139412; PMID:3343248
 A;Accession: A29922
 A;Molecule type: mRNA
 A;Residues: 'EPRNK', 147-229, 'TEP' <CRU>
 A;Cross-references: GB:M18918; NID:g204649; PIDN:AAA41347.1; PID:g554443
 C;Superfamily: heme oxygenase (decylizing)
 C;Keywords: oxidoreductase

Query Match 52.4%; Score 44; DB 1; Length 315;
 Best Local Similarity 40.0%; Pred. No. 6;
 Matches 6; Conservative 7; Mismatches 2; Indels 0; Gaps 0;

QY 1 QERAIIRQVEYFGD 15
 :::::|||||:
 Db 104 RKEALIKMEYFGE 118

RESULT 15

S19365
 hypothetical protein YCL037C - Yeast (*Saccharomyces cerevisiae*)
 C;Species: *Saccharomyces cerevisiae*
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Jun-2000
 C;Accession: S19365
 R;Delgado, M.; Ebleben, M.; Navas, L.
 submitted to the Protein Sequence Database, March 1992
 A;Reference number: S19365
 A;Accession: S19365
 A;Molecule type: DNA
 A;Residues: 1-466
 A;Cross-references: EMBL:X59720; NID:G1907116; PIDN:CAA42379.1; PID:g5326; MIPS:YCL037C
 C;Genetics:
 A;Gene: SGD:SR09
 A;Cross-references: SGD:S0000542; MIPS:YCL037C
 A;Map position: 3L

Query Match 51.2%; Score 43; DB 2; Length 466;
 Best Local Similarity 63.6%; Pred. No. 14;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 IIRQVEYFGD 15
 |||:|||||:
 Db 297 IARQIEYFSE 307

Search completed: September 10, 2004, 18:02:42
 Job time : 15.514 secs

T00677
 hypothetical protein At2g43970 [imported] - Arabidopsis thaliana
 N/Alternate names: hypothetical protein F6E13.10
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001
 C/Accession: T00677, G84872
 R/Rounsaey, S.D.; Kaul, S.; Lin, X.; Kechum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, June 1998
 A/Description: Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence.
 A/Reference number: Z14180
 A/Accession: T00677
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-529 <STO>
 A/Cross-references: EMBL:AC004005; NID:G3212846; PID:G3212854
 A/Experimental source: Cultivar Columbia
 R/Lin, X.; Kaul, S.; Rounsaey, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.; Neus, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
 A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A/Reference number: A84420; MUID:20083487; PMID:10617197
 A/Accession: G84872
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-529 <STO>
 A/Cross-references: GB:AE002093; NID:G3212854; PIDN:AA023405.1; GSPDB:GN00139
 A/Map position: 2
 A/Introns: 200/3; 228/1; 259/3; 283/3; 310/2; 344/3; 367/3; 421/3

Query Match 56.0%; Score 47; DB 2; Length 529;
 Best Local Similarity 72.7%; Pred. No. 3.1;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 IIRQVEYFGD 15
 DB 197 IVQVEYFSD 207

RESULT 11
 T38937
 rna binding protein - fission yeast (Schizosaccharomyces pombe)
 C/Species: Schizosaccharomyces pombe
 C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C/Accession: T38937
 R/Baddock, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, April 1997
 A/Reference number: Z21818
 A/Accession: T38937
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-298 <BAD>
 A/Cross-references: EMBL:Z24864; PIDN:CA08173.1; GSPDB:GN00066; SPDB:SPAC57A10.100
 A/Experimental source: strain 972h-; cosmid c57A10
 C/Genetics:
 A/Map position: 1
 A/Introns: 72/1

Query Match 54.8%; Score 46; DB 2; Length 298;
 Best Local Similarity 50.0%; Pred. No. 2.5;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 ERAIRQVEYFGD 15
 DB 64 EAEVLQVEYFSD 77

RESULT 12
 T43542
 RNA-binding protein Lal homolog - fission yeast (Schizosaccharomyces pombe)

N/Alternate names: la autoantigen; ribonucleoprotein la homolog
 C/Species: Schizosaccharomyces pombe
 C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
 C/Accession: T43542; T43325
 R/Van Horn, D.J.; Yoo, C.J.; Xue, D.; Shi, H.; Molin, S.L. RNA 3, 1434-1443, 1997
 A/Title: The la protein in Schizosaccharomyces pombe: a conserved yet dispensable phospho
 A/Reference number: Z22560; MUID:98067398; PMID:9404894
 A/Accession: T43542
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-298 <VAN>
 A/Cross-references: EMBL:AF022949; PIDN:AA082145.1
 R/Utsumi, R. submitted to the EMBL Data Library, February 1998
 A/Description: Screening of S. pombe cDNA library using E. coli defective in signal tran
 A/Reference number: Z22428
 A/Accession: T43325
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-298 <UTS>
 A/Cross-references: EMBL:AB011371; PIDN:BAA24981.1
 C/Genetics:
 A/Function:
 A/Description: the binding of the la protein to rRNA precursors is required for the endo
 C/Keywords: phosphoprotein; RNA binding

Query Match 54.8%; Score 46; DB 2; Length 298;
 Best Local Similarity 50.0%; Pred. No. 2.5;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 ERAIRQVEYFGD 15
 DB 64 EAEVLQVEYFSD 77

RESULT 13
 H83743
 ABC transporter (permease) BH0752 [imported] - Bacillus halodurans (strain C-125)
 C/Species: Bacillus halodurans
 C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C/Accession: H83743
 R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
 A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A/Reference number: A83650; MUID:20512582; PMID:11058132
 A/Accession: H83743
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-642 <STO>
 A/Cross-references: GB:AP001509; GB:BA000004; NID:G10173176; PIDN:BA004471.1; GSPDB:GN000
 A/Experimental source: strain C-125
 C/Genetics:
 A/Map position: 1
 A/Introns: 72/1

Query Match 54.2%; Score 45.5; DB 2; Length 642;
 Best Local Similarity 60.0%; Pred. No. 7;
 Matches 9; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 1 ERAIRQVEYFGD 15
 DB 471 QSKALVLA-EYFSD 484

RESULT 14
 A35199
 heme oxygenase (decyclizing) (EC 1.14.99.3) 2 [similarity] - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C/Accession: A35199; A29922
 R/Rotenberg, M.O.; Maines, M.D. J. Biol. Chem. 265, 7501-7506, 1990

A;Cross-references: GB:X67859; NID:955778; PIDN:CAA48043.1; PID:955779
 A;Experimental source: liver
 C;Comment: This protein associates with a variety of small RNA molecules, most of which
 ay act as a transcription termination factor.
 C;Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology
 C;Keywords: phosphoprotein; RNA binding
 F;112-178/Domain: ribonucleoprotein repeat homology <RRM>
 F;113-118/Region: RNA-binding RNP2 motif
 F;151-158/Region: RNA-binding RNP1 motif
 F;127-415/Domain: phosphorylated #status predicted <PHY>

Query Match 67.9%; Score 57; DB 1; Length 415;
 Best Local Similarity 66.7%; Pred. No. 0.042;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 2 ERAIRQVEYFDF 16
 Db 14 EAKICHQIEYFDF 28

RESULT 6
 T30953
 hypothetical protein C44E4.4 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
 C;Accession: T30953
 R;Sammons, L.; Wohlmann, P.; Gillam, B.
 submitted to the EMBL Data Library, August 1999
 A;Description: The sequence of C. elegans cosmid C44E4.
 A;Reference number: Z20945
 A;Accession: T30953
 A;Status: preliminary; translated from GB/EMBL/DDBF
 A;Molecule type: DNA
 A;Residues: 1-396 <SAM>
 A;Cross-references: EMBL:AF003140; PIDN:AAB54169.1
 A;Experimental source: strain Bristol N2; clone C44E4
 C;Genetics:
 A;Map position: 1
 A;Intons: 45/1; 114/3
 A;Note: C44E4.4
 C;Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology

Query Match 59.5%; Score 50; DB 2; Length 396;
 Best Local Similarity 57.1%; Pred. No. 0.67;
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 QY 2 ERAIRQVEYFDF 15
 Db 13 DQKITQLEYFDF 26

RESULT 7
 S33817
 ribonucleoprotein la.B - African clawed frog
 N;Alternate names: autoantigen SS-B/la; ribonucleoprotein SS-B
 C;Species: Xenopus laevis (African clawed frog)
 C;Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
 C;Accession: S33817; S28544
 R;Scherly, D.; Stutz, F.; Lin-Marq, N.; Clarkson, S.G.
 J. Mol. Biol. 231, 196-204, 1993
 A;Title: La proteins from Xenopus laevis. cDNA cloning and developmental expression.
 A;Reference number: S33817; MUID:93287095; PMID:8510143
 A;Accession: S33817
 A;Molecule type: mRNA
 A;Residues: 1-427 <SCH>
 A;Cross-references: EMBL:X68818; NID:964875; PIDN:CAA48716.1; PID:964876
 C;Comment: This protein associates with a variety of small RNA molecules, most of which
 ay act as a transcription termination factor.
 C;Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology
 C;Keywords: phosphoprotein; RNA binding
 F;111-177/Domain: ribonucleoprotein repeat homology <RRM>
 F;112-117/Region: RNA-binding RNP2 motif
 F;150-157/Region: RNA-binding RNP1 motif

F;227-427/Domain: phosphorylated #status predicted <PHY>

Query Match 57.1%; Score 48; DB 1; Length 427;
 Best Local Similarity 72.7%; Pred. No. 1.6;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 5 IIRQVEYFDF 15
 Db 16 ICEQIEYFDF 26

RESULT 8
 S33818
 ribonucleoprotein la.A - African clawed frog
 N;Alternate names: autoantigen SS-B/la; ribonucleoprotein SS-B
 C;Species: Xenopus laevis (African clawed frog)
 C;Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
 C;Accession: S33818; S28545
 R;Scherly, D.; Stutz, F.; Lin-Marq, N.; Clarkson, S.G.
 J. Mol. Biol. 231, 196-204, 1993
 A;Title: La proteins from Xenopus laevis. cDNA cloning and developmental expression.
 A;Reference number: S33817; MUID:93287095; PMID:8510143
 A;Accession: S33818
 A;Molecule type: mRNA
 A;Residues: 1-428 <SCH>
 A;Cross-references: EMBL:X68817; NID:964873; PIDN:CAA48715.1; PID:964874
 C;Comment: This protein associates with a variety of small RNA molecules, most of which
 ay act as a transcription termination factor.
 C;Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology
 C;Keywords: phosphoprotein; RNA binding
 F;112-178/Domain: ribonucleoprotein repeat homology <RRM>
 F;113-118/Region: RNA-binding RNP2 motif
 F;151-158/Region: RNA-binding RNP1 motif
 F;228-428/Domain: phosphorylated #status predicted <PHY>

Query Match 57.1%; Score 48; DB 1; Length 428;
 Best Local Similarity 72.7%; Pred. No. 1.6;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 5 IIRQVEYFDF 15
 Db 17 ICEQIEYFDF 27

RESULT 9
 T04453
 hypothetical protein FAD11.80 - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999
 C;Accession: T04453
 R;Bevan, M.; Benes, V.; Rechmann, S.; Borkova, D.; Ansgorge, W.; Hohenseel, J.; Mewes, H.
 submitted to the Protein Sequence Database, April 1998
 A;Reference number: Z15360
 A;Accession: T04453
 A;Molecule type: DNA
 A;Residues: 1-483 <BEV>
 A;Cross-references: EMBL:AL022537
 A;Experimental source: cultivar Columbia; BAC clone FAD11
 C;Genetics:
 A;Map position: 4
 A;Intons: 17/3; 44/1; 141/3; 206/2; 247/2; 345/3; 395/1; 434/2
 A;Note: FAD11.80

Query Match 57.1%; Score 48; DB 2; Length 483;
 Best Local Similarity 53.8%; Pred. No. 1.9;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 QY 3 RAIIRQVEYFDF 15
 Db 12 KTVLRQVEYFDF 24

RESULT 10

Best Local Similarity 100.0%; Pred. No. 8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERATIRQVEYFGDF 15
|||||
Db 50 ERATIRQVEYFGDF 64

RESULT 3

S03849

ribonucleoprotein la - bovine

N/Alternate names: autoantigen SS-B/la; ribonucleoprotein SS-B

C/Species: Bos primigenius taurus (cattle)

C/Date: 31-Dec-1990 #sequence_revision 26-May-1994 #text_change 22-Jun-1999

C/Accession: S03849

R/Chan, E.K.L.; Sullivan, K.F.; Tan, E.M.

Nucleic Acids Res. 17, 2233-2244, 1989

A/Title: Ribonucleoprotein SS-B/la belongs to a protein family with consensus sequences

A/Reference number: S03848; PMID:89202037; PMID:2468131

A/Accession: S03849

A/Molecule type: mRNA

A/Residues: 1-404 <CHA>

A/Cross-references: EMBL:X13698; NID:g755; PIDN:CAA31986.1; PID:g756

A/Note: part of this sequence was confirmed by protein sequencing

C/Comment: This protein associates with a variety of small RNA molecules, most of which

act as a transcription termination factor.

C/Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology

C/Keywords: blocked amino end; phosphoprotein; RNA binding

F/112-178/Domain: ribonucleoprotein repeat homology <RHM>

F/113-118/Region: RNA-binding RNP2 motif

F/151-158/Region: RNA-binding RNP1 motif

F/228-404/Domain: phosphorylated #status predicted <PHY>

Query Match 67.9%; Score 57; DB 1; Length 404;

Best Local Similarity 66.7%; Pred. No. 0.041;

Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Db 14 EAKTCHQIEYFGDF 28

RESULT 4

A31888

ribonucleoprotein la - human

N/Alternate names: autoantigen SS-B/la; ribonucleoprotein SS-B; Sjogren syndrome antigen

C/Species: Homo sapiens (man)

C/Date: 21-May-1990 #sequence_revision 26-May-1994 #text_change 22-Jun-1999

C/Accession: A31888; S03848; A22956; A61051; S11013; I55553; I70205; I70206; A31273

R/Chan, E.K.L.; Sullivan, K.F.; Tan, E.M.

J. Biol. Chem. 263, 18043-18051, 1988

A/Title: Genomic structure and amino acid sequence domains of the human la autoantigen.

A/Reference number: A31888; PMID:89053970; PMID:3192555

A/Accession: A31888

A/Molecule type: mRNA

A/Residues: 1-408 <CHA>

A/Cross-references: GB:J04205; NID:g178686; PIDN:AAA51885.1; PID:g178687

R/Chan, E.K.L.; Sullivan, K.F.; Tan, E.M.

Nucleic Acids Res. 17, 2233-2244, 1989

A/Title: Ribonucleoprotein SS-B/la belongs to a protein family with consensus sequences

A/Reference number: S03848; PMID:89202037; PMID:2468131

A/Accession: S03848

A/Molecule type: mRNA

A/Residues: 1-408 <CH2>

A/Cross-references: EMBL:X13697; NID:g36414; PIDN:CAA31985.1; PID:g36415

R/Chan, E.K.L.; Keene, J.D.

Proc. Natl. Acad. Sci. U.S.A. 82, 2115-2119, 1985

A/Title: Isolation and analysis of cDNA clones expressing human lupus la antigen.

A/Reference number: A22956; PMID:85166283; PMID:3856888

A/Accession: A22956

A/Molecule type: mRNA

A/Residues: 45-97, 'LK' <CH3>

A/Cross-references: GB:J04205

A/Note: this sequence has been revised in reference A31888

R/Nyman, U.; Ringertz, N.R.; Petersson, I.

Immunol. Lett. 22, 65-72, 1989

A/Title: Demonstration of an amino terminal la epitope recognized by human anti-la sera.

A/Reference number: A61051; PMID:89379261; PMID:2476379

A/Accession: A61051

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-19, 'E', 21-47 <HYM>

R/Sturges, A.D.; Peterson, M.G.; McNeillage, L.J.; Whittingham, S.; Coppel, R.L.

J. Immunol. 140, 3212-3218, 1988

A/Title: Characteristics and epitope mapping of a cloned human autoantigen la.

A/Reference number: S11013; PMID:88199081; PMID:2452201

A/Accession: S11013

A/Molecule type: mRNA

A/Residues: 'E', 55-287, 'V', 289-408 <STU>

A/Cross-references: EMBL:M20328; NID:g337456; PIDN:AAA36577.1; PID:g337457

R/Kohaka, H.; Yamamoto, K.; Fujii, H.; Miura, H.; Miyasaka, N.; Nishioke, K.; Miyamoto, J.

Clin. Invest. 85, 1566-1574, 1990

A/Title: Fine epitope mapping the human SS-B/la protein: Identification of a distinct at

A/Reference number: I55553; PMID:90237237; PMID:1692037

A/Accession: I55553

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 81-107 <RES>

A/Cross-references: GB:M35261; NID:g338492; PIDN:AAA36552.1; PID:g338495

A/Accession: I70205

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 174-224 <RR2>

A/Cross-references: GB:M35263; NID:g338492; PIDN:AAA36553.1; PID:g338496

A/Accession: I70206

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 279-342 <RR3>

A/Cross-references: GB:M35262; NID:g338493; PIDN:AAA36554.1; PID:g338497

C/Comment: This protein associates with a variety of small RNA molecules, most of which

act as a transcription termination factor.

C/Genetics:

A/Gene: GDB:SSB

A/Cross-references: GDB:125359; OMIM:109090

A/Map position: 2

A/Introns: 22/3; 57/2; 115/3; 151/3; 185/2; 209/2; 223/3; 264/3; 380/2

C/Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology

C/Keywords: phosphoprotein; RNA binding

F/112-178/Domain: ribonucleoprotein repeat homology <RHM>

F/113-118/Region: RNA-binding RNP2 motif

F/151-158/Region: RNA-binding RNP1 motif

F/228-408/Domain: phosphorylated #status experimental <PHY>

Query Match 67.9%; Score 57; DB 1; Length 408;

Best Local Similarity 66.7%; Pred. No. 0.041;

Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Db 14 EAKTCHQIEYFGDF 28

RESULT 5

JC1494

ribonucleoprotein la - rat

N/Alternate names: autoantigen SS-B/la; ribonucleoprotein SS-B

C/Species: Rattus norvegicus (Norway rat)

C/Date: 24-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999

C/Accession: JC1494; S25145

R/Semel, I.; Troester, H.; Bartsch, H.; Schwemmler, M.; Igloi, G.L.; Bachmann, M.

Gene 126, 265-268, 1993

A/Title: Isolation of rat cDNA clones coding for the autoantigen SS-B/la: Detection of

A/Reference number: JC1494; PMID:93246255; PMID:7916708

A/Accession: JC1494

A/Molecule type: mRNA

A/Residues: 1-415 <SEM>

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:33:11 / Search time 12.514 Seconds
(without alignments)
122.988 Million cell updates/sec

Title: US-09-836-073-19

Perfect score: 84
Sequence: 1 QERAIIRQVEYFQDF 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 28366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.78:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	92.9	390	2	La/SS-B homolog D-
2	78	92.9	390	2	ribonucleoprotein
3	78	92.9	390	2	ribonucleoprotein
4	57	67.9	404	1	ribonucleoprotein
5	57	67.9	408	1	ribonucleoprotein
6	50	59.5	415	1	ribonucleoprotein
7	48	57.1	427	1	ribonucleoprotein
8	48	57.1	428	1	ribonucleoprotein
9	48	57.1	483	2	hypothetical prote
10	46	54.8	529	2	hypothetical prote
11	46	54.8	529	2	RNA-binding protei
12	46	54.8	298	2	ABC transporter (p
13	45.5	54.2	642	2	heme oxygenase (de
14	44	52.4	315	1	hypothetical prote
15	43	51.2	466	2	hypothetical prote
16	43	51.2	469	2	vacuolar protein s
17	43	51.2	569	2	vacuolar protein s
18	43	51.2	569	2	general secretion
19	43	51.2	846	2	RNA-binding protei
20	42	50.0	275	2	hypothetical 44.4
21	42	50.0	393	2	hypothetical prote
22	42	50.0	398	2	hypothetical prote
23	42	50.0	407	2	hypothetical prote
24	42	50.0	788	2	probable proteinase
25	41.5	49.4	334	2	hypothetical prote
26	41	48.8	421	2	hypothetical prote
27	41	48.8	483	2	hypothetical prote
28	41	48.8	520	2	trans-cinnamate 4-
29	40.5	48.2	506	2	T14907

30	40.5	48.2	3078	2	T28432	variant-specific s
31	40	47.6	230	2	C84410	hypothetical prote
32	40	47.6	304	2	H64156	hypothetical prote
33	40	47.6	373	1	KMECDP	chorismate mutase
34	40	47.6	373	2	A10832	prephenate dehydro
35	40	47.6	373	2	C85306	chorismate mutase-
36	40	47.6	373	2	G91061	chorismate mutase-
37	40	47.6	384	2	H96829	probable RNA-bind
38	40	47.6	391	2	H89777	capsular polysacch
39	40	47.6	634	1	A55683	L-iduronidase (EC
40	40	47.6	662	2	S55387	hemocyanin precurs
41	40	47.6	736	1	C69307	conserved hypochet
42	39.5	47.0	335	2	A75179	probable proteinase
43	39	46.4	206	2	A71326	probable V-type At
44	39	46.4	253	2	B71346	probable Spo0' reg
45	39	46.4	267	2	D82593	phosphate ABC tran

ALIGNMENTS

RESULT 1

A53773
La/SS-B homolog D-1a - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
C/Accession: A53773
R/Bat, C./ Li, Z.; Tolia, P.P.
Mol. Cell. Biol. 14, 5123-5129, 1994
A/Title: Developmental characterization of a Drosophila RNA-binding protein homologous
A/Reference number: A53773; MUID:94309632; PMID:8035794
A/Accession: A53773
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-390 <BAT>
A/Cross-references: GB:007652; NID:9464019; PIDN:AAA20518.1; PID:9464020
C/Genetics:
A:Gene: FlyBase:La
A:Gene: FlyBase:La
A/Cross-references: FlyBase:FBgn0011638
C/Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
C/Keywords: leucine zipper; RNA binding

Query Match 92.9%; Score 78; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QERAIIRQVEYFQDF 15
Db 50 QERAIIRQVEYFQDF 64

RESULT 2

A53781
ribonucleoprotein La - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 20-Sep-1999
C/Accession: A53781
R/Yoo, C.J.; Molin, S.L.
Mol. Cell. Biol. 14, 5412-5424, 1994
A/Title: La proteins from Drosophila melanogaster and Saccharomyces cerevisiae: a yeast
A/Reference number: A53781; MUID:94309661; PMID:8035818
A/Accession: A53781
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-390 <YOO>
A/Cross-references: GB:L32988; NID:9488469; PID:9488470
C/Genetics:
A:Gene: FlyBase:La
A:Gene: FlyBase:La
A/Cross-references: FlyBase:FBgn0011638
C/Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
C/Keywords: RNA binding

Query Match 92.9%; Score 78; DB 2; Length 390;

08YOB2 PRELIMINARY; PRT; 451 AA.
 ID 08YOB2;
 AC 08YOB2;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE UDP-N-acetylglucosamine pyrophosphorylase.
 GN A183921.
 OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 CC NCBI_TaxID=103690;
 OK [1]
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21595285; PubMed=11759840;
 RA Kaneo T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
 RA Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 cyanobacterium Anabaena sp. strain PCC 7120.";
 RL DNA Res. 8:205-213(2001).
 DR EMBL; AP003594; BAB75620.1; -.
 DR PIR; AB2296; AB2296.
 DR GO; GO:0003977; F:UDP-N-acetylglucosamine diphosphorylase act. .; IEA.
 DR GO; GO:0009058; P:biosynthesis; IEA.
 DR GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
 DR InterPro; IPR005882; GIMU.
 DR InterPro; IPR001451; Hexapep_transf.
 DR InterPro; IPR005835; NTP_transferase.
 DR Pfam; PF00132; hexapep; 6.
 DR Pfam; PF00483; NTP_transferase; 1.
 DR TIGRfam; TIGR01173; glmu; 1.
 KW Complete proteome.
 SQ SEQUENCE 451 AA; 49191 MW; B1DEB3A6F2170FA7 CRC64;

Query Match 46.7%; Score 42; DB 16; Length 451;
 Best Local Similarity 53.3%; Pred. No. 65;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 LEASTIROEYFGDA 18
 |||: :|||
 DB 187 LEANNNAQKEYVLTDA 201

RESULT 15
 ID 004697 PRELIMINARY; PRT; 632 AA.
 AC 004697;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE DNA-binding protein PD2.
 OS Pisum sativum (Garden pea).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
 CC NCBI_TaxID=3888;
 OK [1]
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Alaska; TISSUE=leaf;
 RA Sato N., Kazuno A.A., Ohta N., Ohshima K.;
 RT "Identification of a novel family of DNA-binding proteins with two AT-
 RT hook motifs from pea."
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X98740; CAA67292.1; -.
 DR PIR; T06586; T06586.
 DR GO; GO:0003677; F:DNA binding; IEA.
 KW DNA-binding.
 SQ SEQUENCE 632 AA; 69498 MW; 9F744E227CD08717 CRC64;

Query Match 46.7%; Score 42; DB 10; Length 632;
 Best Local Similarity 50.0%; Pred. No. 95;

Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 4 LEASTIROEYFGD 17
 :||: :|||
 DB 161 VEAIVSDERYTGD 174

Search completed: September 10, 2004, 18:00:17
 Job time : 44.229 secs

DR ProDom; PD000001; Prot Kinase; 1.
 DR SMART; SM00192; L0LA; 1.
 DR SMART; SM00220; S.TKC; 1.
 DR SMART; SM00219; TYKC; 1.
 DR PROSITE; PS01209; L0LA_1; 1.
 DR PROSITE; PS0068; L0LA_2; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
 DR ATP-Binding; Transferase.
 FT NON TER 1
 SQ SEQUENCE 1161 AA; 124852 MW; 601210E788E8AA41 CRC64;

Query Match 47.2%; Score 42.5; DB 13; Length 1161;
 Best Local Similarity 43.5%; Pred. No. 1.5e+02;
 Matches 10; Conservative 4; Mismatches 4; Indels 5; Gaps 1;

QY 1 VSKLEASTROEYFGD 18
 DB 530 LSKIRSTIMTDNPNNGYFGKA 552

RESULT 11

OS 088YN2 PRELIMINARY; PRT; - 160 AA.
 AC 088YN2;
 DT 01-JUN-2003 (Tremblrel. 24, Created)
 DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 25, Last annotation update)
 DE Ribosomal-protein-alanine N-acetyltransferase (EC 2.3.1.128).
 GN RM11 OR LP 0718.
 OS Lactobacillus plantarum.
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=1590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCIMB 8826 / WCFS1;
 RX MEDLINE=22480296; PubMed=12566566;
 RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
 RA Kijpers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
 RA Piers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
 RA Hofer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
 RA De Vos W.M., Siezen R.J.;
 RT "Complete genome sequence of Lactobacillus plantarum WCFS1";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995 (2003).
 DR EMBL; AL935253; CAD63319.1; -
 DR GO; GO:0008415; F:acetyltransferase activity; IEA.
 DR GO; GO:0008080; F:N-acetyltransferase activity; IEA.
 DR GO; GO:0008999; F:ribosomal-protein-alanine N-acetyltransferase. . .; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR InterPro; IPR00182; GCSAcetyl_trans.
 DR Pfam; PF00583; Acetyltransferase; 1.
 KW Acyltransferase; Transferase; Complete proteome.
 SQ SEQUENCE 160 AA; 18734 MW; 3FD115B0095A526 CRC64;

Query Match 46.7%; Score 42; DB 16; Length 160;
 Best Local Similarity 53.8%; Pred. No. 20;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 EASTIROEYFGD 17
 DB 131 EKTGKRYPGD 143

RESULT 12

OS 088YN2 PRELIMINARY; PRT; 308 AA.
 AC 088YN2;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)

DE Glycosyltransferase.
 GN MM1127.
 OS Methanosarcina mazei (Methanosarcina frisia).
 OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
 OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2209;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Gael / G01 / ATCC BAA-199 / DSM 3647 / OCM 88;
 RX MEDLINE=2210827; PubMed=12125824;
 RA Depgenmeier U., Johann A., Hartisch T., Merkl R., Schmitz R.A.,
 RA Martinez-Arias R., Henne A., Wierzer A., Benner S., Jacobi C.,
 RA Brueggemann H., Lénard T., Christmann A., Boemeke M., Steckel S.,
 RA Bhattacharyya A., Lykdis G.,
 RA Bratz H.-J., Gottschalk G.;
 RT "The genome of Methanosarcina mazei: evidence for lateral gene
 transfer between Bacteria and Archaea";
 RL J. Mol. Microbiol. Biotechnol. 4:453-461 (2002).
 DR EMBL; AE013341; AAM30823.1; -
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR InterPro; IPR01173; Glyco trans 2.
 DR Pfam; PF00535; Glycos transf 2; 1.
 KW Transferase; Complete proteome.
 SQ SEQUENCE 308 AA; 35128 MW; 0C01D9C354DA40DE CRC64;

Query Match 46.7%; Score 42; DB 17; Length 308;
 Best Local Similarity 50.0%; Pred. No. 42;
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 VSKLEASTROEYFG 16
 DB 105 IGLDADTILEENYFG 120

RESULT 13

OS 086119 PRELIMINARY; PRT; 358 AA.
 AC 086119;
 DT 01-JUN-2003 (Tremblrel. 24, Created)
 DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE Hypothetical protein.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RX MEDLINE=22092622; PubMed=12097910;
 RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
 RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
 RA Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
 RT "Sequence and analysis of chromosome 2 of Dictyostelium discoideum";
 RL Nature 418:79-85 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RA Baumgart C.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC117176; AAO52103.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 358 AA; 39920 MW; 021273F80378AF7C CRC64;

Query Match 46.7%; Score 42; DB 5; Length 358;
 Best Local Similarity 53.3%; Pred. No. 50;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 KLEASTROEYFGD 17
 DB 64 KLISKTKQSKYFGS 78

RESULT 14

```
DR GO:0006520; P:amino acid metabolism; IEA.
DR GO:0006535; P:cysteine biosynthesis from serine; IEA.
DR GO:0013343; P:cysteine biosynthesis via cystathione; IEA.
DR InterPro: IPR001926; B6_enzyme_beta.
DR InterPro: IPR000644; CBS_domain.
DR InterPro: IPR005857; Cysa_beta_synth.
DR InterPro: IPR001216; Cys_synthase_BS.
DR Pfam: PF00571; CBS_2.
DR Pfam: PF00291; PALP_1.
DR SMART: SM00116; CBS_2.
DR TIGRFAMs: TIGR01137; cysa_beta_1.
DR PROSITE: PS00301; CYS_SYNTHASE_1.
KW Lyase.
SQ SEQUENCE 507 AA; 56025 MW; 1589165DEB7C8A54 CRC64;

Query Match
Best Local Similarity 47.8%; Score 43; DB 3; Length 507;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 SKLEASTIRQRYFGDA 18
Db 351 SKLEASTIRQRYFGDA 367

RESULT 8
Q8E9H6 PRELIMINARY; PRT; 206 AA.
AC Q8E9H6;
DT 01-MAR-2003 (TREMblrel. 23, Created)
DT 01-MAR-2003 (TREMblrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Conserved hypothetical protein.
GN SO4307.
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Alteromonadales; Shewanella.
OX NCBI_Taxid=70663;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NR-1;
RX MEDLINE=22297686; PubMed=12368813;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N., Mehe B., Clayton R.A.,
RA Meyer R.T., Tsapin R.J., Beaman M., Brinkac L., Daugherty S.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
RA Madupu R., Peterson J.D., Umapati M., White O., Wolf A.M.,
RA Vamathevan J., Weidman J., Umapati M., Lee K., Berry K., Lee C.,
RA Mueller J., Kouri H., Gill J., Uterback T.R., McDonald L.A.,
RA Feldblyum T.V., Smith H.O., Venter J.C., Nelson K.H., Fraser C.M.,
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis."
RL Nat. Biotechnol. 20:1118-1123(2002).
DR EMBL: AEO15863; AAN57276.1; -.
DR TIGR: SO4307; -.
DR InterPro: IPR007435; DUF484.
DR Pfam: PF04340; DUF484; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 206 AA; 24078 MW; D8935EAD40692P10 CRC64;

Query Match
Best Local Similarity 47.2%; Score 42.5; DB 16; Length 206;
Matches 10; Conservative 3; Mismatches 3; Indels 9; Gaps 1;

Qy 1 VSKLEASTIRQRYFG 16
Db 118 ISVLEADVEMKAIMARLKEYFG 142

RESULT 9
Q7ZT10 PRELIMINARY; PRT; 401 AA.
AC Q7ZT10;
DT 01-JUN-2003 (TREMblrel. 24, Created)
```

```
DT 01-JUN-2003 (TREMblrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)
DE Similar to sjogren syndrome antigen B (Autoantigen Ia).
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC045392; AAH45392.1; -.
DR GO:0005634; C:nucleus; IEA.
DR GO:0003723; F:RNA binding; IEA.
DR InterPro: IPR002344; LupaLa.
DR InterPro: IPR00630; LupaLa_dom.
DR InterPro: IPR00504; RNA_rec_mot.
DR Pfam: PF00076; rrm; 1.
DR PRINTS: PR00302; LUPUSLA.
DR SMART: SM00715; LA; 1.
DR SMART: SM00360; RRM; 1.
DR PROSITE: PS50102; RRM; 1.
DR PROSITE: PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 401 AA; 46138 MW; 2EF032FDD3916291 CRC64;

Query Match
Best Local Similarity 47.2%; Score 42.5; DB 13; Length 401;
Matches 10; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

Qy 1 VSKLEASTIRQRYFGD 17
Db 7 MSPLEKVAEOLEYFGD 24

RESULT 10
Q8JFV0 PRELIMINARY; PRT; 1161 AA.
AC Q8JFV0;
DT 01-OCT-2002 (TREMblrel. 22, Created)
DT 01-OCT-2002 (TREMblrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMblrel. 25, Last annotation update)
DE SI:Z107016.1 (Novel protein similar to vertebrate anaplastic lymphoma
DE kinase (ALK) and leukocyte tyrosine kinase receptor precursor (LTK or
DE TYK1) (Fragment).
GN SI:Z107016.1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC Hammond S.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL596022; CAD43463.1; -.
DR GO:0016020; C:membrane; IEA.
DR GO:0005524; F:ATP binding; IEA.
DR GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO:0016740; F:transferase activity; IEA.
DR GO:0004714; F:transmembrane receptor protein tyrosine kin. . .; IEA.
DR GO:0006468; P:protein amino acid phosphorylation; IEA.
DR GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
DR InterPro: IPR002172; LDL_receptor_A.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002011; RecepttyrkinetI.
DR InterPro: IPR002290; Set_tyr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR InterPro: IPR008266; Tyr_kinase_AS.
DR Pfam: PF00057; ldl_recept_a; 1.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
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RC STRAIN=ATCC 12228;
RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
RA Chen Z., Wen Y.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
KW EMBL: A6016750; AAC05481.1; -.
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 116 AA; 14002 MW; C8419BFA9B8A7EA5 CRC64;

Query Match 48.3%; Score 43.5; DB 16; Length 116;
Best Local Similarity 57.9%; Pred. No. 7.5;
Matches 11; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Qy 1 VSKLEAST-IRCEYFEDA 18
: ||| : ||| |||
Db 78 ISKLRSETDERQYVFFDA 96

RESULT 5
09C9B9 PRELIMINARY; PRT; 381 AA.
AC 09C9B9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Sjogren syndrome antigen B.
GN SSB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batelov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kiehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schiraldi L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszewski A., Yoshida K., Hasegawa Y., Kawaji H., Kontecki S.,
RA Hayaishizaki Y.;
RL "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
DR EMBL: AK017822; BAB30957.1; -.
DR MGD; MGI:98423; Ssb.
DR GO; GO:0005634; C:nucleus; IDA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS00102; RRM_1.
DR PROSITE; PS00030; RRM_RNP_1.
SQ SEQUENCE 415 AA; 47657 MW; A7545C7686AC8363 CRC64;

Query Match 48.3%; Score 43.5; DB 11; Length 381;
Best Local Similarity 55.6%; Pred. No. 29;
Matches 10; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Qy 1 VSKLEASTIRO-EYFED 17
: ||| : ||| |||
Db 10 MTALEAKICHOIEYFED 27


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RESULT 6
09BRT4 PRELIMINARY; PRT; 415 AA.
AC 09BRT4;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Sjogren syndrome antigen B.
GN SSB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK088677; BAC40498.1; -.
DR MGD; MGI:98423; Ssb.
DR GO; GO:0005634; C:nucleus; IDA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS00102; RRM_1.
DR PROSITE; PS00030; RRM_RNP_1.
SQ SEQUENCE 415 AA; 47657 MW; A7545C7686AC8363 CRC64;

Query Match 48.3%; Score 43.5; DB 11; Length 415;
Best Local Similarity 55.6%; Pred. No. 32;
Matches 10; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Qy 1 VSKLEASTIRO-EYFED 17
: ||| : ||| |||
Db 10 MTALEAKICHOIEYFED 27

RESULT 7
094073 PRELIMINARY; PRT; 507 AA.
AC 094073;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Cystathionine beta-synthase (EC 4.2.1.22).
GN NBS5.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OC NCBI_TaxId=4932;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=X2180-1A;
RA Tezuka H., Mori T., Okumura Y., Kitabatake K., Tsunuma Y.;
RT "Cloning of a gene suppression hydrogen sulfide production by
RT Saccharomyces cerevisiae and its expression in a brewing yeast.";
RL ASBC Journal 50:130-133(1992).
DR EMBL; D16496; BAA03947.1; -.
DR HSSP; P35520; IUBO.
DR GO; GO:0005737; C:cytosol; IEA.
DR GO; GO:0004122; F:cystathionine beta-synthase activity; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.


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Query Match      58.3%; Score 52.5; DB 5; Length 390;
Best Local Similarity 66.7%; Pred. No. 0.67;
Matches 12; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY      2 SKLEASTIRQ-EYFFGDA 18
      48 TKGERALIRQVEYFFGDA 65

RESULT 2
Q9SV58      PRELIMINARY; PRT; 365 AA.
ID 09VZB8
AC 09VZB8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN F25G13.200 OR ATAG13110.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Pohl T., Weizenegger T., Bancroft I., Mewes H.W.,
RA Mayer K.F.X., Lemcke K., Scheller C.;
RA Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RA Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Pohl T., Weizenegger T., Mewes H.W., Lemcke K., Mayer K.F.X.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL079349; CAB4510.1; -
DR EMBL; AL161535; CAB78353.1; -
DR PIR; T10213; T10213.
DR InterPro; IPR005607; BSD.
DR Pfam; PF03909; BSD; 1.
DR PROSITE; PS00858; BSD; 1.
KM Hypothetical protein.
SQ SEQUENCE 365 AA; 41867 MW; 47BDCAM1B18F43D2 CRC64;

Query Match      48.9%; Score 44; DB 10; Length 365;
Best Local Similarity 38.9%; Pred. No. 22;
Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY      1 VSKLEASTIRQVEYFFGDA 18
      8 IIRGSSCTIRQVEYFFGDA 25

RESULT 3
Q9VZB8      PRELIMINARY; PRT; 512 AA.
ID 09VZB8
AC 09VZB8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE CG12014 protein.
GN CG12014.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.

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RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amaralides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Morten J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Chame M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abil J.F., Agbayani A., An H.-J., Andrews-Pfannkuoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasly E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brockett P., Brockett P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mewlrow G., Miletina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheller F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Weissman D.A., Weisslock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195 (2000).
DR EMBL; AE003478; AAF4771.1; -
DR EMBL; AE003478; AAF4771.1; -
DR FlyBase; FBgn0035445; CG12014.
DR GO; GO:0008484; P:sulfuric ester hydrolase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000917; Sulfatase.
DR Pfam; PF00884; Sulfatase; 1.
DR PROSITE; PS00523; SULFATASE 1; 1.
SQ SEQUENCE 512 AA; 58904 MW; AASB6D8400B6FB3A CRC64;

Query Match      48.9%; Score 44; DB 5; Length 512;
Best Local Similarity 57.1%; Pred. No. 32;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1 VSKLEASTIRQVEY 14
      278 ISPLQAAQIRQSY 291

RESULT 4
Q8CRF1      PRELIMINARY; PRT; 116 AA.
ID 08CRF1
AC 08CRF1;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Conserved hypothetical protein.
GN SE1840.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.

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RESULT 14
ID UL61_HCMVA STANDARD; PRT; 431 AA.
AC P16818;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Hypothetical protein UL61.
GN UL61.
OS Human cytomegalovirus (strain AD169).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Cytomegalovirus.
OX NCBI_TaxID=10360;
RN [1]
RA MEDLINE=90269039; Pubmed=2161319;
RA Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R.,
RA Horsnell T., Hutchinson C.A. III, Kouzarides T., Martignetti J.A.,
RA Peddie B., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
RT "Analysis of the protein-coding content of the sequence of human
RT cytomegalovirus strain AD169."
RT Curr. Top. Microbiol. Immunol. 154:125-169(1990).
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CC -----
DR EMBL; X17403; CAA35376.1; -
DR F01; S09824; S09824.
DR Hypothetical protein.
KM SEQUENCE 431 AA; 44309 MW; 61CC7288FA3B0743 CRC64;
SQ
Query Match 43.3%; Score 39; DB 1; Length 431;
Best Local Similarity 42.9%; Pred. No. 34;
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;
Qy 5 EASTRPOEYFGDA 18
Db 65 QATVRAAFWGA 78
RESULT 15
ID YF59_HUMAN STANDARD; PRT; 533 AA.
AC O9HCL3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical zinc finger protein KIA1559.
GN KIA1559
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RA SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20450683; Pubmed=10997877;
RA Nagase T., Kikuno R., Nakayama M., Hiroseawa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes.
RT XVIII. The complete sequences of 100 new cDNA clones from brain which
RT code for large proteins in vitro."
RL DNA Res. 7:273-281(2000).
CC -1- FUNCTION: May function as a transcription factor.
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: BELONGS TO THE KRUEPEL FAMILY OF C2H2-TYPE ZINC-
CC FINGER PROTEINS.
CC -1- SIMILARITY: Contains 1 KRAB domain.
```

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CC -1- SIMILARITY: Contains 13 C2H2-type zinc fingers.
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CC -----
DR EMBL; AB046779; BAB13385.1; ALT_INIT.
DR HSSP; P25490; IUBD.
DR InterPro; IPR001909; KRAB.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF01352; KRAB; 1.
DR Pfam; PF00096; zf-C2H2; 13.
DR SMART; SM00349; KRAB; 1.
DR SMART; SM00355; Znf_C2H2; 13.
DR PROSITE; PS50805; KRAB; 1.
DR PROSITE; PS50028; ZINC_FINGER_C2H2_1; 13.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 13.
KM Hypothetical protein; Transcription regulation; DNA-binding;
KM Zinc-finger; Metal-binding; Nuclear protein; Repeat.
KW DOMAIN
FT 172 194 C2H2-TYPE 1.
FT 200 222 C2H2-TYPE 2.
FT 228 250 C2H2-TYPE 3.
FT 256 278 C2H2-TYPE 4.
FT 284 306 C2H2-TYPE 5.
FT 312 334 C2H2-TYPE 6.
FT 340 362 C2H2-TYPE 7.
FT 368 390 C2H2-TYPE 8.
FT 396 418 C2H2-TYPE 9.
FT 424 446 C2H2-TYPE 10.
FT 452 474 C2H2-TYPE 11.
FT 480 502 C2H2-TYPE 12.
FT 508 530 C2H2-TYPE 13.
SQ SEQUENCE 533 AA; 63463 MW; E40EF5EC22A99F10 CRC64;
Query Match 43.3%; Score 39; DB 1; Length 533;
Best Local Similarity 53.3%; Pred. No. 42;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy 2 SKLEASTRPOEYFG 16
Db 127 SKIDGKQDQGYFG 141
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Search completed: September 10, 2004, 17:53:12
Job time : 9.24022 secs

DE Cystathionine beta-synthase (EC 4.2.1.22) (Serine sulphydrase)
 DE (beta-chlthase).
 OS Cys4 OR STR4 OR YGR155W OR G6667.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Burkholderia; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomycos.
 CC NCBI_TaxId=4932;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=X2180-1A;
 RC MEDLINE=93374830; PubMed=8366024;
 RA Charest H., Thomas D., Surdin-Kerjan Y.;
 RT "Cysteine biosynthesis in Saccharomyces cerevisiae occurs through the
 RT transsulfuration pathway which has been built up by enzyme
 RT recruitment.";
 RT J. Bacteriol. 175:5366-5374(1993).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=A5-8-1A.
 RC Ono B.I., Inoue T., Kijima K., Matsuda A., Negishi K., Shinoda S.;
 RA Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RC MEDLINE=96158062; PubMed=8585325;
 RA Skala U., Nawrocki A., Goffeau A.;
 RT "The sequence of a 27 kb segment on the right arm of chromosome VII
 RT from Saccharomyces cerevisiae reveals MOI1, NAT2, RPL30B, RSR1, CYS4,
 RT PEM1/CHO2, NSR1 genes and ten new open reading frames.";
 RT Yeast 11:1421-1427(1995).
 RN [4]
 RN SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RC MEDLINE=94294429; PubMed=8022826;
 RA Kruger W.D., Cox D.R.;
 RT "A yeast system for expression of human cystathionine beta-synthase:
 RT structural and functional conservation of the human and yeast genes.";
 RT Proc. Natl. Acad. Sci. U.S.A. 91:6614-6618(1994).
 CC -1- CATALYTIC ACTIVITY: L-serine + L-homocysteine = cystathionine +
 CC H(2)O.
 CC -1- COFACTOR: Pyridoxal phosphate.
 CC -1- PATHWAY: Homocysteine transsulfuration; first step.
 CC -1- SIMILARITY: Belongs to the cysteine synthase/cystathionine beta-
 CC synthase family.
 CC -1- SIMILARITY: Contains 1 CBS domain.
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 DR EMBL: X72922; CAA51426.1; -;
 DR EMBL: D16502; BAA03952.1; -;
 DR EMBL: X85807; CAA59812.1; -;
 DR EMBL: Z72940; CAA97169.1; -;
 DR EMBL: L14578; AAC37401.1; -;
 DR PIR: A48661; A48661.
 DR HSSP: P35520; IJBO.
 DR GenOnline: 141467; -;
 DR SGD: S000387; CYG4.
 DR GO: GO:000537; C:cytoplasm; IDA.
 DR GO: GO:0004122; P:cystathionine beta-synthase activity; IDA.
 DR GO: GO:0019344; P:cysteine biosynthesis; IMP.
 DR InterPro: IPR001926; B6_enzyme_beta.
 DR InterPro: IPR000644; CBS_domain.
 DR InterPro: IPR001216; Cys_synthase_BS.
 DR InterPro: IPR005857; Cysa_beta_synth.
 DR Pfam: PF00051; CBS; 2.
 DR Pfam: PF00291; PALP; 1.
 DR SMART: SM00116; CBS; 2.

DR TIGRfam: TIGR01137; cysa_beta; 1.
 DR PROSITE: P800901; CYS_SYNTHASE; 1.
 KW Cysteine biosynthesis; Lyase; Pyridoxal phosphate; CBS domain.
 FT BINDING 117 117
 FT DOMAIN 311 424
 FT CONFLICT 2 2
 FT CONFLICT 8 8
 FT CONFLICT 63 63
 FT CONFLICT 104 104
 FT CONFLICT 129 129
 FT CONFLICT 163 163
 FT CONFLICT 293 293
 FT CONFLICT 407 407
 FT CONFLICT 436 437
 FT CONFLICT 441 441
 FT CONFLICT 481 481
 FT CONFLICT 481 481
 SQ SEQUENCE 507 AA; 56021 MW; DDC7059B20FD0746 CRC64;
 Query Match 47.8%; Score 43; DB 1; Length 507;
 Best Local Similarity 58.8%; Pred. NO. 7.8;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 2 SKLEASTIROEYFGDA 18
 DB 351 SKLEASTIRKADVFQNA 367

RESULT 9
 YN48 ARCFU STANDARD; PRT; 112 AA.
 ID YN48 ARCFU
 AC 030321;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein AF2348.
 GN AF2348.
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
 OC Archaeoglobaceae; Archaeoglobus.
 CC NCBI_TaxId=2234;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RC MEDLINE=96049343; PubMed=9389475;
 RX Kleink H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
 RA Richardson D.L., Kierlavage A.R., Graham D.E., Kyriakides N.C.,
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 RA Kiriess E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
 RA Cotton M.D., Spriggs T., Arllich P., Kaine B.P., Sykes S.M.,
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Weese C.R.,
 RA Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 RT reducing archaeon Archaeoglobus fulgidus.";
 RL Nature 390:364-370(1997).
 CC -----
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 CC -----
 CC
 DR EMBL: AE001114; AAB91315.1; -;
 DR PIR: D69543; D69543.
 DR TIGR: AF2348; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 112 AA; 13012 MW; C9C6AC0ACD6AC730 CRC64;

RP SEQUENCE FROM N.A.
 RC TISUB=Placenta, and Skeletal muscle;
 RA MEDLINE=22388257; PubMed=1477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
 RA Stedlecken M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinck P., Prange C.,
 RA Rata S.S., Locuelli N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosnak S.A., McEwen K.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield V.S.N., Krzywinski M.T., Skalska U., Smalits D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE OF 54-408 FROM N.A.
 RX MEDLINE=88199081; PubMed=2452201;
 RA Sturgees A.D., Peterson M.G., McNeilage L.J., Whittingham S.,
 RA Coppel R.S.;
 RT "Characteristics and epitope mapping of a cloned human autoantigen
 RT La.";
 RL J. Immunol. 140:3212-3218(1988).
 RN [5]
 RP SEQUENCE OF 54-97 FROM N.A.
 RX MEDLINE=85166283; PubMed=3856888;
 RA Chambers J.C., Keene J.D.;
 RT "Isolation and analysis of cDNA clones expressing human lupus La
 RT antigen.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:2115-2119(1985).
 RN [6]
 RP FUNCTION.
 RX MEDLINE=89251617; PubMed=2470590;
 RA Gottlieb E., Steltz J.A.;
 RT "Function of the mammalian La protein: evidence for its action in
 RT transcription termination by RNA polymerase III.";
 RL EMBO J. 8:851-861(1989).
 RN [7]
 RP PHOSPHORYLATION.
 RX MEDLINE=97207017; PubMed=9054510;
 RA Fan H., Sakulich A.L., Goodier J.L., Zhang X., Qin J., Marale R.J.;
 RT "Phosphorylation of the human La antigen on serine 366 can regulate
 RT recycling of RNA polymerase III transcription complexes.";
 RL Cell 88:707-715(1997).
 RN [8]
 RP INTERACTION WITH DDX15.
 RX MEDLINE=22346609; PubMed=12458796;
 RA Fournoux M.A., Kolkman M.J.M., Van der Heijden A., De Jong A.S.,
 RA Van Venrooij W.J., Pruijn G.J.M.;
 RT "The human La (SS-B) autoantigen interacts with DDX15/hPrp43, a
 RT putative DEAD-box RNA helicase.";
 RL RNA 8:1428-1443(2002).
 RN [9]
 RP FUNCTION: La protein plays a role in the transcription of RNA
 CC polymerase III. It is most probably a transcription termination
 CC factor. Binds to the 3' termini of virtually all nascent
 CC polymerase III transcripts. It is associated with precursor forms
 CC of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S,
 CC and 7-2 RNAs.
 CC -1- SUBUNIT: Interacts with DDX15.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- PTM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES ARE AT THE
 CC C-TERMINAL PART OF THE PROTEIN.
 CC -1- PTM: The N-terminus is blocked.
 CC -1- DISEASE: Sera from patients with systemic lupus erythematosus
 CC often contain antibodies that react with the normal cellular

CC La protein as if this antigen was foreign.
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RNM) domain.
 CC -----
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL: X13697; CAA31985.1; -
 CC EMBL: J04205; AAA51885.1; -
 CC EMBL: BC001289; AAH01289.1; -
 CC EMBL: BC020818; AAH20818.1; -
 CC PIR: A11888; A11888.
 CC GeneW: HGNC:11316; SSB.
 CC MIM: 109090; -
 CC GO: GO:0030529; C:ribonucleoprotein complex; TAS.
 CC GO: GO:0003729; F:RNA binding; TAS.
 CC GO: GO:0000049; F:tRNA binding; TAS.
 CC GO: GO:0008334; P:histone mRNA metabolism; TAS.
 CC GO: GO:0006400; P:tRNA modification; TAS.
 CC InterPro: IPR002344; Lupus_La.
 CC InterPro: IPR006630; Lupus_La_dom.
 CC InterPro: IPR00504; RNA_rec_mot.
 CC Pfam: PF05383; tm; 1.
 CC Pfam: PF00076; tm; 1.
 CC PRINTS: PR00302; LUPUSLA.
 CC SMART: SMO0715; LA; 1.
 CC SMART: SMO0360; RNM; 1.
 CC PROSITE: PS01002; RNM; 1.
 CC PROSITE: PS00030; RNM_RNP_1; 1.
 CC KMW: Systemic lupus erythematosus; RNA-binding; Phosphorylation;
 CC Nuclear protein.
 CC FT: DOMAIN 111 187 RNA-BINDING (RNM).
 CC FT: MOD RES 366 366 PHOSPHORYLATION (BY CK2).
 CC SQ: SEQUENCE 408 AA; 46837 MW; EC15315F9187FC4 CRC64;
 CC -----
 CC Query Match 48.3%; Score 43.5; DB 1; Length 408;
 CC Best Local Similarity 55.6%; Pred. No. 5;
 CC Matches 10; Conservative 2; Mismatches 5; Indels 1; Gaps 1;
 CC -----
 CC QY 1 VSKLRASTIRQ-EYFPGD 17
 CC Db 10 MALEAKICHOIEYFPGD 27
 CC [1]
 CC RESULT 6
 CC LA_MOUSE STANDARD; PRT; 415 AA.
 CC AC P32067;
 CC DT 01-OCT-1993 (Rel. 27, Created)
 CC DT 01-OCT-1993 (Rel. 27, Last sequence update)
 CC DT 15-MAR-2004 (Rel. 43, Last annotation update)
 CC DE Lupus La protein homolog (La ribonucleoprotein) (La autoantigen
 CC homolog).
 CC GN SSB OR SS-B.
 CC OS Mus musculus (Mouse).
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC RX MEDLINE=93203630; PubMed=8454877;
 CC RA Topfer F., Gordon T., McCluskey J.;
 RT "Characterization of the mouse autoantigen La (SS-B). Identification
 RT of conserved RNA-binding motifs, a putative ATP binding site and
 RT reactivity of recombinant protein with poly(U) and human
 RL J. Immunol. 150:3091-3100(1993).
 CC [2]
 CC SEQUENCE FROM N.A.

[1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=MAF030309;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asanizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Ideesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.,
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 Mesorhizobium loti."
 RL DNA Res. 7:331-338(2000).
 CC -1- CATALYTIC ACTIVITY: ATP + L-histidine + tRNA(His) = AMP +
 CC dihydrophate + L-histidyl-tRNA(His).
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
 CC -----
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 CC -----
 CC EMBL; AF003010; BAB53120.1; -.
 DR HAMAP; MF_00127; -; 1.
 DR InterPro; IPR004154; HGRP_anticonodon.
 DR InterPro; IPR004516; HisP.
 DR InterPro; IPR002314; tRNA-synt_2b.
 DR InterPro; IPR006195; tRNA_ligase_1t.
 DR Pfam; PF03129; HGRP_anticonodon; 1.
 DR Pfam; PF00587; tRNA-synt_2b; 1.
 DR TIGRFAMs; TIGR00442; hisS; 1.
 DR PROSITE; PS50862; AA tRNA LIGASE II; 1.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 SQ SEQUENCE 500 AA; 54546 MW; 290E8B18CA2DF84 CRC64;
 QY
 Db 1 VKLEASTRQRYFGDA 18
 398 VSELRAAGIRSEWYLGGA 415
 Query Match 50.0%; Score 45; DB 1; Length 500;
 Best Local Similarity 55.6%; Pred. No. 3.4;
 Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

CC polymerase III. It is most probably a transcription termination
 CC factor. Binds to the 3' termini of virtually all nascent
 CC polymerase III transcripts. It is associated with precursor forms
 CC of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S,
 CC and 7-2 RNAs.
 CC -1- SUBUNIT: Interacts with DDX15 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- PTM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES ARE AT THE
 CC C-TERMINAL PART OF THE PROTEIN.
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X13698; CAA31986.1; -.
 DR PIR; S03849; S03849.
 DR InterPro; IPR002344; Lups_La.
 DR InterPro; IPR00630; Lups_La_dom.
 DR InterPro; IPR00504; RNA_rec_mot.
 DR Pfam; PF05383; La; 1.
 DR Pfam; PF00076; rrm; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PS50102; RRM; 1.
 DR PROSITE; PS00030; RRM_RNP_1; 1.
 KW RNA-binding; Nuclear protein; Phosphorylation.
 FT DOMAIN 111
 187
 RNA-BINDING (RRM).
 SQ SEQUENCE 404 AA; 46534 MW; 4EE30B5C262A26A1 CRC64;
 QY
 Db 1 VKLEASTRQRYFGD 17
 10 MALEAKICHQIEYFGD 27
 Query Match 48.3%; Score 43.5; DB 1; Length 404;
 Best Local Similarity 55.6%; Pred. No. 5;
 Matches 10; Conservative 2; Mismatches 5; Indels 1; Gaps 1;
 RESULT 5
 LA HUMAN
 ID LA HUMAN STANDARD; PRT; 408 AA.
 AC P05455;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Lups La protein (Sjogren syndrome type B antigen) (SS-B) (La
 DE ribonucleoprotein) (La autoantigen).
 GN SSB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RX MEDLINE=89053970; PubMed=2468131;
 RA Chan E.K.L., Sullivan K.F., Tan E.M.;
 RT "Ribonucleoprotein SS-B/La belongs to a protein family with consensus
 RT sequences for RNA-binding."
 RT Nucleic Acids Res. 17:2233-2244(1989).
 RN [12]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89053970; PubMed=3192525;
 RA Chambers J.C., Kenan D., Martin B.J., Keane J.D.;
 RT "Genomic structure and amino acid sequence domains of the human La
 RT autoantigen."
 RN J. Biol. Chem. 263:18043-18051(1988).
 RN [3]

DB 40 VSKLEASTIRQLEYFGDA 58

RESULT 2

LA DROME STANDARD; PRT; 390 AA.

AC P40796; Q24375; Q9VIN2;

DT 01-FEB-1995 (Rel. 31, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE La protein homolog (La ribonucleoprotein) (La autoantigen homolog).

GN LA OR CG10922.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RP [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Canton-S; TISSUE=Ovary;

RC MEDLINE=94309632; PubMed=8035794;

RA Bai C., Li Z., Tolias P.P.;

RT "Developmental characterization of a Drosophila RNA-binding protein homologous to the human systemic lupus erythematosus-associated La/SS-B autoantigen";

RT Mol. Cell. Biol. 14:5123-5129 (1994).

RN [2]

RN SEQUENCE FROM N.A.

RX MEDLINE=94309661; PubMed=8035818;

RX Yoo C.J., Molin S.L.;

RT "La proteins from Drosophila melanogaster and Saccharomyces cerevisiae: a yeast homolog of the La autoantigen is dispensable for growth";

RT Mol. Cell. Biol. 14:5412-5424 (1994).

RN [3]

RN SEQUENCE FROM N.A.

RC STRAIN=Berkley;

RC MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle J.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abail J.F., Agbayani A., An H.-J., Andrews-Pfankuch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.V., Benos P.V., Bertan B.P., Bhandari D., Bolshakov S., Borkov D., Botchan M.R., Bouck J., Brokstein P., Brothier P., Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fowler C., Gabrielian A.E., Gang N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclik J.M., Palazuelos M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier B., Spradling A.C., Stapleton M., Strong R., Sun E., Svoboda R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RT Science 287:2185-2195 (2000).

CC -1- FUNCTION: May be involved in transcription termination by RNA polymerase III. Binds RNA and DNA. Binds to precursors of RNA development.

CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).

CC -1- DEVELOPMENTAL STAGE: Expressed throughout embryonic, larval, pupal, and adult development. Expression throughout the embryo is followed by a restricted pattern of mesodermal expression that is later confined to the visceral mesoderm, gonads, gut, and salivary glands.

CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.

CC -1- SIMILARITY: TO VERTEBRATE PROTEIN LA.

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CC -----

DR EMBL; U07652; AAA20518.1; -

DR EMBL; L32988; AAA21776.1; -

DR EMBL; AE003666; AA53885.1; -

DR PIR; A53773; A53773.

DR PIR; A53781; A53781.

DR FLYBase; FBgn0011638; La.

DR GO; GO:0008098; P:5S rRNA primary transcript binding; IDA.

DR GO; GO:0003723; F:RNA binding; NAS.

DR InterPro; IPR002344; Lupus_La.

DR InterPro; IPR006630; Lupus_La_dom.

DR InterPro; IPR00504; RNA_rec_mot.

DR Pfam; PF05383; La; 1.

DR Pfam; PF00076; rrm; 1.

DR PRINTS; PR00302; LUPUSLA.

DR SMART; SM00715; LA; 1.

DR SMART; SM00360; RRM; 1.

DR PROSITE; PS50102; RRM; 1.

DR PROSITE; PS00303; RRM_NRP_1; 1.

DR KEGG; K04499; Nuclear protein; DNA-binding.

FT DOMAIN 149 234

FT CONFLICT 169 169 A -> T (IN REF. 1).

FT CONFLICT 182 183 KH -> NS (IN REF. 1).

FT CONFLICT 283 283 A -> R (IN REF. 1).

FT CONFLICT 329 329 K -> N (IN REF. 1).

SO SEQUENCE 390 AA; 44884 MW; A809928B8904655 CRC64;

QY 2 SKLEASTIRQLEYFGDA 18

DB 48 TKQERATIRQLEYFGDA 65

Query Match 58.3%; Score 52.5; DB 1; Length 390;

Best local similarity 66.7%; Pred. No. 0.12;

Matches 12; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

RESULT 3

SYN_RHIL0 STANDARD; PRT; 500 AA.

AC Q98770;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase) (HISRS).

GN HIS5 OR MUR6928.

OS Rhizobium loti (Mesorhizobium loti).

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Phyllobacteriaceae; Mesorhizobium.

OX NCBI_TaxID=381;

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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:01:41; Search time 7.24022 Seconds
(without alignments)
129,452 Million cell updates/sec

Title: US-09-836-073-18

Perfect score: 90

Sequence: 1 VSKLEASTTROEYFGDA 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	79.5	88.3	383	1 LA_AEDAL	Q26457 aedes albop
2	52.5	58.3	390	1 LA_DROME	P40796 drosophila
3	45	50.0	500	1 SYH_RHILLO	Q98760 rhizobium 1
4	43.5	48.3	404	1 LA_BOVIN	P10981 bos taurus
5	43.5	48.3	408	1 LA_HUMAN	P05455 homo sapien
6	43.5	48.3	415	1 LA_MOUSE	P32067 mus musculu
7	43.5	48.3	415	1 LA_MOUSE	P32582 rattus norv
8	43	47.8	507	1 CBS_YEAST	P30321 archaeoglob
9	40	44.4	112	1 YN48_ARCFU	P23292 saccharomyc
10	40	44.4	546	1 CK12_YEAST	Q99ct1 staphylococ
11	40	44.4	876	1 SYA_STAM	Q8nw87 staphylococ
12	40	44.4	876	1 SYA_STAM	Q8nw87 staphylococ
13	39	43.3	314	1 PYRB_DEIRA	Q9rvco delinococcus
14	39	43.3	431	1 UL61_HCVIVA	P16818 human cytom
15	39	43.3	533	1 YFS9_HUMAN	Q9hcl3 homo sapien
16	39	43.3	550	1 SYR_CORGL	P35868 corynebacte
17	39	43.3	778	1 SZ1B_BRARE	Q9w686 brachydanio
18	39	43.3	904	1 SYA_SULO	Q971j4 sulfolobus
19	38.5	42.8	1234	1 CFAH_MOUSE	F06909 mus musculu
20	38	42.2	212	1 OMPW_ECOLI	P21364 escherichia
21	38	42.2	230	1 VIB8_AGRU	P09781 agrobacteri
22	38	42.2	230	1 VIB8_AGRU	P09781 agrobacteri
23	38	42.2	540	1 Y968_TREPA	Q83934 treponema p
24	38	42.2	551	1 SYR_CHLITE	Q83934 treponema p
25	38	42.2	607	1 HTPG_FUSNN	Q9hgm4 fusobacteri
26	38	42.2	727	1 VK82_SCHPO	Q9hgm4 fusobacteri
27	38	42.2	771	1 SM3A_HUMAN	Q14563 homo sapien
28	38	42.2	772	1 SM3A_CHICK	Q90607 gallus gall
29	38	42.2	772	1 SM3A_MOUSE	Q90607 gallus gall
30	38	42.2	772	1 SM3A_MOUSE	Q90607 gallus gall
31	38	42.2	876	1 SYA_STARP	Q83548 rattus norv
32	37.5	41.7	387	1 SUCC_MYCTU	Q83548 rattus norv
33	37.5	41.7	393	1 SUCC_MYCTU	Q83548 rattus norv

34	37.5	41.7	428	1 LAA_XENLA	P28048 xenopus lae
35	37	41.1	268	1 Y1AJ_HAEIN	P44996 haemophilus
36	37	41.1	312	1 KPR5_CAUCR	Q9496 caulobacter
37	37	41.1	332	1 MYOD_DROME	P22816 drosophila
38	37	41.1	339	1 MURG_THEMA	Q9w774 thermotoga
39	37	41.1	422	1 U183_CAEEL	P34692 caenorhabdi
40	37	41.1	427	1 LAB_XENLA	P28049 xenopus lae
41	37	41.1	433	1 SUDB_SCHPO	Q94415 schizosacch
42	37	41.1	471	1 YMT1_CAEEL	P98080 caenorhabdi
43	37	41.1	550	1 SYR_MYCSM	Q9x5m0 mycobacteri
44	37	41.1	556	1 SYR_LISIN	Q927t2 listeria in
45	37	41.1	556	1 SYR_LISMO	Q8y493 listeria mo

ALIGNMENTS

RESULT 1
LA_AEDAL STANDARD; PRT; 383 AA.
AC Q26457;
DT 15-JUL-1998 (rel. 36, Last sequence update)
DT 15-JUL-1998 (rel. 36, Last sequence update)
DT 28-FEB-2003 (rel. 41, Last annotation update)
DE La protein homolog (la ribonucleoprotein) (la autoantigen homolog).
OS Aedes albopictus (Forest day mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes.
ON NCBI_Taxid=7160;
RX MEDLINE=96135233; PubMed=8551578;
RA Pardigon N., Straus J.H.;
RT "Mosquito homolog of the la autoantigen binds to Sindbis virus RNA.";
RL J. Virol. 70:1173-1181 (1996).
CC -1- FUNCTION: May be involved in transcription termination by RNA
CC polymerase III. Binds RNA and DNA. Binds to the 3' end of the
CC minus strand of Sindbis virus RNA. This may be significant for
CC Sindbis virus RNA replication.
CC -1- SUBCELLULAR LOCATION: Nuclear. Primarily nuclear, but significant
CC amounts are present in the cytoplasm.
CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
CC -1- SIMILARITY: TO VERTEBRATE PROTEIN LA.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; S80954; AAB35931.1; -
DR InterPro; IPR002344; Lupus Ia.
DR InterPro; IPR006630; Lupus Ia dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00715; La; 1.
DR SMART; SM00715; La; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PSS0102; RRM; 1.
DR PROSITE; PSS0030; RRM_RNP_1; FALSE NEG.
KW RNA-Binding; Nuclear protein; DNA-Binding.
FT DOMAIN 141 228 RNA-BINDING (RRM).
SQ SEQUENCE 383 AA; 44430 MW; 4E5CC8F21C40F452 CRC64;
Query Match 88.3%; Score 79.5; DB 1; Length 383;
Best Local Similarity 94.7%; Pred. No. 1.8e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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A;introns: 29/1

Query Match 45.6%; Score 41; DB 2; Length 633;
 Best Local Similarity 53.3%; Pred. No. 37;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 KLEASTIROEYFGD 17
 | : | | | | : |
 DB 353 KKDARTIIQYFLSD 367

RESULT 14

D70117

acridiavine resistance protein (acrB) homolog - Lyme disease spirochete

C;Species: Borrelia burgdorferi (Lyme disease spirochete)

C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 17-Mar-2000

C;Accession: D70117

R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Iathigra, R.; White

son, D.; Peterson, J.; Ketzavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,

i Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997

A;Authors: Smith, H.O.; Venter, J.C.

A;Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.

A;Reference number: A70100; PMID:9805943; PMID:9403685

A;Accession: D70117

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-1036 <KLE>

A;Cross-references: GB:AE000783; TIGR:BB0140

A;Experimental source: strain B31

C;Superfamily: cation efflux system membrane protein czcA

Query Match 45.6%; Score 41; DB 2; Length 1036;
 Best Local Similarity 50.0%; Pred. No. 65;
 Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 VSKLEASTIROEYFG 16
 | | | | | : | | | |
 DB 82 VSKKSTIVSLRPHG 97

RESULT 15

D69543

hypothetical protein AF2348 - Archaeoglobus fulgidus

C;Species: Archaeoglobus fulgidus

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999

C;Accession: D69543

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

. ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A;Authors: Ueterbach, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Woese, C.R.; Venter, J.C.

A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

A;Reference number: A69250; PMID:98049343; PMID:9389475

A;Accession: D69543

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-112 <KLE>

A;Cross-references: GB:AE001114; GB:AE000782; NID:92689437; PIDN:AAB91315.1; PID:9265074

C;Superfamily: Archaeoglobus fulgidus hypothetical protein AF2348

Query Match 44.4%; Score 40; DB 2; Length 112;
 Best Local Similarity 47.1%; Pred. No. 7.6;
 Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 SKLEASTIROEYFGDA 18
 | : | | | | : |
 DB 3 SRSRKSIVLQDYRGS 19

Search completed: September 10, 2004, 18:02:39
 Job time: 16.0782 secs

Query Match 46.7%; Score 42; DB 2; Length 451;
 Best Local Similarity 53.3%; Pred. No. 16;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 4 LEASTROEYFGDA 18
 |||:|:|:|:|:|
 Db 187 LEANNAOKEYVLTDA 201

RESULT 9

T06586
 DNA-binding protein PD2 - garden pea
 C:Species: Pisum sativum (garden pea)
 C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
 C:Accession: T06586
 R:Sato, N.; Kazuno, A.A.; Ohta, N.; Ohshima, K.
 submitted to the EMBL Data Library, June 1996
 A:Description: Identification of a novel family of DNA-binding proteins with two AT-hook
 A:Reference number: Z15774
 A:Accession: T06586
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-632 <SAT>
 A:Cross-references: EMBL:X98740; NID:e995229; PIDN:CAA67292.1; PID:e275185
 A:Experimental source: cv. Alaska

Query Match 46.7%; Score 42; DB 2; Length 632;
 Best Local Similarity 50.0%; Pred. No. 24;
 Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 LEASTROEYFGD 17
 |||:|:|:|:|:|
 Db 161 VEATVSDDEYTYGD 174

RESULT 10

H83743
 ABC transporter (permease) BH0752 [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C:Accession: H83743
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirai
 Nucleic Acids Res. 28, 4317-4331, 2000
 A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: H83743
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-642 <STO>
 A:Cross-references: GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BAE04471.1; GSPDB:GN00
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH0752

Query Match 46.7%; Score 42; DB 2; Length 642;
 Best Local Similarity 53.8%; Pred. No. 24;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 EASTROEYFGD 17
 |||:|:|:|:|:|
 Db 472 EKALVHBEYFGD 484

RESULT 11

C96636
 hypothetical protein T7P1.19 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: C96636
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: C96636
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-322 <STO>
 A:Cross-references: GB:AE005173; NID:g6751694; PIDN:AAF27677.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: T7P1.19
 A:Map position: 1

Query Match 45.6%; Score 41; DB 2; Length 322;
 Best Local Similarity 64.3%; Pred. No. 17;
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VSKLEASTROEY 14
 |||:|:|:|:|:|
 Db 44 VSKLMSQIRRPY 57

RESULT 12

B87591
 cytochrome c-type biogenesis protein Cych [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 30-Sep-2002
 C:Accession: B87591
 R:Nierman, W.C.; Feldblym, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.U.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon,
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A>Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: B87591
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-370 <STO>
 A:Cross-references: GB:AE005673; NID:g13424358; PIDN:AAK24726.1; GSPDB:GN00148
 C:Genetics:
 A:Gene: CC2762
 C:Superfamily: cych protein

Query Match 45.6%; Score 41; DB 2; Length 370;
 Best Local Similarity 43.8%; Pred. No. 20;
 Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 KLEASTROEYFGDA 18
 |||:|:|:|:|:|
 Db 220 KVDAADVARYYLGRA 235

RESULT 13

T06703
 hypothetical protein T29H11.90 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 22-Oct-1999
 C:Accession: T06703
 R:Querier, F.; Choisme, N.; Robert, C.; Brottier, P.; Wincker, P.; Catolico, L.; Artigun,
 submitted to the Protein Sequence Database, April 1999
 A:Reference number: Z15793
 A:Accession: T06703
 A:Molecule type: DNA
 A:Residues: 1-633 <QUE>
 A:Cross-references: EMBL:AL049659; GSPDB:GN00061; ATSP:T29H11.90
 A:Experimental source: cultivar Columbia; BAC clone T29H11
 C:Genetics:
 A:Gene: ATSP:T29H11.90
 A:Map position: 3

F:112-178/Domain: ribonucleoprotein repeat homology <RRM>
 A:Reference number: S42686; MUID:94287710; PMID:8017103
 A:Accession: S42686
 F:151-158/Region: RNA-binding RNP1 motif
 F:228-408/Domain: phosphorylated #status experimental <PHY>

Query Match 48.3%; Score 43.5; DB 1; Length 408;
 Best Local Similarity 55.6%; Pred. No. 7.7;
 Matches 10; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 1 VKLEASTIRQ-EYFGD 17
 DB 10 MALEAKICHQIEYFGD 27

RESULT 6
 UCI494

ribonucleoprotein la - rat
 N:Alternate names: autoantigen SS-B/la; ribonucleoprotein SS-B
 C:Species: Rattus norvegicus (Norway rat)

C>Date: 24-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999

A:Accession: UCI494; S25145

R:Semmel, I.; Troester, H.; Bartsch, H.; Schwemmler, M.; Igloi, G.L.; Bachmann, M.

Gene 126, 265-268, 1993

A:Title: Isolation of rat cDNA clones coding for the autoantigen SS-B/la: Detection of B

A:Reference number: UCI494; MUID:93246255; PMID:7916708

A:Accession: UCI494

A:Molecule type: mRNA

A:Residues: 1-415 <SEM>

A:Cross-references: GB:X67859; NID:955778; PIDN:CAA48043.1; PID:955779

A:Experimental source: liver

C:Comment: This protein associates with a variety of small RNA molecules, most of which

act as a transcription termination factor.

C:Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology

C:Keywords: phosphoprotein; RNA binding

F:112-178/Domain: ribonucleoprotein repeat homology <RRM>

F:113-118/Region: RNA-binding RNP1 motif

F:151-158/Region: RNA-binding RNP1 motif

F:227-415/Domain: phosphorylated #status predicted <PHY>

Query Match

Best Local Similarity 55.6%; Score 43.5; DB 1; Length 415;
 Pred. No. 7.9;
 Matches 10; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 1 VKLEASTIRQ-EYFGD 17
 DB 10 MALEAKICHQIEYFGD 27

RESULT 7

cyathionine beta-synthase (EC 4.2.1.22) - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein G667; protein YGR155w

C:Species: Saccharomyces cerevisiae

C>Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 21-Jul-2000

A:Accession: A48601; S48505; S42686; S60445; B55760; S64464; S33202

R:Cherest, H.; Thomas, D.; Surdin-Kerjan, Y.

U. Bacteriol. 175, 5366-5374, 1993

A:Title: Cysteine biosynthesis in Saccharomyces cerevisiae occurs through the transsulfit

A:Reference number: A48601; MUID:93374830; PMID:8366024

A:Accession: A48601

A:Molecule type: DNA

A:Residues: 1-507 <CHE>

A:Cross-references: GB:X72922; NID:9296134; PIDN:CAA51426.1; PID:9296135

R:Ono, B.I.; Inoue, T.; Kijima, K.; Matsuda, A.; Negishi, K.; Shinoda, S.

submitted to the EMBL Data Library, June 1993

A:Description: Identification of the structural gene of cyathionine beta-synthase in S

A:Reference number: S48505

A:Accession: S48505

A:Molecule type: DNA

A:Residues: 1-292, 'r', 294-507 <ONO>

A:Cross-references: EMBL:DJ6502; NID:9391939; PIDN:BA03952.1; PID:9416161

R:Ono, B.I.; Kijima, K.; Inoue, T.; Miyoshi, S.I.; Matsuda, A.; Shinoda, S.

Yeast 10, 333-339, 1994

A:Title: Purification and properties of Saccharomyces cerevisiae cyathionine beta-syn

A:Reference number: S42686; MUID:94287710; PMID:8017103

A:Accession: S42686

A:Molecule type: protein

A:Residues: 2-11 <ON2>

R:Skala, U.; Nawrocki, A.; Goffeau, A.

Yeast 11, 1421-1427, 1995

A:Title: The sequence of a 27 kb segment on the right arm of chromosome VII from Saccha

A:Reference number: S60435; MUID:96158062; PMID:858525

A:Accession: S60445

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-507 <SKA>

A:Cross-references: EMBL:X85807; NID:91045249; PIDN:CAA59812.1; PID:91045260

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1995

R:Kluger, W.D.; Cox, D.R.

Proc. Natl. Acad. Sci. U.S.A. 91, 6614-6618, 1994

A:Title: A yeast system for expression of human cyathionine beta-synthase: structural

A:Reference number: A55760; MUID:94294429; PMID:8022826

A:Accession: B55760

A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tr

A:Molecule type: DNA

A:Residues: 1-61,63-128,'V',130-406,'Y',408-435,'VE',438-440,'V',442-480,'E',482-507 <K

A:Cross-references: GB:J14578

R:Van Dyck, L.; Skala, U.; de Wergifosse, P.; Purnelle, B.; Talia, E.; Nawrocki, A.; Del

submitted to the Protein Sequence Database, May 1996

A:Reference number: S64428

A:Accession: S64464

A:Molecule type: DNA

A:Residues: 1-507 <EMV>

A:Cross-references: EMBL:Z72940; NID:91323262; PIDN:CAA97169.1; PID:91323263; MIPS:YGR1

A:Experimental source: strain S288C

C:Genetics: SCD:CY84, STR4

A:Gene: SCD:CY84, STR4

A:Cross-references: SGD:S0003387; MIPS:YGR155w

A:May position: 7R

C:Keywords: carbon-oxygen lyase; cyathionine beta-synthase; homotetramer; hydro-lyase; phos

F:2-507/Product: cyathionine beta-synthase #status experimental <MAT>

F:376-424/Domain: CBS homology <CBS>

F:53/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 47.8%; Score 43; DB 2; Length 507;
 Best Local Similarity 58.8%; Pred. No. 12;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 SKLEASTIRQYFGDA 18
 DB 351 SKLEASTIRQYFGDA 367

RESULT 8
 AB2296
 UDP-N-acetylglucosamine pyrophosphorylase [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

A>Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

A:Accession: AB2296

R:Kaneko, T.; Nakamura, Y.; Wolik, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuch

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata,

DNA Res. 8, 205-213, 2001

A:Title: Complete genomic sequence of the filamentous Nitrogen-fixing Cyanobacterium An

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AB2296

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-451 <NUR>

A:Cross-references: GB:BA000019; PIDN:BA075620.1; PID:gl7133055; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: alr3921

C:Superfamily: N-acetylglucosamine-1-phosphate uridylyltransferase

Best Local Similarity 66.7%; Pred. No. 0.17;
Matches 12; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Oy 2 SKLEASTIRQ-EYFGDA 18
Db 48 TKQERAIRQVYFPGDA 65

RESULT 3

T10213
hypothetical protein F25G13.200 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999

C:Accession: T10213

R:Chan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Meyer, K.F.X.; Lemcke

submitted to the Protein Sequence Database, June 1999

A:Reference number: Z16991

A:Accession: T10213

A:Molecule type: DNA

A:Residues: 1-365 <BEV>

A:Cross-references: EMBL:X13697; GSPDB:GN00062; ATSP:F25G13.200

A:Experimental source: cultivar Columbia; BAC clone F25G13

C:Genetics:

A:Gene: ATSP:F25G13.200

A:Map position: 4

A:Introns: 55/2

Query Match 48.9%; Score 44; DB 2; Length 365;
Best Local Similarity 38.9%; Pred. No. 5.5;
Matches 7; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Oy 1 VSKLEASTIRQVYFGDA 18
Db 8 ILRCSSCTMRSEYFPHDA 25

RESULT 4

S03849
ribonucleoprotein La - bovine

N:Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B

C:Species: Bos primigenius taurus (cattle)

C:Date: 31-Dec-1990 #sequence_revision 26-May-1994 #text_change 22-Jun-1999

C:Accession: S03849

R:Chan, E.K.L.; Sullivan, K.F.; Tan, E.M.

Nucleic Acids Res. 17, 2233-2244, 1989

A:Title: Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences

A:Reference number: S03848; MUID:89202037; PMID:2468131

A:Accession: S03849

A:Molecule type: mRNA

A:Residues: 1-404 <CHA>

A:Cross-references: EMBL:X13698; NID:9755; PIDN:CAA31986.1; PID:9756

A>Note: part of this sequence was confirmed by protein sequencing

C:Comment: This protein associates with a variety of small RNA molecules, most of which

act as a transcription termination factor.

C:Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology

C:Keywords: blocked amino end; phosphoprotein; RNA binding

F:113-118/Region: ribonucleoprotein repeat homology <RNR>

F:113-118/Region: RNA-binding RNP2 motif

F:151-158/Region: RNA-binding RNP1 motif

F:128-404/Domain: phosphorylated #status predicted <PHY>

Query Match 48.3%; Score 43.5; DB 1; Length 404;
Best Local Similarity 55.6%; Pred. No. 7.6;
Matches 10; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Oy 1 VSKLEASTIRQ-EYFGD 17
Db 10 MAALAKICHQIEYFGD 27

RESULT 5

A31888
ribonucleoprotein La - human

N:Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B; Sjogren syndrome antigen

C:Species: Homo sapiens (man)

C:Date: 21-May-1990 #sequence_revision 26-May-1994 #text_change 22-Jun-1999

C:Accession: A31888; S03848; A22956; A61051; S11013; I55553; I70205; I70206; A31273

R:Chambers, J.C.; Kenan, D.; Martin, B.J.; Keene, J.D.

J. Biol. Chem. 263, 18043-18051, 1988

A:Title: Genomic structure and amino acid sequence domains of the human La autoantigen.

A:Reference number: A31888; MUID:89053970; PMID:3192525

A:Accession: A31888

A:Molecule type: mRNA

A:Residues: 1-408 <CHA>

A:Cross-references: GB:J04205; NID:9178686; PIDN:AAA51885.1; PID:9178687

R:Chan, E.K.L.; Sullivan, K.F.; Tan, E.M.

Nucleic Acids Res. 17, 2233-2244, 1989

A:Title: Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences

A:Reference number: S03848; MUID:89202037; PMID:2468131

A:Accession: S03848

A:Molecule type: mRNA

A:Residues: 1-408 <CH2>

A:Cross-references: EMBL:X13697; NID:936414; PIDN:CAA31985.1; PID:936415

R:Chambers, J.C.; Keene, J.D.

Proc. Natl. Acad. Sci. U.S.A. 82, 2115-2119, 1985

A:Title: Isolation and analysis of cDNA clones expressing human lupus La antigen.

A:Reference number: A22956; MUID:85166283; PMID:3856888

A:Accession: A22956

A:Molecule type: mRNA

A:Residues: 45-97, 'LK' <CH3>

A:Cross-references: GB:J04205

A>Note: this sequence has been revised in reference A31888

R:Nyman, U.; Ringertz, N.R.; Petersson, I.

Immunol. Lett. 22, 65-72, 1989

A:Title: Demonstration of an amino terminal La epitope recognized by human anti-La sera.

A:Reference number: A61051; MUID:89379261; PMID:2476379

A:Accession: A61051

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-19, 'E', '21-47 <NYM>

R:Sturges, A.D.; Peterson, M.G.

J. Immunol. 140, 3212-3218, 1988

A:Title: Characteristics and epitope mapping of a cloned human autoantigen La.

A:Reference number: S11013; MUID:88199081; PMID:2425201

A:Accession: S11013

A:Molecule type: mRNA

A:Residues: 'E', 55-287, 'V', 289-408 <STU>

A:Cross-references: EMBL:M20328; NID:9337456; PIDN:AAA6577.1; PID:9337457

R:Kohsaka, H.; Yamamoto, K.; Fujii, H.; Mura, H.; Miyasaka, N.; Nishioaka, K.; Miyamoto, J.

Clin. Invest. 85, 1566-1574, 1990

A:Title: Fine epitope mapping the human SS-B/La protein: Identification of a distinct au

A:Reference number: I55553; MUID:90237237; PMID:1692037

A:Accession: I55553

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 81-107 <RES>

A:Cross-references: GB:M5261; NID:9338491; PIDN:AAA36652.1; PID:9338495

A:Accession: I70205

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 174-224 <RE2>

A:Cross-references: GB:M5263; NID:9338492; PIDN:AAA36653.1; PID:9338496

A:Accession: I70206

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 279-342 <RE3>

A:Cross-references: GB:M5262; NID:9338493; PIDN:AAA36654.1; PID:9338497

C:Comment: This protein associates with a variety of small RNA molecules, most of which

act as a transcription termination factor.

C:Genetics:

A:Gene: GDB:SSB

A:Cross-references: GDB:125359; OMIM:109090

A:Map position: 2

A:Introns: 22/3; 57/2; 115/3; 151/3; 185/2; 209/2; 223/3; 264/3; 380/2

C:Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology

C:Keywords: phosphoprotein; RNA binding

; PRIOR FILING DATE: 1999-05-21
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 19
 ; LENGTH: 16,
 ; TYPE: PRT
 ; ORGANISM: Drosophila
 US-09-836-073-19

Query Match 52.6%; Score 50; DB 9; Length 16;
 Best Local Similarity 57.1%; Pred. No. 0.37;
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 QY 4 DQRIKQLEYYFEN 17
 Db 2 ERAIRQVEYFED 15

Search completed: September 10, 2004, 18:11:57
 Job time : 41.424 secs

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RESULT 11
US-10-424-599-254664
; Sequence 254664, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 254664
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_71985C.1.pep
US-10-424-599-254664

Query Match          53.7%; Score 51; DB 12; Length 395;
Best Local Similarity 52.9%; Pred. No. 7.6;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy      1 DDADQRIIKQLEYFGNI 17
Db      101 EDLKLKIKQVEYFSD 117

RESULT 12
US-10-767-701-46290
; Sequence 46290, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 46290
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBR-28WAY03-C18446_1.pep
US-10-767-701-46290

Query Match          53.7%; Score 51; DB 16; Length 489;
Best Local Similarity 50.0%; Pred. No. 9.5;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy      1 DDADQRIIKQLEYFGNI 18
Db      133 DEVVHKITKQVEYFSDI 150

RESULT 13
US-10-425-114-69520
; Sequence 69520, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
```

```
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 69520
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73030C03_FLI.pep
US-10-425-114-69520

Query Match          53.7%; Score 51; DB 12; Length 490;
Best Local Similarity 50.0%; Pred. No. 9.5;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy      1 DDADQRIIKQLEYFGNI 18
Db      131 DEVVHKITKQVEYFSDI 148

RESULT 14
US-10-437-963-106767
; Sequence 106767, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 106767
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_11181C.1.pep
US-10-437-963-106767

Query Match          53.7%; Score 51; DB 16; Length 511;
Best Local Similarity 50.0%; Pred. No. 10;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy      1 DDADQRIIKQLEYFGNI 18
Db      117 DEVVHKITKQVEYFSDI 134

RESULT 15
US-09-836-073-19
; Sequence 19, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
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Best Local Similarity 52.9%; Pred. No. 2.4;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 DDADQRIIKOLEYFGN 17
|:|:|:|:|:|:|:
DB 132 DELCDRIYKQVEYFSD 148

RESULT 7

US-10-437-963-179489
; Sequence 179489, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 179489
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_76947C.1.pep
US-10-437-963-179489

Query Match 56.8%; Score 54; DB 16; Length 453;
Best Local Similarity 38.9%; Pred. No. 2.9;
Matches 7; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDADQRIIKOLEYFGN 18
|:|:|:|:|:|:|:
DB 105 EDVARRVKQVEYFSDV 122

RESULT 8

US-10-437-963-134637
; Sequence 134637, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 134637
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_36391C.1.pep
US-10-437-963-134637

Query Match 55.8%; Score 53; DB 16; Length 405;
Best Local Similarity 52.9%; Pred. No. 3.7;

Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 DDADQRIIKOLEYFGN 17
|:|:|:|:|:|:|:
DB 85 DELCDRIYKQVEYFSD 101

RESULT 9

US-10-424-599-254661
; Sequence 254661, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 254661
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_71982C.1.pep
US-10-424-599-254661

Query Match 53.7%; Score 51; DB 12; Length 143;
Best Local Similarity 52.9%; Pred. No. 2.6;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 DDADQRIIKOLEYFGN 17
|:|:|:|:|:|:|:
DB 101 EDLKLKIKQVEYFSD 117

RESULT 10

US-10-425-114-66921
; Sequence 66921, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack B
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 66921
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB71148E12_Flt.pep
US-10-425-114-66921

Query Match 53.7%; Score 51; DB 12; Length 357;
Best Local Similarity 55.6%; Pred. No. 6.8;
Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DDADQRIIKOLEYFGN 18
|:|:|:|:|:|:|:
DB 163 DDVPRKIKQVEYFSDI 180

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; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 258877
; LENGTH: 174
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_75790C.1.pep
US-10-424-599-258877

Query Match      62.1%; Score 59; DB 12; Length 174;
Best Local Similarity 50.0%; Pred. No. 0.17;
Matches 9; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy      1 DDADQRIIKQLEYFGNT 18
Db      156 DEASQKILNQVEYFSDL 173

RESULT 3
US-10-424-599-258874
; Sequence 258874, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 258874
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(467)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_75788C.1.pep
US-10-424-599-258874

Query Match      62.1%; Score 59; DB 12; Length 467;
Best Local Similarity 50.0%; Pred. No. 0.48;
Matches 9; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy      1 DDADQRIIKQLEYFGNT 18
Db      148 DEASQKILNQVEYFSDL 165

RESULT 4
US-10-177-478-8
; Sequence 8, Application US/10177478
; Publication No. US20030165903A1
; GENERAL INFORMATION:
; APPLICANT: Dang Van-Dinh
; APPLICANT: Okamura, Jack
; TITLE OF INVENTION: Chimeric Histone Acetyltransferase
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 11696-037001
; CURRENT APPLICATION NUMBER: US/10/177,478
; CURRENT FILING DATE: 2002-06-21
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; PRIOR APPLICATION NUMBER: U.S. 60/300,135
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-177-478-8

Query Match      60.0%; Score 57; DB 14; Length 411;
Best Local Similarity 52.9%; Pred. No. 0.87;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy      1 DDADQRIIKQLEYFGN 17
Db      90 DELNQKILNQVEYFSD 106

RESULT 5
US-09-836-073-15
; Sequence 15, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baladya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 22002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Xenopus
US-09-836-073-15

Query Match      57.9%; Score 55; DB 9; Length 18;
Best Local Similarity 56.2%; Pred. No. 0.067;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy      2 DADQRIIKQLEYFGN 17
Db      2 DLDTRKICQIYFQGD 17

RESULT 6
US-10-767-701-45524
; Sequence 45524, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 45524
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28WAY03-C33606_1.pep
US-10-767-701-45524

Query Match      56.8%; Score 54; DB 16; Length 376;
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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:52:06 ; Search time 40.324 Seconds
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Title: US-09-836-073-17

Sequence: 1 DDADQRIIKQLEYFGNI 18

Scoring table: BLOSUM62

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Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

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15: /cgn2_6/prodata/1/pubppa/US10_PUBCOMB.pep:*
16: /cgn2_6/prodata/1/pubppa/US10_NEW_PUB.pep:*
17: /cgn2_6/prodata/1/pubppa/US60_NEW_PUB.pep:*
18: /cgn2_6/prodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the distribution.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	100.0	18	9	US-09-836-073-17
2	59	62.1	174	12	Sequence 17, Appl
3	59	62.1	467	12	Sequence 258877,
4	57	60.0	411	14	Sequence 258874,
5	55	57.9	18	9	US-10-424-599-258874
6	54	56.8	376	16	US-10-177-478-8
7	54	56.8	453	16	US-09-836-073-15
8	53	55.8	405	16	US-10-437-963-145524
9	51	53.7	143	12	Sequence 179489,
10	51	53.7	357	12	Sequence 134637,
11	51	53.7	395	12	Sequence 254661,
12	51	53.7	489	16	Sequence 66921, A
13	51	53.7	490	12	Sequence 254664,
14	51	53.7	490	12	Sequence 46290, A
15	50	52.6	511	16	Sequence 69520, A
					Sequence 106767,
					Sequence 19, Appl

16	49	51.6	303	12	US-10-425-114-45759	Sequence 45759, A
17	49	51.6	401	12	US-10-424-599-254663	Sequence 254663,
18	49	51.6	488	12	US-10-424-599-272690	Sequence 272690,
19	48	50.5	112	16	US-10-624-080-3	Sequence 3, Appl
20	48	50.5	112	16	US-10-624-080-9	Sequence 9, Appl
21	48	50.5	112	16	US-10-624-080-10	Sequence 10, Appl
22	48	50.5	112	16	US-10-624-080-11	Sequence 11, Appl
23	48	50.5	112	16	US-10-624-080-12	Sequence 12, Appl
24	48	50.5	112	16	US-10-624-080-5	Sequence 5, Appl
25	48	50.5	385	14	US-10-242-943-16	Sequence 16, Appl
26	48	50.5	385	16	US-10-624-080-1	Sequence 1, Appl
27	48	50.5	397	9	US-09-738-628-5064	Sequence 5064, Ap
28	48	50.5	420	16	US-10-437-963-128072	Sequence 128072,
29	48	50.5	936	14	US-10-174-677-52	Sequence 52, Appl
30	47	49.5	108	14	US-10-006-869-41	Sequence 41, Appl
31	47	49.5	108	15	US-10-395-032-41	Sequence 41, Appl
32	47	49.5	199	16	US-10-767-701-59379	Sequence 59379, A
33	47	49.5	343	16	US-10-437-963-111769	Sequence 111769,
34	46	48.4	39	9	US-09-843-676-26	Sequence 26, Appl
35	46	48.4	39	9	US-09-766-253-26	Sequence 26, Appl
36	46	48.4	39	10	US-09-438-486-26	Sequence 26, Appl
37	46	48.4	39	12	US-10-325-810-216	Sequence 216, Appl
38	46	48.4	39	14	US-10-053-758-26	Sequence 26, Appl
39	46	48.4	39	14	US-10-054-295-26	Sequence 26, Appl
40	46	48.4	39	14	US-10-054-611-26	Sequence 26, Appl
41	46	48.4	161	16	US-10-437-963-201436	Sequence 201436,
42	45	47.4	18	9	US-09-836-073-2	Sequence 2, Appl
43	45	47.4	123	12	US-10-296-115-1147	Sequence 1147, Ap
44	45	47.4	228	12	US-10-005-168-2	Sequence 2, Appl
45	45	47.4	1076	14	US-10-116-949-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-836-073-17
Sequence 17, Application US/09836073
Patent No. US20020173475A1
GENERAL INFORMATION:
APPLICANT: Daegu, Asim
APPLICANT: Daegu, S.
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
PRIOR FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 17
LENGTH: 18
TYPE: PRT
ORGANISM: C. elegans
US-09-836-073-17

Query Match 100.0%; Score 95; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.7e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDADQRIIKQLEYFGNI 18
DB 1 DDADQRIIKQLEYFGNI 18

RESULT 2
US-10-424-599-258877
Sequence 258877, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Roga Thomas J
APPLICANT: Kovalic David K

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: US/08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-854-050-26

Query Match 48.4%; Score 46; DB 3; Length 39;
Best Local Similarity 63.6%; Pred. No. 0.63;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 7 IIKQLEYYFGN 17
|:|:|:|:|:
DB 1 ILRQVEYYFGD 11

RESULT 15
US-09-430-323-26
Sequence 26, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US/08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US/08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US/08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-430-323-26

Query Match 48.4%; Score 46; DB 4; Length 39;
Best Local Similarity 63.6%; Pred. No. 0.63;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 7 IIKQLEYYFGN 17
|:|:|:|:|:
DB 1 ILRQVEYYFGD 11

Search completed: September 10, 2004, 18:05:11
Job time: 16.8883 secs

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-851-843A-26

Query Match 48.4%; Score 46; DB 3; Length 39;
Best Local Similarity 63.6%; Pred. No. 0.63;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 7 IIRQVEYFGN 17
|:::|||||:
1 IIRQVEYFGD 11

Db 1 IIRQVEYFGD 11

RESULT 13
US-08-974-549A-216
Sequence 216, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morlin, Gregg B.
APPLICANT: Harley, Calvin H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 216:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-216

Query Match 48.4%; Score 46; DB 3; Length 39;
Best Local Similarity 63.6%; Pred. No. 0.63;
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 7 IIRQVEYFGN 17
|:::|||||:
1 IIRQVEYFGD 11

Db 1 IIRQVEYFGD 11

RESULT 14
US-08-854-050-26
Sequence 26, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morlin, Gregg B.
APPLICANT: Harley, Calvin H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESSES:


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Query Match      50.5%;   Score 48;   DB 5;   Length 385;
Best Local Similarity 50.0%;   Pred. No. 3;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy      1 DDADQRIIKQLLEYRGNI 18
      | : | | | : | : | |
Db      256 DQSDQRIIKKLNHYGNI 273

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RESULT 8
US-09-187-859-41

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: Patent No 6358920
:
: GENERAL INFORMATION:
:
: APPLICANT: Blaschuk, Orest W.
:
: APPLICANT: Gout, Barbara J.
:
: TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
:
: TITLE OF INVENTION: CADERLIN-MEDIATED FUNCTIONS
:
: FILE REFERENCE: 100086.40701
:
: CURRENT APPLICATION NUMBER: US/09/187,859A
:
: CURRENT FILING DATE: 1998-11-06
:
: NUMBER OF SEQ ID NOS: 4052
:
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 41
:
: LENGTH: 108
:
: TYPE: PR1
:
: ORGANISM: Mus musculus
:
US-09-187-859-41

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Qy	2	DADQRITKQLEYFGNT	18
Db	26	DADGINKKELIYFFSNL	42

Query Match 49.5%; Score 47; DB 4; Length 108;
 Best Local Similarity 47.1%; P-Val 1.4;
 Matches 8; Conservative 5; Mismatches 4; Indels 0;
 Gaps 0;

```

RESULT 9
US-09-839-542B-41
: Sequence 41. Application US/09839542B
: Patent No. 656996
: GENERAL INFORMATION:
: APPLICANT: Blachuk, Orest W.
: APPLICANT: Symonds, James Matthew
: APPLICANT: Gaur, Barbara J.
: TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
: FILE REFERENCE: 100086,407D1
: FILE REFERENCE: CADHERIN-MEDIATED FUNCTIONS
: CURRENT APPLICATION NUMBER: US/09/839,542B
: CURRENT FILING DATE: 2001-04-20
: NUMBER OF SEQ ID NOS: 4052
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 41
: LENGTH: 108
: TYPE: PRT
: ORGANISM: Mus musculus
US-09-839-542B-41

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Query Match	49.5%	Score 47;	DB 4;	Length 108;
Best Local Similarity	47.1%	Pred. No. 1.4;		
Matches	8;	Conservative	5;	Mismatches 4;
				Indels 0;
				Gaps 0;
QY	2	DADQRIRKQLEYFGNI	18	
Db	26	DADGINKKILYFFSNL	42	

RESULT 10
US-09-535-852-41
; Sequence 41, Application US/09535852
; Patent No. 6638911
; GENERAL INFORMATION:

```

APPLICANT: Blachuk, Orest W.
APPLICANT: Symonds, James M.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING
TITLE OF INVENTION: DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100066.407C6
CURRENT APPLICATION NUMBER: US/09/535,852
CURRENT FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 2009
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 41
LENGTH: 108
TYPE: PRT
ORGANISM: Mus musculus
US-09-535-852-41

Query Match          49.5%  Score 47;  DB 4;  Length 108;
Best Local Similarity 47.1%;  Pred. No. 1.4;
Matches      8;  Conservative      5;  Mismatches      4;  Indels      0;  Gaps      0

Oy      2  DADQRIIKOLEYVFGNI 18
      |||:| |:| |:|
Db      26 DADGINKKELIYFNSNL 42

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RESULT 11
US-09-540-236-2229
: Sequence 2229, Application US/09540236
: Patent No. 6673910
: GENERAL INFORMATION:
: APPLICANT: Gary L. Breton et al.
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARR
: TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 2709-2005-001
: CURRENT APPLICATION NUMBER: US/09/540,236
: CURRENT FILING DATE: 2000-04-04
: NUMBER OF SEQ ID NOS: 3840
: SEQ ID NO 2229
: LENGTH: 191
: TYPE: PRT
: ORGANISM: M.catarhalis
US-09-540-236-2229

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Query	March	49.5%	Score 47;	DB 4;	Length 191;
	Best Local Similarity	47.1%;	Pred. No. 2.6;		
Matches	8;	Conservative	5;	Mismatches	4;
				Indels	0;
				Gaps	0;
Qy	1	DDADQRIIKOLEFFYFGN	17		
		::: :::			
Db	140	DDLPOLIKOLEFFHSH	156		

RESULT 12
US-08-851-843A-26
Sequence 26, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Nakamura, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Hartley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

REFERENCE/DOCKET NUMBER: 44301-Z/JPM/AGL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-516-801-2

Query Match 50.5%; Score 48; DB 2; Length 385;
Best Local Similarity 50.0%; Pred. No. 3.9;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DDADQRIIKOLEYFFGNI 18
|:||||:|:|:|
Db 256 DQSDQRVIIKLNHVGNI 273

RESULT 5
US-08-248-355-2
Sequence 2, Application US/08248355
Patent No. 6222024
GENERAL INFORMATION:
APPLICANT: Goff, Stephen P.
APPLICANT: Kaipana, Ganjam V.
TITLE OF INVENTION: A cDNA Clone of the Human Ini-1 Gene Encoding
TITLE OF INVENTION: A Protein That Binds to the HIV-1 Integrase;
TITLE OF INVENTION: and Its Use in Antiviral Therapy
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/248,355
FILING DATE: 24-May-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44301
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-248-355-2

Query Match 50.5%; Score 48; DB 3; Length 385;
Best Local Similarity 50.0%; Pred. No. 3.9;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DDADQRIIKOLEYFFGNI 18
|:||||:|:|:|
Db 256 DQSDQRVIIKLNHVGNI 273

RESULT 6

US-09-167-206-16
Sequence 16, Application US/09167206A
Patent No. 6476193
GENERAL INFORMATION:
APPLICANT: Nandabalan, Krishnan
APPLICANT: Schulz, Vincent P.
APPLICANT: Yang, MeiJa
TITLE OF INVENTION: NIK1 PROTEIN AND NIK1 PROTEIN COMPLEXES
FILE REFERENCE: 15966-521 NIK1 protein complexes
CURRENT APPLICATION NUMBER: US/09/167,206A
CURRENT FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 385
TYPE: PRT
ORGANISM: Homo sapiens
US-09-167-206-16

Query Match 50.5%; Score 48; DB 4; Length 385;
Best Local Similarity 50.0%; Pred. No. 3.9;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DDADQRIIKOLEYFFGNI 18
|:||||:|:|:|
Db 256 DQSDQRVIIKLNHVGNI 273

RESULT 7
PCT-US95-06683-2
Sequence 2, Application PC/TUS9506683
GENERAL INFORMATION:
APPLICANT: Goff, Stephen P.
APPLICANT: Kaipana, Ganjam V.
TITLE OF INVENTION: A cDNA Clone of the Human Ini-1 Gene Encoding
TITLE OF INVENTION: a Protein That Binds to the HIV-1 Integrase;
TITLE OF INVENTION: and Its Use in Antiviral Therapy
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06683
FILING DATE: 24-May-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/248,355
FILING DATE: 24-May-1994
ATTORNEY/AGENT INFORMATION:
NAME: White Esq., John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 44301-A-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-06683-2

Db 77 DQSDQVITKINHVGNI 94

RESULT 2

US-08-248-355-3
Sequence 3, Application US/08248355

Patent No. 6222024

GENERAL INFORMATION:

APPLICANT: Goff, Stephen P.

APPLICANT: Kalpana, Ganjam V.

TITLE OF INVENTION: A cDNA Clone of the Human Int-1 Gene Encoding

TITLE OF INVENTION: a Protein That Binds to the HIV-1 Integrase;

TITLE OF INVENTION: and Its Use in Antiviral Therapy

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/248,355

FILING DATE: 24-May-1994

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: White Esq., John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 44301

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550

TELEFAX: (212) 664-0525

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 204 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: N

ANTI-SENSE: N

FRAGMENT TYPE: N-terminal

US-08-248-355-3

Query Match 50.5%; Score 48; DB 3; Length 204;

Best Local Similarity 50.0%; Pred. No. 1.9;

Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DDADQRIIKOLEYFYFNGI 18
|:||||:|:|:|
Db 77 DQSDQVITKINHVGNI 94

RESULT 3

PCT-US95-06683-3

Sequence 3, Application PC/TUS9506683

GENERAL INFORMATION:

APPLICANT: Goff, Stephen P.

APPLICANT: Kalpana, Ganjam V.

TITLE OF INVENTION: A cDNA Clone of the Human Int-1 Gene Encoding

TITLE OF INVENTION: a Protein That Binds to the HIV-1 Integrase;

TITLE OF INVENTION: and Its Use in Antiviral Therapy

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/06683

FILING DATE: 24-May-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/248,355

FILING DATE: 24-May-1994

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: White Esq., John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 44301-A-PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 204 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: N

ANTI-SENSE: N

FRAGMENT TYPE: N-terminal

PCT-US95-06683-3

Query Match 50.5%; Score 48; DB 5; Length 204;

Best Local Similarity 50.0%; Pred. No. 1.9;

Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

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Db 77 DQSDQVITKINHVGNI 94

RESULT 4

US-08-516-801-2

Sequence 2, Application US/08516801

Patent No. 5872213

GENERAL INFORMATION:

APPLICANT: Goff, Stephen P.

APPLICANT: Kalpana, Ganjam V.

TITLE OF INVENTION: A cDNA Clone of the Human Int-1 Gene Encoding a

TITLE OF INVENTION: Protein That Binds to the HIV-1 Integrase; and Its Use in Anti

TITLE OF INVENTION: and Its Use in Antiviral Therapy

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/516,801

FILING DATE: 18-August-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: John P. White, Esq.

REGISTRATION NUMBER: 28,678

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:43:01; Search time 15.8883 Seconds
(without alignments)
58.488 Million cell updates/sec

Title: US-09-836-073-17

Perfect score: 95

Sequence: 1 DDADQRIIKOLEYFGNI 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/2/iaa/5A COMB.pep:*
2: /cgn2_6/prodata/2/iaa/5B COMB.pep:*
3: /cgn2_6/prodata/2/iaa/6A COMB.pep:*
4: /cgn2_6/prodata/2/iaa/6B COMB.pep:*
5: /cgn2_6/prodata/2/iaa/6CTUS COMB.pep:*
6: /cgn2_6/prodata/2/iaa/6ackfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match Length	DB ID	Description
1	48	50.5	204 2	US-08-516-801-3 Sequence 3, Appl1
2	48	50.5	204 3	US-08-248-355-3 Sequence 3, Appl1
3	48	50.5	204 5	PCT-US95-06683-3 Sequence 3, Appl1
4	48	50.5	385 2	US-08-516-801-2 Sequence 2, Appl1
5	48	50.5	385 3	US-08-248-355-2 Sequence 2, Appl1
6	48	50.5	385 4	US-09-167-206-16 Sequence 16, Appl1
7	48	50.5	385 5	PCT-US95-06683-2 Sequence 2, Appl1
8	47	49.5	108 4	US-09-187-859-41 Sequence 41, Appl1
9	47	49.5	108 4	US-09-839-542B-41 Sequence 41, Appl1
10	47	49.5	108 4	US-09-535-852-41 Sequence 41, Appl1
11	47	49.5	191 4	US-09-540-236-2229 Sequence 2229, Ap
12	46	48.4	39 3	US-08-851-843A-26 Sequence 26, Appl1
13	46	48.4	39 3	US-08-974-549A-216 Sequence 216, Appl1
14	46	48.4	39 3	US-08-854-050-26 Sequence 26, Appl1
15	46	48.4	39 3	US-09-430-323-26 Sequence 26, Appl1
16	46	48.4	39 4	US-09-402-181B-216 Sequence 216, App
17	46	48.4	39 4	US-09-721-456-216 Sequence 216, App
18	45	47.4	1076 4	US-09-470-443-6 Sequence 6, Appl1
19	45	47.4	1145 4	US-09-470-443-2 Sequence 2, Appl1
20	45	47.4	1145 4	US-09-470-443-4 Sequence 4, Appl1
21	45	47.4	3074 4	US-09-543-681A-5508 Sequence 5508, Ap
22	44	46.3	18 3	US-09-316-630-3 Sequence 3, Appl1
23	44	46.3	18 3	US-09-316-630-4 Sequence 4, Appl1
24	43	45.3	38 3	US-08-851-843A-25 Sequence 25, Appl1
25	43	45.3	38 3	US-08-974-549A-215 Sequence 215, App
26	43	45.3	38 3	US-08-854-050-25 Sequence 25, Appl1
27	43	45.3	38 4	US-09-430-323-25 Sequence 25, Appl1

28	43	45.3	38 4	US-09-402-181B-215 Sequence 215, App
29	43	45.3	38 4	US-09-721-456-215 Sequence 215, App
30	43	45.3	498 4	US-09-107-532A-6991 Sequence 6991, Ap
31	41	43.2	21 4	US-08-475-955-20 Sequence 20, Appl1
32	41	43.2	108 4	US-09-187-859-43 Sequence 43, Appl1
33	41	43.2	108 4	US-09-839-542B-43 Sequence 43, Appl1
34	41	43.2	108 4	US-09-535-852-43 Sequence 43, Appl1
35	41	43.2	265 4	US-09-328-352-4347 Sequence 4347, Ap
36	41	43.2	626 4	US-09-489-039A-9106 Sequence 9106, Ap
37	41	43.2	775 2	US-08-966-388-4 Sequence 4, Appl1
38	41	43.2	775 3	US-09-188-403-4 Sequence 4, Appl1
39	41	43.2	775 3	US-09-188-404-4 Sequence 4, Appl1
40	41	43.2	775 3	US-09-281-259-4 Sequence 4, Appl1
41	40	42.1	108 4	US-09-149-476-552 Sequence 552, App
42	40	42.1	185 3	US-08-984-295-1 Sequence 1, Appl1
43	40	42.1	186 4	US-09-149-476-394 Sequence 394, App
44	40	42.1	335 4	US-09-540-236-2030 Sequence 2030, Ap
45	39	41.1	72 4	US-09-107-532A-3822 Sequence 3822, Ap

ALIGNMENTS

RESULT 1
US-08-516-801-3
Sequence 3, Application US/08516801
Patent No. 5872213
GENERAL INFORMATION:
APPLICANT: Gott, Stephen P.
APPLICANT: Kalpana, Ganjam V.
TITLE OF INVENTION: A CDNA Clone of the Human Int-1 Gene Encoding a
TITLE OF INVENTION: Protein That Binds to the HIV-1 Integrase; and Its Use in Ant
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSES: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/516,801
FILING DATE: 18-August-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: John P. White, Esq.
REGISTRATION NUMBER: 28,578
REFERENCE/DOCKET NUMBER: 44301-Z/JFW/AGL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
INFORMATION FOR SEQ. ID NO. 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
TOPOLOGY: linear
HYPOTHETICAL: N
ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
US-08-516-801-3
Query Match 50.5%; Score 48; DB 2; Length 204;
Best Local Similarity 50.0%; Pred. No. 1.9;
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

DB 51 ERAIRKOVYFPGD 64

RESULT 10

ID Q940X9 PRELIMINARY; PRT; 826 AA.

AC Q940X9;

DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DT AT5G21160/T10F18_190 (Prolin-rich protein family).

GN AT5G21160.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eucotyle II; Brassicales; Brassicaceae; Arabidopsis.

OC NCBI_TaxID=3702;

OX NCBI_TaxID=3702;

[1]

SEQUENCE FROM N.A.

RP Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,

Bann J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,

Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,

Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,

Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,

Pham P.K., Quach H.J., Sakurai T., Satou M., Seki M., Southwick A.,

Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,

Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,

"Arabidopsis cDNA clones."

RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

[2]

SEQUENCE FROM N.A.

RP Shinn P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P.,

Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,

Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,

Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,

Nguyen M., Palm C.J., Quach H.J., Sakurai T., Satou M., Seki M.,

Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,

Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A.,

Ecker J.R.,

"Arabidopsis ORF clones."

RT Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.

RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.

[3]

SEQUENCE FROM N.A.

RP STRAIN-CV. Columbia;

RA Town C.D., Haas B.J., Maiti R., Hannick L.I., Chan A.P., Rongning C.M.,

Smith Jr R.K., Arabogast T., Tallon L.V., Utterback T.R., Vanhaken S.E.,

Reidlyum T.V., Yu C., Wortman J.R., White O., Fraser C.M.,

"Arabidopsis thaliana chromosome 5 BAC F13M1 genomic sequence."

RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

RL EMBL: AY052365; AAK96556.1; -

DR EMBL: AY139801; AAO73903.1; -

DR EMBL: AC140977; AAO73903.1; -

DR GO: GO:0003743; P:translational initiation factor activity; IEA.

DR GO: GO:0006413; P:translational initiation; IEA.

DR InterPro: IPR006630; Lupus la dom.

DR InterPro: IPR002965; P rich extensn.

DR InterPro: IPR001950; TIF_SUTL.

DR Pfam: PF05383; La; 1.

DR PRINTS: PR01217; PRICHEXTENS.

DR PROSITE: PS01118; SUTL 1; 1.

SO SEQUENCE 826 AA; 91377 MW; 8D4192285B609D9A CRC64;

Query Match 52.6%; Score 50; DB 10; Length 826;

Best Local Similarity 50.0%; Pred. No. 18;

Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

DB 277 DLRDVKOVYFPGD 292

RESULT 11
Q77881

ID Q77881 PRELIMINARY; PRT; 93 AA.

AC Q77881;

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Envelope protein (Fragment).

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retroviruses; Retroviridae; Lentivirus.

OC NCBI_TaxID=11676;

OX NCBI_TaxID=11676;

[1]

SEQUENCE FROM N.A.

RP MEDLINE=95191002; PubMed=7884875;

RA Mulder-Kampinga G.A., Simonon A., Kuiken C.L., Dekker J.,

Scherpber H.J., de Perre P., Boer K., Goudemir J.,

"Similarity in env and gag genes between genomic RNAs of human

immunodeficiency virus type 1 (HIV-1) from mother and infant is

unrelated to time of HIV-1 RNA positivity in the child."

RL J. Virol. 69:2285-2296(1995).

DR EMBL: Z47894; CAA87908.1; -

DR GO: GO:0019028; C:viral capsid; IEA.

DR GO: GO:0019031; C:viral envelope; IEA.

DR GO: GO:0005198; P:structural molecule activity; IEA.

DR InterPro: IPR00777; GP120.

DR Pfam: PF00516; GP120; 1.

KW AIDS; Coat protein; Glycoprotein.

FT NON_TER 1 93

FT SEQUENCE 93 AA; 10561 MW; 4941876B9B6FFA8 CRC64;

Query Match 51.6%; Score 49; DB 15; Length 93;

Best Local Similarity 61.5%; Pred. No. 2.9;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

DB 73 OKVTLQVLEFGN 85

RESULT 12

ID Q91WT4

AC Q91WT4; PRELIMINARY; PRT; 170 AA.

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Env glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retroviruses; Retroviridae; Lentivirus.

OC NCBI_TaxID=11676;

OX NCBI_TaxID=11676;

[1]

SEQUENCE FROM N.A.

RP STRAIN=85CD225;

RA MEDLINE=21134754; PubMed=11242522;

Yang C., Dash B., Hanna S.L., Frances H.S., Nzilambi N.,

Colobanders R.C., St Louis M., Quinn T.C., Folke T.M., Lal R.B.,

"Prevalence of HIV type 1 subtype G among commercial sex workers

from Kinshasa, Democratic Republic of Congo."

RT AIDS Res. Hum. Retroviruses 17:361-365(2001).

DR EMBL: AF260442; AAF71590.1; -

DR GO: GO:0019028; C:viral capsid; IEA.

DR GO: GO:0019031; C:viral envelope; IEA.

DR GO: GO:0005198; P:structural molecule activity; IEA.

DR InterPro: IPR00777; GP120.

DR Pfam: PF00516; GP120; 1.

KW AIDS; Coat protein; Glycoprotein.

FT NON_TER 1 170

FT SEQUENCE 170 AA; 19351 MW; 177B41DAF67F7B7E CRC64;

Query Match 51.6%; Score 49; DB 15; Length 170;

Best Local Similarity 52.9%; Pred. No. 5.3;

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RT clone:011414.E05";
RL Submitted (MAR-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AP003375; BAB90138.1; -.
DR Gramene; Q85078; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002344; LupaLs_La.
DR InterPro; IPR006630; LupaLs_La_dom.
DR Pfam; PF05383; La; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
SQ SEQUENCE 389 AA; 42100 MW; 10C1863EAB6FA7B7 CRC64;

Query Match 55.8%; Score 53; DB 10; Length 389;
Best Local Similarity 52.9%; Pred. No. 2.7;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 DDADRIKOLEYFGN 17
Db 85 DELCDRIYKQVYFSD 101

RESULT 7
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AC O80H15.
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Untranslated region binding-protein.
GN UBP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauira; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA L'Ecuyer T.J., Fang H.-L.;
RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF467897; AAL76269.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002344; LupaLs_La.
DR InterPro; IPR006630; LupaLs_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 206 AA; 23992 MW; 965B62F7DFFB90E9 CRC64;

Query Match 54.7%; Score 52; DB 13; Length 206;
Best Local Similarity 57.1%; Pred. No. 2.1;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 4 DORIKOLEYFGN 17
Db 14 ESKICQLEYFGN 27

RESULT 8
O7ZBB0 PRELIMINARY; PRT; 211 AA.
AC O7ZBB0.
DT 01-JUN-2003 (TRENBLrel. 24, Created)
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.

```

```

OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TM08A7146;
RX MEDLINE=22483018; PubMed=12596722;
RA Kapiga S., Essex M.;
RA Kijeli I.E., Remylo B., Chaplin B., Sam N., Nkya W.M.M., Shao J.,
RT "HIV Type 1 Subtypes Among Bar and Hotel Workers in Moshi, Tanzania.";
RT AIDS Res. Hum. Retroviruses 19:57-64 (2003).
DR EMBL; AY123866; AAM95850.1; -.
DR GO; GO:0019031; C:viral envelope; IEA.
DR InterPro; IPR007777; GP120.
DR Pfam; PF00516; GP120; 1.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 211 AA; 23512 MW; D94732D39FC1497B CRC64;

Query Match 52.6%; Score 50; DB 15; Length 211;
Best Local Similarity 69.2%; Pred. No. 4.5;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 5 ORIKOLEYFGN 17
Db 71 QVAKOLEYFGN 83

RESULT 9
O8TBV5 PRELIMINARY; PRT; 390 AA.
AC O8TBV5.
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE AT2034P.
GN LA OR CG10922.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Ceiniker S.;
RL Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY075257; AAL68124.1; -.
DR FLYbase; FBGN011638; La.
DR GO; GO:0008098; F:5S rRNA primary transcript binding; IDA.
DR GO; GO:0003723; F:RNA binding; NAS.
DR InterPro; IPR002344; LupaLs_La.
DR InterPro; IPR006630; LupaLs_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 390 AA; 44869 MW; 797FDE26B903C909 CRC64;

Query Match 52.6%; Score 50; DB 5; Length 390;
Best Local Similarity 57.1%; Pred. No. 8.5;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 4 DORIKOLEYFGN 17

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DR GO:0003723; F:RNA binding; IEA.
DR InterPro: IPR002344; Lupus_La.
DR InterPro: IPR006530; Lupus_La_dom.
DR InterPro: IPR005054; RNA_rec_moc.
DR Pfam: PF00076; rtm; 1.
DR PRINTS: PR00302; LUPUSLA.
DR SMART: SM00715; LA; 1.
DR SMART: SM00360; RRM; 2.
DR PROSITE: PS50102; RRM; 1.
SQ SEQUENCE 427 AA; 4896 MW; 1E7CD82D8A9C69A CRC64;

Query Match
Best Local Similarity 57.9%; Score 55; DB 13; Length 427;
Pred. No. 1.4;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 DDADRIIKQLEYFGN 17
DB 11 DDDTICQEIYFPGD 26

RESULT 5
080567 PRELIMINARY; PRT; 545 AA.
AC 080567; Q9CSX1;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Expressed protein (VirF-interacting protein F1P1) (Hypothetical
protein) (At2g43970/F6E13.10/AT2G43970).
GN AT2G43970 OR F6E13.10/AT2G43970.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia;
RC Roundley S.D., Kaul S., Lin X., Ketchum K.A., Crosby M.L.,
RA Brandon R.C., Sykes S.M., Mason T.M., Kerlavage A.R., Adams M.D.,
RA Somerville C.R., Venter J.C.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Town C.D., Kaul S.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Mayda E., Tzfira T., Citovsky V.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G.,
RA Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C.,
RA Koeseema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shim P.,
RA Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Koeseema E., Meyers M.C., Shim P.,
RA Banh J., Bowser L., Carninci P., Chung M.K., Goldsmith A.D.,

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RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yu G., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,
RA Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,
RA Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,
RA Davis R.W., Theologis A., Ecker J.R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RA Shinn P., Chen H., Cheuk R., Kim C.J., Banh J., Bowser L.,
RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [9]
RP Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC004005; AAC23405.2; -
DR EMBL; AF332565; AAK06847.1; -
DR EMBL; AY056238; AAL07087.1; -
DR EMBL; AF375410; AAK52994.1; -
DR EMBL; AF367277; AAK56266.1; -
DR EMBL; AY129474; AAM91060.1; -
DR PIR; T00677; T00677.
DR GO:0005634; C:nucleus; IEA.
DR GO:0003723; F:RNA binding; IEA.
DR InterPro: IPR002344; Lupus_La.
DR InterPro: IPR006530; Lupus_La_dom.
DR Pfam; PR00302; LUPUSLA.
DR PRINTS; PR00302; LUPUSLA.
KW Hypothetical protein.
SQ SEQUENCE 545 AA; 60589 MW; E1A933261FE1ED80 CRC64;

Query Match
Best Local Similarity 56.8%; Score 54; DB 10; Length 545;
Pred. No. 2.6;
Matches 8; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

QY 1 DDADRIIKQLEYFGN 18
DB 191 EDSIQKIVQVEYFSDL 208

RESULT 6
080578 PRELIMINARY; PRT; 389 AA.
AC 080578;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE RNA-binding protein-like.
GN O1414_R05.3.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_Taxid=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nippondare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP "Oryza sativa nippondare(GA3) genomic DNA, chromosome 1, BAC

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0S Arabidopsis thaliana (Mouse-ear cress) .
0C Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
0C Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
0C eurosids II; Brassicales; Brassicaceae; Arabidopsits.
OX NCBI_TaxID=3702;
RN
RP SEQUENCE FROM N.A.
RA Shun P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
RA Bahj J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones";
RL Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P.,
RA Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,
RA Hewan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,
RA Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
RA Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis ORF clones";
RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
RN
RP EMBL, AY050403; AA91419.1; -.
DR EMBL, BT000588; AAA18157.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; LaI_1.
DR Pfam; PF00076; Itm_1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PSS0102; RRM; 1.
SQ SEQUENCE 422 AA; 46842 MW; 4ECABBBF1E068F0E CRC64;

Query Match 60.0%; Score 57; DB 10; Length 422;
Best Local Similarity 52.9%; Pred. No. 0.65;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 DDADORTIKOLEYYFGN 17
   |:::|||::|||::
DB 101 DELNQKIIROVEYFSD 117

RESULT 4
O7ZTK2 PRELIMINARY; PRT; 427 AA.
AC O7ZTK2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
DE Similar to lupus Ia protein homolog B.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachina; Pipidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strauberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databaes.
RE EMBL, BC046654; AAH46654.1; -.
RR GO; GO:0005634; C:nucleus; IEA.
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:29:01; Search time 41.229 Seconds
(without alignments)
137.751 Million cell updates/sec

Title: US-09-836-073-17

Perfect score: 95
Sequence: 1 DDADQRIKQLEFYFGNT 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL.25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	92	96.8	396	5	001806
2	97	60.0	411	10	09FL36
3	57	60.0	422	10	09A438
4	55	57.9	427	13	07ZTK2
5	54	56.8	545	10	080567
6	53	55.8	389	10	0850T8
7	52	54.7	206	13	08QHT5
8	50	52.6	211	15	07ZB80
9	50	52.6	390	5	08TRV5
10	50	52.6	826	10	0940X9
11	49	51.6	93	15	077881
12	49	51.6	170	15	091WT4
13	48	50.5	30	15	069711
14	48	50.5	341	15	07ZQ80
15	48	50.5	342	15	07ZQR9
16	48	50.5	342	15	07ZQP5

17	48	50.5	342	15	07ZQP4	Q7ZQP4 human immun
18	48	50.5	342	15	07ZQP3	Q7ZQP3 human immun
19	48	50.5	376	11	09ESU0	Q9ESU0 mus musculus
20	48	50.5	385	4	09UBH2	Q9UBH2 homo sapien
21	48	50.5	385	11	09ESU1	Q9ESU1 mus musculus
22	48	50.5	394	4	09H836	Q9H836 homo sapien
23	48	50.5	397	16	08NOL9	Q8NOL9 corynebacte
24	48	50.5	859	15	011947	Q11947 human immun
25	48	50.5	863	15	08JBB4	Q8JBB4 human immun
26	48	50.5	890	4	08N4R3	Q8N4R3 homo sapien
27	47	49.5	102	15	09QAP7	Q9QAP7 human immun
28	47	49.5	114	15	09YL33	Q9YL33 human immun
29	47	49.5	115	15	09YL52	Q9YL52 human immun
30	47	49.5	115	15	074722	Q74722 human immun
31	47	49.5	143	15	09J6A7	Q9J6A7 human immun
32	47	49.5	343	10	094LD0	Q94LD0 oryza sativ
33	47	49.5	401	13	07ZT10	Q7ZT10 brachydanio
34	47	49.5	898	11	088193	Q88193 mus musculu
35	47	49.5	934	11	091Y15	Q91Y15 mus musculu
36	46	48.4	102	15	090AW6	Q90AW6 human immun
37	46	48.4	102	15	090AN7	Q90AN7 human immun
38	46	48.4	102	15	090AY3	Q90AY3 human immun
39	46	48.4	128	15	09QMB7	Q9QMB7 human immun
40	46	48.4	342	15	07ZQR1	Q7ZQR1 human immun
41	46	48.4	351	15	07ZQ03	Q7ZQ03 human immun
42	46	48.4	351	15	07ZQ02	Q7ZQ02 human immun
43	46	48.4	351	15	07ZQ01	Q7ZQ01 human immun
44	46	48.4	351	15	07ZQ00	Q7ZQ00 human immun
45	46	48.4	351	15	07ZQP9	Q7ZQP9 human immun

ALIGNMENTS

RESULT 1
ID 001806 PRELIMINARY; PRT; 396 AA.
AC 001806; 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE C4AE4.4 protein.
GN C4AE4.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RT "The sequence of C. elegans cosmid C4AE4.";
RN Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (JUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003140; AAB54169.1; -;
DR PIR; T30953; T30953.
DR WormPep; C4AE4.4; CE08718.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002344; Lupus La.
DR InterPro; IPR006630; Lupus_La_dom.

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DR EMBL, X67859; CAA48043.1; -
DR PIR, JCI494; JCI494.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La.dom.
DR InterPro; IPR000504; RNA_rec_mob.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
DR Rfam-binding; Nuclear Protein; Phosphorylation.
FT DOMAIN 111 187
SQ SEQUENCE 415 AA; 47777 MW; 033FD9CCE1475F98 CRC64;

Query Match
Best Local Similarity 46.3%; Score 44; DB 1; Length 415;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 DQRIIKOLEYFGN 17
Db 14 EAKICHOIEYFGD 27

RESULT 15
DPOE MOUSE STANDARD; PRT; 2283 AA.
AC 09WVF7; Q9OX50;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE DNA polymerase epsilon, catalytic subunit A (EC 2.7.7.7) (DNA
GN POLYMERASE II subunit A).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP MEDLINE=99296371; PubMed=10366722;
RX Huang D., Knutti R., Palosaari H., Pospiech H., Sytaoja J.E.;
RT "cDNA and structural organization of the gene Pof1 for the mouse DNA
RL Biochim. Biophys. Acta 1445:363-371(1999).
CC -1- FUNCTION: Participates in DNA repair and in chromosomal DNA
CC replication.
CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + (DNA) (N).
CC -1- SUBUNIT: Consists of two subunits (258 kDa and 55 kDa).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- DOMAIN: The DNA polymerase activity domain resides in the
CC N-terminal half of the protein, while the C-terminus is necessary
CC for complexing subunits B and C. The C-terminus may also regulate
CC the catalytic activities of the enzyme.
CC -1- SIMILARITY: Belongs to the DNA polymerase type-B family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
DR EMBL, AF123502; AAD45244.1; -
DR EMBL, AF126398; AAD46482.1; -
DR EMBL, AF126377; AAD46482.1; JOINED.
DR EMBL, AF126378; AAD46482.1; JOINED.
DR EMBL, AF126379; AAD46482.1; JOINED.
DR EMBL, AF126380; AAD46482.1; JOINED.
DR EMBL, AF126381; AAD46482.1; JOINED.

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DR EMBL, AF126382; AAD46482.1; JOINED.
DR EMBL, AF126383; AAD46482.1; JOINED.
DR EMBL, AF126384; AAD46482.1; JOINED.
DR EMBL, AF126385; AAD46482.1; JOINED.
DR EMBL, AF126386; AAD46482.1; JOINED.
DR EMBL, AF126387; AAD46482.1; JOINED.
DR EMBL, AF126388; AAD46482.1; JOINED.
DR EMBL, AF126389; AAD46482.1; JOINED.
DR EMBL, AF126390; AAD46482.1; JOINED.
DR EMBL, AF126391; AAD46482.1; JOINED.
DR EMBL, AF126392; AAD46482.1; JOINED.
DR EMBL, AF126393; AAD46482.1; JOINED.
DR EMBL, AF126394; AAD46482.1; JOINED.
DR EMBL, AF126395; AAD46482.1; JOINED.
DR EMBL, AF126396; AAD46482.1; JOINED.
DR EMBL, AF126397; AAD46482.1; JOINED.
DR MGD; MGI:1196391; Pole.
DR InterPro; IPR006172; DNA_pol_B.
DR InterPro; IPR006134; DNA_pol_B_dom.
DR InterPro; IPR006133; DNA_pol_B_exo.
DR Pfam; PF00136; DNA_pol_B; 1.
DR SMART; SM03104; DNA_pol_B_exo; 1.
DR SMART; SM00486; POLBc; 1.
KW Transferase; DNA-directed DNA polymerase; DNA replication; DNA repair;
KW DNA-binding; Zinc-finger; Nuclear protein.
FT ZN_FING 2155 2235
FT CONFLICT 205 205 D -> E (IN REF. 1; AAD45244).
FT CONFLICT 284 284 T -> K (IN REF. 1; AAD45244).
FT CONFLICT 1309 1309 G -> E (IN REF. 1; AAD45244).
FT CONFLICT 1320 1320 K -> R (IN REF. 1; AAD45244).
FT CONFLICT 1386 1388 ALP -> GLFL (IN REF. 1; AAD45244).
FT CONFLICT 1665 1665 T -> I (IN REF. 1; AAD45244).
FT CONFLICT 2086 2086 I -> V (IN REF. 1; AAD45244).
FT CONFLICT 2111 2111 L -> Q (IN REF. 1; AAD45244).
SQ SEQUENCE 2283 AA; 262025 MW; 7005C34354E465F3 CRC64;

Query Match
Best Local Similarity 46.3%; Score 44; DB 1; Length 2283;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DADQRIIKOLEYFG 15
Db 73 DEDKRLVSAVDYDF 86

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Search completed: September 10, 2004, 17:53:10
Job time : 8.24022 secs

Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 DORIKOLEYFGN 17
: : : : :
Db 14 EAKICHQIERYFGD 27

RESULT 13

LA MOUSE STANDARD; PRT; 415 AA.

AC P32067;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Lupus La protein homolog (La ribonucleoprotein) (La autoantigen homolog).
GN SSB OR SS-B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93203630; PubMed=8454877;
RA Topfer F., Gordon T., McCluskey J.;
RT "Characterization of the mouse autoantigen La (SS-B). Identification of conserved RNA-binding motifs, a putative ATP binding site and reactivity of recombinant protein with poly(U) and human autoantibodies.";
RT J. Immunol. 150:3091-3100(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary gland;
RX MEDLINE=23388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haib F., Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Mullan S.J., Raha S.S., Loughell N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Harte S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [3]
RP SEQUENCE OF 1-11 FROM N.A.
RA Groetz D., Bachmann M.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termin of virtually all nascent polymerase III transcripts. It is associated with precursor forms of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S, and 7-2 RNAs.
CC -1- SUBUNIT: Interacts with DDX15 (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- PTM: Phosphorylated (By similarity).
CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
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CC EMBL; L00993; AAA39415.1; -
CC EMBL; BC003820; AA03820.1; -
CC EMBL; Y07951; CAA69249.1; -
CC MGD; MG1:98423; Ssb.
CC GO; GO:0005634; C:nucleus; IDA.
CC InterPro; IPR002344; Lupus_La.
CC InterPro; IPR00504; RNA_rec_mot.
CC Pfam; PF00076; rrm; 1.
CC PRINTS; PR00302; LUPUSLA.
CC SMART; SM00715; LA; 1.
CC SMART; SM00360; RRM; 1.
CC PROSITE; PS50102; RRM; 1.
CC PROSITE; PS00030; RRM_RNP_1; 1.
CC RNA-binding; Nuclear protein; Phosphorylation.
CC FT DOMAIN 111 187 RNA-BINDING (RRM).
SQ SEQUENCE 415 AA; 47756 MW; 2D75197692FDC933 CRC64;

Query Match 46.3%; Score 44; DB 1; Length 415;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 DORIKOLEYFGN 17
: : : : :
Db 14 EAKICHQIERYFGD 27

RESULT 14

LA RAT STANDARD; PRT; 415 AA.

AC P38656;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lupus La protein homolog (La ribonucleoprotein) (La autoantigen homolog).
GN SSB OR SS-B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93246255; PubMed=7916708;
RA Semsei I., Troester H., Bartsch H., Schwemmler M., Igloi G.L., Bachmann M.;
RT "Isolation of rat cDNA clones coding for the autoantigen SS-B/La: detection of species-specific variations.";
RT Gene 126:265-268(1993).
CC -1- FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termin of virtually all nascent polymerase III transcripts. It is associated with precursor forms of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S, and 7-2 RNAs.
CC -1- SUBUNIT: Interacts with DDX15 (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- PTM: Phosphorylated (By similarity).
CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
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DB 14 EAKICHQIEYRGD 27

RESULT 12

LA_HUMAN STANDARD: PRT; 408 AA.

AC P05455:

DT 01-NOV-1988 (Rel. 09, Created)

DT 01-JUL-1989 (Rel. 11, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Lupus La protein (Sjogren syndrome type B antigen) (SS-B) (La ribonucleoprotein) (La autoantigen).

GN SSB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_Taxid=9606;

RM [1]

RP MEDLINE=89202037; PubMed=2468131;

RA Chan E.K.L., Sullivan K.F., Tan E.M.;

RT "Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences for RNA-binding."

RL Nucleic Acids Res. 17:2233-2244 (1989).

RN [2]

RP SEQUENCE FROM N.A.

RA MEDLINE=89053970; PubMed=3192525;

RA Chambers J.C., Kenan D., Martin B.J., Keene J.D.;

RT "Genomic structure and amino acid sequence domains of the human La autoantigen."

RL J. Biol. Chem. 263:18043-18051 (1988).

RN [3]

RP SEQUENCE FROM N.A.

RA TISSUE=Placenta, and Skeletal muscle;

RC MEDLINE=22388257; PubMed=12477932;

RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Urdin T.B., Toshiyuki S., Carinci P., Prange C., Raha S.S., Loguelfano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosack S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumarane P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton B., Kettner M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schin J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [4]

RP SEQUENCE OF 54-408 FROM N.A.

RA MEDLINE=88199081; PubMed=2452201;

RA Sturgeons A.D., Peterson M.G., McNeillage L.J., Whittingham S., Coppel R.S.;

RT "Characteristics and epitope mapping of a cloned human autoantigen La."

RL J. Immunol. 140:3212-3218 (1988).

RN [5]

RP SEQUENCE OF 54-97 FROM N.A.

RA MEDLINE=8516283; PubMed=3856888;

RA Chambers J.C., Keene J.D.;

RT "Isolation and analysis of cDNA clones expressing human lupus La antigen."

RL Proc. Natl. Acad. Sci. U.S.A. 82:2115-2119 (1985).

RN [6]

RP FUNCTION.

RA MEDLINE=89251617; PubMed=2470590;

RA Göttlieb E., Steltz J.A.;

RT "Function of the mammalian La protein: evidence for its action in transcription termination by RNA polymerase III."

RL EMBO J. 8:851-861 (1989).

RN [7]

RP PHOSPHORYLATION.

RA MEDLINE=97207017; PubMed=9054510;

RT Fan H., Sakulich A.L., Goodier J.L., Zhang X., Qin J., Marate R.J.;

RT "Phosphorylation of the human La antigen on serine 366 can regulate recycling of RNA polymerase III transcription complexes."

RL Cell 88:707-715 (1997).

RN [8]

RP INTERACTION WITH DDX15.

RA MEDLINE=22346609; PubMed=12458796;

RA Fouraux M.A., Kolkmann M.J.M., Van der Heijden A., De Jong A.S., Van Veenrooij W.J., Pruijn G.J.M.;

RT "The human La (SS-B) autoantigen interacts with DDX15/hPrp43, a putative DEAD-box RNA helicase."

RL RNA 8:1428-1443 (2002).

CC -1- FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor forms of RNA polymerase III transcripts including rRNA and 4.5S, 5S, 7S, and 7-2 RNAs.

CC -1- SUBUNIT: Interacts with DDX15.

CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).

CC -1- PTM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES ARE AT THE C-TERMINAL PART OF THE PROTEIN.

CC -1- PTM: The N-terminus is blocked.

CC -1- DISEASE: Sera from patients with systemic lupus erythematosus often contain antibodies that react with the normal cellular La protein as if this antigen was foreign.

CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.

CC -----

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CC -----

DR EMBL: X13597; CAA31985.1; -.

DR EMBL: J04205; AA51885.1; -.

DR EMBL: BC001289; AAH01289.1; -.

DR EMBL: BC020818; AAH20818.1; -.

DR PIR: A11888; A11888.

DR Gene: HGNC:11316; SSB.

DR MIM: 109090; -.

DR GO: GO:0030529; C:ribonucleoprotein complex; TAS.

DR GO: GO:0003729; F:mRNA binding; TAS.

DR GO: GO:0000049; F:RNA binding; TAS.

DR GO: GO:0008334; P:histone mRNA metabolism; TAS.

DR GO: GO:0006400; P:RNA modification; TAS.

DR InterPro: IPR002344; Lupus_La.

DR InterPro: IPR006630; Lupus_La_dom.

DR InterPro: IPR00504; RNA_rec_mot.

DR Pfam: PF05383; La; 1.

DR Pfam: PF00076; rrm; 1.

DR PRINTS: PR00302; LUPUSLA.

DR SMART: SM00715; LA; 1.

DR SMART: SM00360; RRM; 1.

DR PROSITE: PS50102; RRM; 1.

DR PROSITE: PS00030; RRM_RNP_1; 1.

DR Systemic lupus erythematosus; RNA-binding; Phosphorylation; Nuclear protein.

FT DOMAIN 111 187 RNA-BINDING (RRM).

FT MOD_RES 366 366 PHOSPHORYLATION (BY CK2).

FT SEQUENCE 408 AA; 46837 MW; EC153C15F9187FC4 CRC64;

Query Match 46.3%; Score 44; DB 1; Length 408;

Best Local Similarity 50.0%; Pred. No. 11;

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RL Mech. Dev. 37:69-80(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Chame M., Pfeiffer B.D.,
RA Wan C.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abriil J.F., Agbayani A., An H.-J., Andrews-Plankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Bence P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,
RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Gang N.S., Gelbart W.M., Glaser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai X.,
RA Lascko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merklow G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Munz D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K.A., Nusskern D.R., Pacleb J.M.,
RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Sanders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson W., Skupski M.P., Smith T.,
RA Spier E.C., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -1- FUNCTION: May play a key role in egg organization. It may be a
CC transcriptional regulator.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: Oocyte specific.
CC -1- DEVELOPMENTAL STAGE: Expressed at all oogenic stages.
CC -1- PTM: The N-terminus is blocked.
CC
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CC
CC EMBL, X63503; CAA45074.1; -.
CC EMBL, AE003768; AAP56858.2; -.
CC PIR, A56678; A56678.
DR FlyBase; FBgn0005586; yem-alpha.
KW Nuclear protein; DNA-binding; Repeat.
FT DOMAIN 80 85 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 207 217 POLY-SER.
FT DOMAIN 219 261 ASP/GUT-RICH (ACIDIC).
FT DOMAIN 230 253 2 X 12 AA TANDEM REPEATS.
FT REPEAT 230 241 1.
FT REPEAT 242 253 2.
FT VARIANT 698 698 S -> L.
SQ SEQUENCE 1002 AA; 109310 MW; EE69A384EBA24D2F CRC64;
Query Match 47.4%; Score 45; DB 1; Length 1002;

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Best Local Similarity 52.9%; Pred. No. 19;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 DDADRIIKOLEYFGN 17
DB 105 DDDVARIVELEAKYGN 121
RESULT 11
LA BOVIN STRAND: PRT; 404 AA.
AC P10881;
DT 01-JUL-1989 (rel. 11, Created)
DT 01-JUL-1989 (rel. 11, Last sequence update)
DT 28-FEB-2003 (rel. 41, Last annotation update)
DE Lupus la protein homolog (La ribonucleoprotein) (La autoantigen
DE homolog).
GN SSB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Plutitary;
RX MEDLINE=89202037; PubMed=2468131;
RA Chan E.K.L., Sullivan K.F., Tan E.M.;
RT "Ribonucleoprotein SSB/La belongs to a protein family with consensus
RL Nucleic Acids Res. 17:2233-2244(1989).
CC -1- FUNCTION: La protein plays a role in the transcription of RNA
CC polymerase III. It is most probably a transcription termination
CC factor. Binds to the 3' terminus of virtually all nascent
CC polymerase III transcripts. It is associated with precursor forms
CC of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S,
CC and 7-2 RNAs.
CC -1- SUBUNIT: Interacts with DDX15 (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- PTM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES ARE AT THE
CC C-TERMINAL PART OF THE PROTEIN.
CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
CC
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CC
CC EMBL, X13698; CAA31986.1; -.
CC PIR, S03849; S03849.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
KW RNA-binding; Nuclear protein; Phosphorylation.
FT DOMAIN 111 187 RNA-BINDING (RRM).
SQ SEQUENCE 404 AA; 46534 MW; 4EE30B5C262AD6A1 CRC64;
Query Match 46.3%; Score 44; DB 1; Length 404;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 4 DORIRKOLEYFGN 17

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parthill J., Achman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holtroyd S.,
RA Jagals K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrall B.G.;
RT meningitidis Z2491."
RL Nature 404:502-506(2000).
CC -1- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
CC -1- COFACTOR: Binds 4 magnesium ions per subunit. Other metal ions can
CC support activity, but at a lower rate. Two magnesium ions are
CC required for the activation of the enzyme and are present before
CC substrate binds, two additional magnesium ions form complexes with
CC substrate and product (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the Pase family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR PIR: G816754; CAB84132.1; -
DR HAMAP: P17288; IFAMJ.
DR InterPro: IPR008163; Inorg_pphsph.
DR InterPro: IPR008162; Pyrophosphatase.
DR Pfam: PF00719; Pyrophosphatase; 1.
DR PROSITE: PS002014; Inorg_pphsph; 1.
DR PROSITE: PS00387; PPASE; 1.
KW Hydrolyase; Metal-binding; Magnesium; Complete proteome.
FT METAL 67 67 MAGNESIUM 1 (BY SIMILARITY).
FT METAL 72 72 MAGNESIUM 1 AND 2 (BY SIMILARITY).
FT METAL 104 104 MAGNESIUM 1 (BY SIMILARITY).
SQ SEQUENCE 177 AA; 19799 MW; 1DAB8F80F8FC06F CRC64;

Query Match 47.4%; Score 45; DB 1; Length 177;
Best Local Similarity 43.8%; Pred. No. 3.3;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 DADQRIKQLEYFGN 17
DB 126 DLPOOLIKQIEHFHFNH 141

RESULT 9
ID IPYR_NEIMB STANDARD; PRT; 177 AA.
AC Q9K0G4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
DE hydrolase) (Pase).
GN PPA OR NMB0641.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,

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RA- Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy O., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Macon T., Clacko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,
RA Cotton M.D., Utechtack T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Maignani V., Piza M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappunli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."; 287:1809-1815(2000).
RL Science 287:1809-1815(2000).
CC -1- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
CC -1- COFACTOR: Binds 4 magnesium ions per subunit. Other metal ions can
CC support activity, but at a lower rate. Two magnesium ions are
CC required for the activation of the enzyme and are present before
CC substrate binds, two additional magnesium ions form complexes with
CC substrate and product (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the Pase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE002419; AAF1064.1; -
DR PIR: F81175; F81175.
DR HAMAP: P17288; IFAMJ.
DR InterPro: IPR008163; Inorg_pphsph.
DR InterPro: IPR008162; Pyrophosphatase.
DR Pfam: PF00719; Pyrophosphatase; 1.
DR PROSITE: PS002014; Inorg_pphsph; 1.
DR PROSITE: PS00387; PPASE; 1.
KW Hydrolyase; Metal-binding; Magnesium; Complete proteome.
FT METAL 67 67 MAGNESIUM 1 (BY SIMILARITY).
FT METAL 72 72 MAGNESIUM 1 AND 2 (BY SIMILARITY).
FT METAL 104 104 MAGNESIUM 1 (BY SIMILARITY).
SQ SEQUENCE 177 AA; 19811 MW; 6017182C446A8567 CRC64;

Query Match 47.4%; Score 45; DB 1; Length 177;
Best Local Similarity 43.8%; Pred. No. 3.3;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 DADQRIKQLEYFGN 17
DB 126 DLPOOLIKQIEHFHFNH 141

RESULT 10
ID YEMA_DROME STANDARD; PRT; 1002 AA.
AC P25992; Q9VAP4;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Yemanuclein-alpha.
GN YEM-ALPHA OR YEMA OR YG4.5 OR CG11879.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Canton-S;
RX MEDLINE=92297435; PubMed=1606021;
RA Alé-Ahmed O., Bellon B., Capri M., Joblet C., Thomas-Dejaage M.;
RT "The Yemanuclein-alpha: a new Drosophila DNA binding protein specific
RT for the oocyte nucleus.";

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CC      Name=2;
CC      IsoId=Q9Y5H7-2; Sequence=VSP_000679, VSP_000680;
CC      Name=3;
CC      IsoId=Q9Y5H7-3; Sequence=VSP_0006704, VSP_0006705;
CC      Note=No experimental confirmation available;
CC      -1 SIMILARITY: Contains 6 cadherin domains.
CC      -----
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CC      or send an email to license@ib-sib.ch).
CC      -----
DR      EMBL; AF152313; AAD3707.1; -
DR      EMBL; AF152483; AAD3744.1; -
DR      EMBL; AC005609; AAC34321.1; -
DR      EMBL; BC033735; AAH3375.1; -
DR      Genew; HGNC:6671; PCDH5.
DR      MIM; 606311; -
DR      MIM; 604966; -
DR      InterPro; IPR002126; Cadherin.
DR      Pfam; PF00028; cadherin; 5.
DR      PRINTS; PR00205; CADHERIN.
DR      SMART; SMO0112; CA; 6
DR      PROSITE; PS00232; CADHERIN_1; 5.
DR      PROSITE; PS50268; CADHERIN_2; 6.
KW      Calcium-binding; Cell adhesion; Glycoprotein; Signal; Repeat;
KW      Transmembrane; Alternative splicing; Multigene family.
FT      SIGNAL 1 28
FT      CHAIN 29 936
FT      DOMAIN 29 696
FT      TRANSMEM 697 717
FT      DOMAIN 718 936
FT      DOMAIN 33 132
FT      DOMAIN 156 241
FT      DOMAIN 242 349
FT      DOMAIN 350 454
FT      DOMAIN 455 564
FT      DOMAIN 580 677
FT      DOMAIN 909 916
FT      DOMAIN 773 890
FT      REPEAT 773 776
FT      REPEAT 773 776
FT      REPEAT 785 788
FT      REPEAT 818 821
FT      REPEAT 873 876
FT      REPEAT 877 890
FT      CARBOHYD 264 264
FT      CARBOHYD 547 547
FT      CARBOHYD 785 816
FT      VARSPLIC
FT      FT
FT      FT
FT      VARSPLIC 817 936
FT      FT
FT      VARSPLIC 868 890
FT      FT
FT      VARSPLIC 891 936
FT      CONFLICT 237 237
FT      SEQUENCE 936 AA; 102047 MM; 7143ECCETIA357CD6 CRC64;
SQ
OY      Query Match 50.5%; Score 48; DB 1; Length 936;
OY      Best Local Similarity 47.1%; Pred. No. 5.7;
OY      Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0
DB      2 DADORIIKOLEYVFENI 18
DB      267 DADGINKETIYVFENI 283

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ID	LA	AEAL	STANDARD	PRT	363 AA
AC	Q26457				
DT	15-JUL-1998	(Rel. 36, Created)			
DT	15-JUL-1998	(Rel. 36, Last sequence update)			
DT	28-FEB-2003	(Rel. 41, Last annotation update)			
DE	The protein homolog (La ribonucleoprotein) (La autoantigen homolog) .				
OS	Aedes albopictus (Forest day mosquito) .				
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes.				
OX	NCBI_TaxID=7160;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				
RX	MEDLINE=96135233; PubMed=8551578;				
RA	Parignon N., Struss U.H.,				
RT	"Mosquito homolog of the La autoantigen binds to Sindbis virus RNA.";				
RL	J. Virol. 70:1173-1181(1996).				
CC	-1- FUNCTION: May be involved in transcription termination by RNA polymerase III. Binds RNA and DNA. Binds to the 3' end of the minus strand of Sindbis virus RNA. This may be significant for Sindbis virus RNA replication.				
CC	-1- SUBCELLULAR LOCATION: Nuclear. Primarily nuclear, but significant amounts are present in the cytoplasm.				
CC	-1- SIMILARITY: Contains 1 RNA recognition motif (RWM) domain.				
CC	-1- SIMILARITY: TO VERTEBRATE PROTEIN LA.				
CC	-----				
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CC	-----				
DR	EMBL, S80954; AAB35931.1; -.				
DR	InterPro, IPR002344; Lupus_La.				
DR	InterPro, IPR006630; Lupus_La.dom.				
DR	InterPro, IPR000504; RNA_rec_mot.				
DR	Pfam, PF05383; La; 1.				
DR	Pfam, PF00076; rrm; 1.				
DR	PRINTS, PR00302; LUPUSLA.				
DR	SMART, SM00715; LA; 1.				
DR	SMART, SM00360; RRM; 1.				
DR	PROSITE, PS50102; RRM; 1.				
DR	PROSITE, PS00030; RRM_RNP_1; FALSE_NEG.				
FW	RNA-binding; Nuclear protein; DNA-binding.				
FT	DOMAIN 141 228 RNA-BINDING (RRM).				
SQ	SEQUENCE 363 AA; 44430 MW; 4B5C89F21C40F452 CRC64;				
Query Match					
Best Local Similarity		49.5%;	Score 47;	DB 1;	Length 383;
Matches		8; Conservative	2; Mismatches	0; Indels	0; Gaps
QY	8 IKOLEYFRGN 17	:			
DB	48 IROLLEYFGD 57				
RESULT 8					
ID	IPYR_NEIMA	STANDARD;	PRT;	177 AA.	
AC	Q9JVG3;				
DT	28-FEB-2003 (Rel. 41, Created)				
DT	28-FEB-2003 (Rel. 41, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-hydrolyase) (Ppase).				
GN	PPA OR NMA0851.				
OS	Neisseria meningitidis (serogroup A).				
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.				
OX	NCBI_TaxID=65699;				

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palczolo M., Pittman G.S., Pan S., Pollard J., Put V., Reese M.G.,
RA Reibert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpston M., Skupski M.P., Smith T.,
RA Spier B., Spirdling A.C., Stapleton M., Strong R., Sun E.,
RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Massarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
CC -1- FUNCTION: May be involved in transcription termination by RNA
CC polymerase III. Binds RNA and DNA. Binds to precursors of RNA
CC polymerase III transcripts. May play a specialized role during fly
CC development.
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- DEVELOPMENTAL STAGE: Expressed throughout embryonic, larval,
CC pupal, and adult development. Expression throughout the embryo is
CC followed by a restricted pattern of mesodermal expression that is
CC later confined to the visceral mesoderm, gonads, gut, and salivary
CC glands.
CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
CC -1- SIMILARITY: TO VERTERATE PROTEIN LA.
CC -----
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CC -----
CC EMBL; U07652; AAA20518.1; -
CC EMBL; L32988; AAA21776.1; -
CC EMBL; AB003666; AAF5385.1; -
CC PIR; A53773; A53773.
CC PIR; A53781; A53781.
CC FLYBASE; FBgn0011638; La.
CC GO; GO:0008098; F:5S rRNA primary transcript binding; IDA.
CC GO; GO:0003723; F:RNA binding; NAS.
CC InterPro; IPR002344; Lupus_La.
CC InterPro; IPR006630; Lupus_La_dom.
CC InterPro; IPR000504; RNA_rec_mot.
CC Pfam; PF00383; La; 1.
CC Pfam; PF00076; rrm; 1.
CC PRINTS; PR00302; LUPUSLA.
CC SMART; SM00715; LA; 1.
CC SMART; SM00360; RRM; 1.
CC PROSITE; PSS0102; RRM; 1.
CC PROSITE; PSS0030; RRM_RNP_1; 1.
CC KWA; KWA-Binding; Nuclear protein; DNA-binding.
CC FT DOMAIN 149 234 RNA-BINDING (RRM).
CC FT CONFICT 169 169 A -> T (IN REF. 1).
CC FT CONFICT 182 183 KH -> NS (IN REF. 1).
CC FT CONFICT 283 283 A -> R (IN REF. 1).
CC FT CONFICT 329 329 K -> N (IN REF. 1).
CC SEQUENCE 390 AA; 44884 MW; A8099288B90446A5 CRC64;

AC Q12824; O75784; O95474;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE SWI/SNF related, matrix associated, actin dependent regulator of
DE chromatin subfamily B member 1 (Integrase interactor 1 protein)
DE (hsNF5) (BAF47).
DE SMARCB1 OR SNF5L1 OR INT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95099327; PubMed=7801128;
RA Kalpana G.V., Marmon S., Wang W., Crabtree G.R., Goff S.P.;
RT "Binding and stimulation of HIV-1 integrase by a human homolog of
RT yeast transcription factor SNF5.";
RL Science 266:2002-2006(1994).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=99225325; PubMed=10208879;
RA Bruder C.E., Dumanski J.P., Kedra D.;
RT "The mouse ortholog of the human SMARCB1 gene encodes two splice
RT forms.";
RL Biochem. Biophys. Res. Commun. 257:886-890(1999).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98334382; PubMed=9671307;
RA Versteeg E.I., Sevenet N., Lange J., Rousseau-Merck M.F., Ambros P.,
RA Handgretinger R., Aurias A., Delattre O.;
RT "Truncating mutations of hSNF5/INT1 in aggressive paediatric cancer.";
RL Nature 394:203-206(1998).
CC -1- FUNCTION: Involved in chromatin-remodeling. Part of a complex that
CC opens the chromatin to facilitate the transcriptional machinery to
CC access their targets.
CC -1- SUBUNIT: Binds tightly to the human immunodeficiency virus-type 1
CC (HIV-1) integrase in vitro and stimulates its DNA-joining
CC activity.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=A; Synonyms=INT1A;
CC IsoId=Q12824-1; Sequence=displayed;
CC Name=B; Synonyms=INT1B;
CC IsoId=Q12824-2; Sequence=VSP_004399;
CC -1- DISEASE: TUMOR SUPPRESSOR. INACTIVATED IN MALIGNANT RHABDOID
CC TUMORS (MRT). MRT'S ARE EXTREMELY AGGRESSIVE CANCERS OF EARLY
CC CHILDHOOD.
CC -1- SIMILARITY: Belongs to the SNF5 family.
CC -1- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC WWW="http://www.infobiogen.fr/services/chronocancer/Genes/SMARCB1ID169.html".
CC -----
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CC -----
CC EMBL; U04847; AAA81905.1; -
CC EMBL; AJ011738; CAA09759.1; -
CC EMBL; Y17118; CAA76639.1; ALT_SEQ.
CC EMBL; Y17119; CAA76639.1; JOINED.
CC EMBL; Y17120; CAA76639.1; JOINED.
CC EMBL; Y17121; CAA76639.1; JOINED.
CC EMBL; Y17122; CAA76639.1; JOINED.
CC EMBL; Y17123; CAA76639.1; JOINED.
CC EMBL; Y17124; CAA76639.1; JOINED.
CC EMBL; Y17125; CAA76639.1; JOINED.
CC EMBL; Y17126; CAA76639.1; JOINED.
CC Genew; HGNC:11103; SMARCB1.

Query Match 52.6%; Score 50; DB 1; Length 390;
Best Local Similarity 57.1%; Pred. No. 1.1;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 4 DORIIOLEYFFGN 17
Db 51 ERAIRIOLEYFFGD 64

RESULT 4
SNF5_HUMAN
ID SNF5_HUMAN STANDARD; PRT; 385 AA.

DR PROSITE; PS00030; RRM_RNP_1; 1.
 KM RNA-binding; Nuclear protein; Phosphorylation.
 FT DOMAIN 111 203 RNA-BINDING (RRM).
 FT DOMAIN 196 212 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 316 332 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 SQ SEQUENCE 428 AA; 48864 MW; AEB3A38B7D2B3EC3 CRC64;
 Query Match 60.0%; Score 57; DB 1; Length 428;
 Best Local Similarity 56.2%; Pred. No. 0.082;
 Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 Oy 2 DADQRIIKOLEYFGN 17
 Db 12 DSDTKICEQIEYFGD 27

RESULT 2
 LAB_XENLA STANDARD; PRT; 427 AA.
 AC P28049;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Lupus la protein homolog B (La ribonucleoprotein B) (la autoantigen homolog B).
 GN LAB1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8335;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Oocyte;
 RX MEDLINE=93287095; PubMed=8510143;
 RA Scherly D., Stutz F., Lin-Marq N., Clarkson S.G.;
 RT "La proteins from Xenopus laevis. cDNA cloning and developmental expression.";
 RU J. Mol. Biol. 231:196-204(1993).
 CC -1- FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' terminus of virtually all nascent polymerase III transcripts (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- DEVELOPMENTAL STAGE: Barely detectable in stage I/II oocytes, accumulate in stage III/IV oocytes, then exhibit a roughly constant steady state level in mature oocytes, eggs, and early embryos.
 CC -1- PTM: Phosphorylated (Probable).
 CC -1- MISCELLANEOUS: There are two forms of La, Laa and Lab, in xenopus.
 CC -1- SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN.
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
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 CC -----
 CC EMBL; X68818; CAA48716.1; -
 CC PIR; S33817; S33817.
 CC InterPro; IPR002344; Lupus_La.
 CC InterPro; IPR00630; Lupus_La_dom.
 CC InterPro; IPR000504; RRM_rec_mot.
 CC Pfam; PF05383; La; 1.
 CC Pfam; PF00076; rrm; 1.
 CC PRINTS; PR00302; LUPUSLA.
 CC SMART; SM00715; LA; 1.
 CC SMART; SM00360; RRM; 1.
 CC PROSITE; PS50102; RRM; 1.
 CC PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.

KM RNA-binding; Nuclear protein; Phosphorylation.
 FT DOMAIN 110 202 RNA-BINDING (RRM).
 FT DOMAIN 315 331 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 SQ SEQUENCE 427 AA; 48995 MW; 45F3146F8934A355 CRC64;
 Query Match 57.9%; Score 55; DB 1; Length 427;
 Best Local Similarity 56.2%; Pred. No. 0.18;
 Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Oy 2 DADQRIIKOLEYFGN 17
 Db 11 DSDTKICEQIEYFGD 26

RESULT 3
 LA_DROME STANDARD; PRT; 390 AA.
 AC P40796; Q24375; Q9VIN2;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE La protein homolog (La ribonucleoprotein) (La autoantigen homolog).
 GN LA OR CG10922.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Canton-S; TISSUE=Ovary;
 RX MEDLINE=94309632; PubMed=8035794;
 RA Bai C., Li Z., Tolias P.P.;
 RT "Developmental characterization of a Drosophila RNA-binding protein homologous to the human systemic lupus erythematosus-associated La/SS-B autoantigen.";
 RU Mol. Cell. Biol. 14:5123-5129(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94309661; PubMed=8035818;
 RA Yoo C.-J., Wolin S.L.;
 RT "La proteins from Drosophila melanogaster and Saccharomyces cerevisiae: a yeast homolog of the La autoantigen is dispensable for growth.";
 RU Mol. Cell. Biol. 14:5412-5424(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celihner S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton R.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Baer A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.T., Benos P.V., Berman B.P., Bhandari D., Bolintsov S., Botkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P., Butlis J.M., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.K., Chuam D.A., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Durkin B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferriz C., Ferrier S., Fleischmann W., Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jatala M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.S., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Laake P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:01:41; Search time 7.24022 Seconds
(without alignments)
129.452 Million cell updates/sec

Title: US-09-836-073-17

Perfect score: 95

Sequence: 1 DDADQRIIKOLEYFGNI 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	60.0	428	1	LAA_XENILA
2	55	57.9	427	1	P28048 xenopus lae
3	50	52.6	390	1	LA_DROME
4	48	50.5	385	1	SNF5_HUMAN
5	48	50.5	385	1	SNF5_MOUSE
6	48	50.5	385	1	CDAS_HUMAN
7	47	49.5	383	1	LA_AEDAL
8	45	47.4	177	1	IPYR_NEIMA
9	45	47.4	177	1	IPYR_NEIMA
10	45	47.4	1002	1	YEMA_DROME
11	44	46.3	404	1	LA_BOVIN
12	44	46.3	408	1	LA_HUMAN
13	44	46.3	415	1	LA_MOUSE
14	44	46.3	415	1	LA_MOUSE
15	44	46.3	2283	1	DPOE_MOUSE
16	43	45.3	176	1	IPYR_HAEIN
17	43	45.3	1290	1	RPOC_MYCN
18	42	44.2	183	1	IPYR_MYCP
19	42	44.2	214	1	EOT4_ACTPO
20	42	44.2	222	1	KADC_MAIZE
21	42	44.2	365	1	ROAL_DROME
22	42	44.2	880	1	CADF_XENILA
23	42	44.2	884	1	CADF_XENILA
24	41.5	43.7	729	1	KEXI_YEAST
25	41	43.2	178	1	COAD_ZYMMO
26	41	43.2	211	1	TRMB_ZYMY3
27	41	43.2	214	1	KAD_MYCUB
28	41	43.2	298	1	LAHI_SCHPO
29	41	43.2	315	1	H02_RAT
30	41	43.2	350	1	Y535_SUISO
31	41	43.2	361	1	YPDF_ECOLI
32	41	43.2	466	1	SYH_BIFIO
33	41	43.2	1170	1	SMC2_YEAST

34	41	43.2	1292	1	RPOC_MYCBE	P47582 mycoplasma
35	40	42.1	108	1	Y165_UREPA	Q9p0x9 ureaplasma
36	40	42.1	339	1	DG11_THENT	Q8t5r4 thelmanae
37	40	42.1	500	1	SYH_RHILU	Q987t0 rhizobium
38	40	42.1	594	1	SYA_BORBU	O51238 borrelia bu
39	40	42.1	618	1	DNK_STRGR	O54215 streptomyce
40	40	42.1	832	1	TENL_CANAL	P43075 candida alb
41	40	42.1	1132	1	NTU1_YEAST	P53114 saccharomyc
42	39	41.1	106	1	RBS_CYAPA	P18062 cyanophora
43	39	41.1	139	1	RBS_GUITH	P14960 guillardia
44	39	41.1	180	1	RBSA_SOLTU	P26575 solanum tub
45	39	41.1	180	1	RBSB_SOLTU	P26576 solanum tub

ALIGNMENTS

RESULT 1
ID LAA_XENILA STANDARD; PRT; 428 AA.
AC P28048;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Lupus La protein homolog A (La ribonucleoprotein A) (La autoantigen homolog A).
GN LAA1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxId=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocyte;
RA MEDLINE=93287095; PubMed=8510143;
RX Scherly D., Stutz F., Lin-Marg N., Clarkson S.G.;
RT "La proteins from Xenopus laevis. cDNA cloning and developmental expression.";
RT J. Mol. Biol. 231:196-204(1993).
RL
CC -1- FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' terminus of virtually all nascent polymerase III transcripts (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- DEVELOPMENTAL STAGE: Barely detectable in stage I/II oocytes, accumulate in stage III/IV oocytes, then exhibit a roughly constant steady state level in mature oocytes, eggs, and early embryos.
CC -1- PTM: Phosphorylated (Probable).
CC -1- MISCELLANEOUS: There are two forms of La, Laa and Lab, in xenopus.
CC -1- SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN.
CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL laboratory - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X68817; CAA48715.1; -.
CC PIR: S33818; S33818.
CC InterPro: IPR002344; Lupus_La.
CC InterPro: IPR006630; Lupus_La_dom.
CC InterPro: IPR000504; RNA_rec_mot.
CC Pfam: PF05383; La; 1.
CC Pfam: PF00076; Rrm; 1.
CC PRINTS: PR00302; LUPUSLA.
CC SMART: SM00715; LA; 1.
CC SMART: SM00360; RRM; 1.
CC PROSITE: PSS0102; RRM; 1.

A:Reference number: AB1775; MUID:20222556; PMID:10761919
A:Accession: G81930
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-177 <PAR>
A:Cross-references: GB:AL162754; GB:AL157959; NID:97379424; PIDN:CA884132.1; PID:9737956
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: ppa; NMA0851
C:Superfamily: inorganic pyrophosphatase
C:Keywords: hydrolase

Query Match 47.4%; Score 45; DB 2; Length 177;
Best Local Similarity 43.8%; Pred. No. 6.4;
Matches 7; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DADGRIIKOLEYFGN 17
Db 126 DLPOOLIKQIEHFVNH 141

RESULT 12
A56678
Yemanuclein-alpha - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jun-2002
C:Accession: A56678; S22146
R:Alt-Alied: O.; Belton, B.; Capri, M.; Uoblet, C.; Thomas-DeLaage, M.
Mech. Dev. 37, 69-80, 1992
A:Title: The yemanuclein-alpha: a new *Drosophila* DNA binding protein specific for the oc
A:Reference number: A56678; MUID:92297435; PMID:1606021
A:Accession: A56678
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1002 <AIE>
A:Cross-references: GB:X63503; NID:98837; PID:98838
C:Genetics:
A:Gene: FlyBase:yem-alpha
A:Cross-references: FlyBase:FBgn0005596
A:Introns: 80/3; 154/3; 428/1 477/2; 557/2
C:Keywords: DNA binding; oocyte

Query Match 47.4%; Score 45; DB 2; Length 1002;
Best Local Similarity 52.9%; Pred. No. 42;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DDADGRIIKOLEYFGN 17
Db 105 DDVARIYKELEAKYGN 121

RESULT 13
F64526
adenine/cytosine DNA methyltransferase - *Helicobacter pylori* (strain 26695)
C:Species: *Helicobacter pylori*
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C:Accession: F64526
R:Tomd, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliq, H.G.; Glodek, A.; McKenna, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watney, L. Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.
A:Reference number: A64520; MUID:9739467; PMID:9252185
A:Accession: F64526
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-823 <TOM>
A:Cross-references: GB:AE000527; GB:AE000511; NID:92313131; PIDN:AA07124.1; PID:9231313

Query Match 46.8%; Score 44.5; DB 2; Length 823;
Best Local Similarity 42.1%; Pred. No. 41;
Matches 8; Conservative 6; Mismatches 2; Indels 3; Gaps 1;

Qy 2 DADGRIIKOLEYFGN 17
Db 65 ETKELIKQIEFYSKFGN 83

RESULT 14
AD2410
hypothetical protein alr4836 [imported] - *Nostoc* sp. (strain PCC 7120)
C:Species: *Nostoc* sp. PCC 7120
A:Note: *Nostoc* sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AD2410
R:Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi, N.; Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana-*
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AD2410
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-158 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA876535.1; PID:917133973; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr4836

Query Match 46.3%; Score 44; DB 2; Length 158;
Best Local Similarity 50.0%; Pred. No. 8.3;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 5 ORRIKOLEYFGN 18
Db 19 QRLIKSPQYWTGNL 32

RESULT 15
A13101
transcription regulator, *lyrA* family Atv4437 [imported] - *Agrobacterium tumefaciens* (str
C:Species: *Agrobacterium tumefaciens*
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: A13101
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L. erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell. ; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ; ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: A13101
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-300 <KUR>
A:Cross-references: GB:AE006889; PIDN:AL45231.1; PID:917742913; GSPDB:GN00187
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atv4437
A:Map position: linear chromosome
C:Superfamily: probable transcription regulator *lyrA*

Query Match 46.3%; Score 44; DB 2; Length 300;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 ADGRIIKOLEYFGN 17
Db 31 AVSRQINLELYFGS 45

Search completed: September 10, 2004, 18:02:37
Job time : 16.0782 secs

F:151-158/Region: RNA-binding RNP1 motif
F:228-428/Domain: phosphorylated #status predicted <PHY>

Query Match 60.0%; Score 57; DB 1; Length 428;
Best Local Similarity 56.2%; Pred. No. 0.18;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy 2 DADRIIKOLEYFGN 17
Db 12 DSDTKICEQIEYFGD 27

RESULT 3

S33817
ribonucleoprotein La-B - African clawed frog
N:Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
C:Species: Xenopus laevis (African clawed frog)
C>Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C:Accession: S33817; S28544
R:Schery, D.; Stutz, F.; Lin-Marg, N.; Clarkson, S.G.
J. Mol. Biol. 231, 196-204, 1993

A:Title: La proteins from *Xenopus laevis*. cDNA cloning and developmental expression.
A:Reference number: S33817; MUID:93287095; PMID:8510143
A:Accession: S33817

A:Molecule type: mRNA
A:Residues: 1-427 <SCH>

A:Cross-references: EMBL:X68818; NID:G64875; PIDN:CAA48716.1; PID:G64876
A:Comment: This protein associates with a variety of small RNA molecules, most of which
act as a transcription termination factor.

C:Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology

C:Keywords: phosphoprotein; RNA binding

F:111-177/Domain: ribonucleoprotein repeat homology <RNM>

F:112-117/Region: RNA-binding RNP2 motif

F:150-157/Region: RNA-binding RNP1 motif

F:227-427/Domain: phosphorylated #status predicted <PHY>

Query Match 57.9%; Score 55; DB 1; Length 427;
Best Local Similarity 56.2%; Pred. No. 0.37;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 2 DADRIIKOLEYFGN 17
Db 11 DSDTKICEQIEYFGD 26

RESULT 4

T00677
hypothetical protein At2g43970 [imported] - Arabidopsis thaliana
N:Alternate names: hypothetical protein FEEL3.10
C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001
C:Accession: T00677; G84872

R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
submitted to the EMBL Data Library, June 1998

A:Description: Arabidopsis thaliana chromosome II BAC FEEL3 genomic sequence.

A:Reference number: Z14180

A:Accession: T00677

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-529 <ROU>

A:Cross-references: EMBL:AC004005; NID:G3212846; PID:G3212854

A:Experimental source: cultivar Columbia

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.

enus, D.; Merman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Frazer, C.M.; Venter, J
Nature 402, 761-766, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A:Reference number: A64420; MUID:20083487; PMID:10617197

A:Accession: G84872

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-529 <STO>

A:Cross-references: GB:AB02093; NID:G3212854; PIDN:AAC23405.1; GSPDB:GN00139

C:Genetics:
A:Gene: FEEL3.10; At2g43970

A:Map:position: 2

A:introns: 200/3; 228/1; 259/3; 283/3; 310/2; 344/3; 367/3; 421/3

Query Match 56.8%; Score 54; DB 2; Length 529;
Best Local Similarity 44.4%; Pred. No. 0.63;
Matches 8; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Oy 1 DDADRIIKOLEYFGNI 18
Db 191 EDSIOKIVNQYEFSD 208

RESULT 5

A53773
La/SS-B homolog D-1a - fruit fly (*Drosophila melanogaster*)

C:Species: *Drosophila melanogaster*

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000

C:Accession: A53773

R:Bat, C.; Li, Z.; Tollas, P.P.

Mol. Cell. Biol. 14, 5123-5129, 1994

A:Title: Developmental characterization of a *Drosophila* RNA-binding protein homologous t

A:Reference number: A53773; MUID:94309632; PMID:8035794

A:Accession: A53773

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-390 <BAI>

A:Cross-references: GB:U07652; NID:G464019; PIDN:AAA20518.1; PID:G464020

A:Genes: FlyBase:la

A:Cross-references: FlyBase:FBgn0011638

C:Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology

C:Keywords: leucine zipper; RNA binding

Query Match 52.6%; Score 50; DB 2; Length 390;
Best Local Similarity 57.1%; Pred. No. 2.3;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Oy 4 DORIIKOLEYFGN 17
Db 51 ERATIRQYEFYFGD 64

RESULT 6

A53781
ribonucleoprotein La - fruit fly (*Drosophila melanogaster*)

C:Species: *Drosophila melanogaster*

C>Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 20-Sep-1999

C:Accession: A53781

R:Yoo, C.J.; Molin, S.L.

Mol. Cell. Biol. 14, 5412-5424, 1994

A:Title: La proteins from *Drosophila melanogaster* and *Saccharomyces cerevisiae*: a yeast t

A:Reference number: A53781; MUID:94309661; PMID:8035818

A:Accession: A53781

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-390 <YOO>

A:Cross-references: GB:L32988; NID:G488469; PID:G488470

C:Genetics:

A:Gene: FlyBase:la

A:Cross-references: FlyBase:FBgn0011638

C:Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology

C:Keywords: RNA binding

Query Match 52.6%; Score 50; DB 2; Length 390;
Best Local Similarity 57.1%; Pred. No. 2.3;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Oy 4 DORIIKOLEYFGN 17
Db 51 ERATIRQYEFYFGD 64

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:33:11; Search time 14.0782 Seconds
(without alignments)
122.988 Million cell updates/sec

Title: US-09-836-073-17

Perfect score: 95

Sequence: 1 DDADQRIIKQLEYFGNI 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	92	96.8	396	2	T30953	hypothetical prote
2	57	60.0	428	1	S33818	ribonucleoprotein
3	55	57.9	427	1	S33817	ribonucleoprotein
4	54	56.8	529	2	T00677	hypothetical prote
5	50	52.6	390	2	A53773	la/SS-B homolog D-
6	50	52.6	390	2	A53781	ribonucleoprotein
7	48	50.5	385	2	S54705	transcription fact
8	46	48.4	391	2	H89777	capsular polysacch
9	45	47.4	156	2	D75605	hypothetical prote
10	45	47.4	177	2	F81175	inorganic pyrophos
11	45	47.4	177	2	G81930	probable inorganic
12	45	47.4	1002	2	A56578	yemamuclein-alpha
13	44.5	46.8	823	2	F64526	adenine/cytosine D
14	44	46.3	158	2	AD2410	hypothetical prote
15	44	46.3	300	2	A13101	transcription regu
16	44	46.3	332	2	A96185	probable transcrip
17	44	46.3	334	2	G97972	conserved hypotet
18	44	46.3	404	1	S03849	ribonucleoprotein
19	44	46.3	408	1	A31888	ribonucleoprotein
20	44	46.3	415	1	JC1494	ribonucleoprotein
21	44	46.3	455	2	G95104	hypothetical prote
22	44	46.3	176	2	G64049	inorganic pyrophos
23	43	45.3	342	2	A70183	hypothetical prote
24	43	45.3	780	2	T27659	hypothetical prote
25	43	45.3	1290	2	S73653	DNA-directed RNA p
26	42	44.2	183	2	F90570	hypothetical prote
27	42	44.2	222	2	S45634	adenylate kinase (
28	42	44.2	340	2	A89798	hypothetical prote
29	42	44.2	365	2	A26459	helix-destabilizin

30	42	44.2	840	2 B87467	conserved hypotet
31	42	44.2	895	1 IXLCP	EP-cadherin precu
32	42	44.2	905	2 S43064	cadherin - African
33	41.5	43.7	188	2 B97104	phospholipase D fa
34	41.5	43.7	729	2 A29651	KEX1 protein precu
35	41	43.2	178	2 S77850	probable histidine
36	41	43.2	192	1 S75273	hypothetical prote
37	41	43.2	214	2 G90582	adenylate kinase (
38	41	43.2	298	2 T38937	RNA-binding protei
39	41	43.2	298	2 T43542	heme oxygenase (de
40	41	43.2	315	1 A35199	hypothetical prote
41	41	43.2	346	2 S78647	acyl carrier prote
42	41	43.2	350	2 G90199	hypothetical prote
43	41	43.2	361	1 F65012	putative sulfatas
44	41	43.2	434	2 AC0512	hypothetical prote
45	41	43.2	450	2 T21931	

ALIGNMENTS

RESULT 1
T30953
hypothetical protein C44E4.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
C:Accession: T30953
R:Sammons, L.; Wohldmann, P.; Gillam, B.
Submitted to the EMBL Data Library, August 1999
A:Description: The sequence of C. elegans cosmid C44E4.
A:Reference number: Z20945
A:Accession: T30953
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-396 <SAM>
A:Cross-references: EMBL:AF003140; PIDN:AMB54169.1
A:Experimental source: stratum Bristol NZ; clone C44E4
C:Genetics:
A:Map position: 1
A:Introns: 45/1; 114/3
A:Note: C44E4.4
C:Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology

Query Match 96.8%; Score 92; DB 2; Length 396;
Best Local Similarity 94.4%; Pred. No. 2.8e-07;
Matches 17; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DDADQRIIKQLEYFGNI 18
|||:|||||||
DB 10 DDADQRIIKQLEYFGNI 27

RESULT 2
S33818
ribonucleoprotein la.A - African clawed frog
N:Alternate names: autoantigen SS-B/la; ribonucleoprotein SS-B
C:Species: Xenopus laevis (African clawed frog)
C:Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C:Accession: S33818; S28545
C:Schery, D.; Stutz, F.; Lin-Marg, N.; Clarkon, S.G.
J. Mol. Biol. 231, 196-204, 1993
A>Title: La proteins from Xenopus laevis. cDNA cloning and developmental expression.
A:Reference number: S33817; MIDID:93287095; PMID:8510143
A:Accession: S33818
A:Molecule type: mRNA
A:Residues: 1-428 <SCH>
A:Cross-references: EMBL:X68817; NID:G64873; PIDN:CAA48715.1; PID:G64874
C:Comment: This protein associates with a variety of small RNA molecules, most of which
ay act as a transcription termination factor.
C:Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology
C:Keywords: phosphoprotein; RNA binding
F:112-178/Domain: ribonucleoprotein repeat homology <RRM>
F:113-118/Region: RNA-binding RNP2 motif

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PA (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuk OM, Gour BJ, Byers S;

XX WPI, 2000-038791/03.

DR
XX
PT New cadherin modulating agents, used for modulating nonclassical cadherin-mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease.

XX
PS Disclosure; Fig 2; 252pp; English.

XX
CC The present invention describes cadherin modulating agents (MA) comprising peptides which comprise a nonclassical cadherin cell adhesion recognition (CAR) sequence. The MA can be used for modulating nonclassical cadherin-mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, enhancing delivery of a drug to a tumour in a mammal, treating cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-expressing cell, preventing or treating obesity in a mammal, stimulating blood vessel regression in a mammal, enhancing drug delivery to the central nervous system, treating a demyelinating neurological disease, increasing vasopermeability in a mammal, enhancing adhesion of nonclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for e.g. enhancing or directing neurite outgrowth, facilitating wound healing or reducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age-related macular degeneration, multiple sclerosis and diabetes. The products can also be used for detection and diagnosis and in bioreactors. AA60592 to AA64572 represent specifically claimed peptides, and CC AA64573 to AA64643 and AA23183 to AA23186 represent sequences used in the exemplification of the present invention

XX
SQ Sequence 108 AA:

Query Match 49.5%; Score 47; DB 3; Length 108;
Best Local Similarity 47.1%; Pred. No. 5.5;
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 DADQRIKQLEYYEGNI 18

DB 26 DADEGINKETLTPFSNL 42

Search completed: September 10, 2004, 17:51:53
Job time : 59.4128 secs

XX 16-DEC-1999; 99UP-00377484.
 PR 07-APR-2000; 2000JP-00159162.
 PR 03-AUG-2000; 2000JP-00280988.
 XX
 PA (KYOWA) KYOWA HAKKO KOGYO KK.
 XX
 PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;
 PI Tateishi N, Senoh A, Ikeda M, Ozaki A;
 XX
 DR MPI; 2001-376931/40.
 DR N-PSDB; AAH66529.
 XX
 PT Novel polynucleotides derived from Corynebacterium bacteria, for identifying
 PT mutation point of a gene, measuring expression of a gene, analyzing
 PT expression profile or pattern of a gene and identifying homologous gene.
 PS
 XX Claim 17; SEQ ID NO 5064; 246bp + Sequence Listing; English.
 CC The present invention provides a number of nucleotide and protein
 CC sequences from the Corynebacterium glutamicum. These
 CC are useful for identifying the mutation point of a gene derived from a
 CC mutant of corynebacterium, measuring expression amount and analysing
 CC the expression profile or expression pattern of a gene derived from
 CC Corynebacterium, and identifying a homologue of a gene derived from
 CC corynebacterium. Corynebacterium bacteria are useful for producing amino
 CC acids, nucleic acids, vitamins, saccharides and organic acids,
 CC particularly L-lysine. The present sequence is a protein described in the
 CC exemplification of the invention. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from the European Patent Office
 XX
 SQ Sequence 397 AA;
 Query Match 50.5%; Score 48; DB 4; Length 397;
 Best Local Similarity 50.0%; Pred. No. 17;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 2 DADQRIIKOLEYFGN 17
 DB 138 DAQOSLDRMEYFGN 153
 RESULT 14
 ABG01240
 ID ABG01240 standard; protein; 650 AA.
 XX
 AC ABG01240;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #1231.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX
 PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Drmanac RT, Liu C, Tang YT;
 PI MPI; 2001-639362/73.
 DR N-PSDB; AAS65427.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID NO 31599; 103bp; English.
 CC
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (II) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 650 AA;
 Query Match 50.5%; Score 48; DB 4; Length 650;
 Best Local Similarity 47.1%; Pred. No. 30;
 Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 2 DADQRIIKOLEYFGNI 18
 DB 223 DADGINKELIVFNSL 239
 RESULT 15
 AAY64613
 ID AAY64613 standard; peptide; 108 AA.
 XX
 AC AAY64613;
 XX
 DT 02-MAR-2000 (first entry)
 XX
 DE Nonclassical cadherin extracellular domain SEQ ID NO.41.
 XX
 KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease.
 XX
 OS Mammalia.
 XX
 PN WO9957149-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 05-MAY-1999; 99WO-CA000363.
 XX
 PR 05-MAY-1998; 98US-00073040.
 PR 06-NOV-1998; 98US-00187859.
 PR 20-JAN-1999; 99US-00234395.
 PR 08-MAR-1999; 99US-00264516.
 XX

CC replication of viruses that utilise internal ribosome entry site (IRES)

4 DÖRIKÖLEYFEN 17

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PR 29-OCT-1999; 99US-0162122P.

Query Match 56.8%; Score 54; DB 3; Length 923;
Best Local Similarity 44.4%; Pred. No. 4.4;
Matches 8; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
QY 1 DDADRIIKOLEYFQNI 18
DB 121 EDSDIKVNOVEYFSDL 138
RESULT 6
AA647712
ID AA647712 standard; protein; 993 AA.
XX
AC AA647712;
XX
DT 18-OCT-2000 (First entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 60166.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-00301439.
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XX 25-FEB-1999; 99US-0121825P.
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PR 08-APR-1999; 99US-0128714P.
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PR 24-SEP-1999; 99US-0156559P.
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PR 29-OCT-1999; 99US-0162142P.

Query Match 56.8%; Score 54; DB 3; Length 913;
Best Local Similarity 44.4%; Pred. No. 4.4;
Matches 8; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Cy i DDADRRITKOLEYFGNI 18
Db 111 EDSIOKIVNQVYRPSDL 128

RESULT 5
AAG47713

ID AAG47713 standard; protein; 923 AA.

AC AAG47713;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 60167.

KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

OS Arabidopsis thaliana.

PN BP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

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RESULT 2

ABP70526
ID ABP70526 standard; protein; 411 AA.

DE Histone deacetylase chromatin-associated protein complex subunit MXC.
XX
KM Histone acetyltransferase; histone deacetylase; gene expression profile.
KM chromatin-associated protein; gene expression.

PR 22-JUN-2001; 2001US-0300135P

PT New chimeric polypeptide comprising a histone acetyltransferase
PT polypeptide segment and a segment comprising a histone deacetylase
PT chromatin-associated protein complex subunit, useful for modulating gene
PT expression in cells.

The specification describes chimeric histone acetyltransferase polypeptides. The chimeric polypeptides comprises a polypeptide segment that exhibits histone acetyltransferase activity, and a polypeptide segment having 40% or greater sequence identity to a subunit of a histone deacetylase chromatin-associated protein complex. The chimeric polypeptides are useful for determining gene expression profiles in specific cells, for modulating gene expression in specific cells, and for making genetically modified eukaryotes. The present sequence represents an exemplary histone deacetylase chromatin-associated protein complex subunit, which can be used to produce chimeric polypeptides of the invention.

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Best Local Similarity 52.9%; Pred. No. 0.53;
Matches 9; Conservative 6; Mismatches 2; Indels 0; Gaps 0
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RESULT 3
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ID ABG72115 standard; peptide; 18 AA
XX

AC ABG72115;

DT 28-JAN-2003 (first entry)

DE Viral replication inhibiting peptide, XENOPUS.

KM viral replication inhibitor; IRES initiated translation; LBP internal ribosome entry site initiated translation; La antigen protein viral life cycle; antiviral therapy; pharmaceutical; veterinary; agricultural; horticultural; virucide; xenopus.

PF 12-APR-2002; 2002WO-US011589.

PR 16-APR-2001; 2001US-00836073.

PA (UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT

PI Dasgupta A, Das S, Baidya N;

PT New compound containing acidic and aromatic amino acids, useful as
PT antiviral therapy in pharmaceutical, veterinary or
PT agricultural/horticultural applications.

CC The present invention relates to copeptides and methods of inhibiting
CC replication of viruses that utilize internal ribosome entry site (IRES)
CC initiated translation, and/or inhibiting viruses that utilize the La
CC antigen protein (LAP) in any phase of their life cycle. The peptides of
CC the invention compete with LAP and inhibit the utilization of various
CC biochemical and physiological functions of LAP required for a productive
CC life cycle. The methods and compositions are useful as antiviral therapy
CC in pharmaceutical, veterinary or agricultural/norticultural applications
CC AB5712101-AB5712119 represent peptides useful as antiviral agents

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Best Local Similarity	56.2%	Pred. No. 0.03;		
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ID AAG47714 standard; protein; 913 AA

Arabidopsis thaliana protein fragment SEQ ID NO: 60168

Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter termination sequence.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2004, 16:58:20 : Search time 56.3129 Seconds
(without alignments)
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Title: US-09-836-073-17

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Total number of hits satisfying chosen parameters: 1586107

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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5	54	56.8	923	3 AAG47713	Aag47713 Arabidops
6	54	56.8	993	3 AAG47712	Aag47712 Arabidops
7	50	52.6	16	6 ABG72119	Abg72119 Viral rep
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14	48	50.5	650	4 ABG01240	Abg01240 Novel hum
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16	47	49.5	176	6 AAE34638	Aae34638 Moraxella
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25	45	47.4	1002	4 ABB58137	Abb58137 Drosophila

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27	45	47.4	1062	4 AAB62238	Aab62238 Human cal
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ALIGNMENTS

RESULT 1	ABG72117	standard; peptide; 18 AA.
ID	ABG72117	standard; peptide; 18 AA.
AC	ABG72117	
DT	28-JAN-2003	(first entry)
DE	Viral replication inhibiting peptide, C. ELEGANS.	
XX	Viral replication inhibitor; IRES initiated translation; IAP;	
XX	Internal ribosome entry site initiated translation; Ia antigen protein;	
XX	Viral life cycle; antiviral therapy; pharmaceutical; veterinary;	
XX	agricultural; horticultural; virucide.	
OS	Caenorhabditis elegans.	
PN	W0200283858-A2.	
PD	24-OCT-2002.	
XX	12-APR-2002; 2002WO-US011589.	
PF	16-APR-2001; 2001US-00836073.	
PR	(UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.	
PA	Dasgupta A, Das S, Baidya N;	
XX	WPI; 2003-058634/05.	
PT	New compound containing acidic and aromatic amino acids, useful as	
PT	antiviral therapy in pharmaceutical, veterinary or	
PT	agricultural/horticultural applications.	
XX	Claim 1; Page 15; 19pp; English.	
XX	The present invention relates to peptides and methods of inhibiting the	
XX	replication of viruses that utilise internal ribosome entry site (IRES)	
XX	initiated translation, and/or inhibiting viruses that utilise the Ia	
XX	antigen protein (IAP) in any phase of their life cycle. The peptides of	
XX	the invention compete with IAP and inhibit the utilisation of various	
XX	biochemical and physiological functions of IAP required for a productive	
XX	life cycle. The methods and compositions are useful as antiviral therapy	
XX	in pharmaceutical, veterinary or agricultural/horticultural applications.	
XX	ABG72101-ABG72119 represent peptides useful as antiviral agents	
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us-09-836-073-16.rapb

Page 5

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; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
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US-09-836-073-12

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Db 1 AALEAKICHQI-EYFGDF 18

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; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
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US-09-836-073-10

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; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
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; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
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US-09-836-073-3

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; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-4

Query Match      73.6%; Score 76.5; DB 9; Length 18;
Best Local Similarity 93.8%; Pred. No. 4.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Cy 4 EAKICHQIEEYFGDF 19
   ||||| ||||| |||||
Db 4 EAKICHQI-EYFGDF 18
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-102-806-695

Query Match
Best Local Similarity 85.1%; Score 88.5; DB 14; Length 460;
Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 AALEAKICHQIEEYFGDF 19
Db 63 AALEAKICHQI-EYFGDF 80

RESULT 7
US-10-264-049-2643
; Sequence 2643, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P413P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2643
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-2643

Query Match
Best Local Similarity 85.1%; Score 88.5; DB 15; Length 460;
Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 AALEAKICHQIEEYFGDF 19
Db 63 AALEAKICHQI-EYFGDF 80

RESULT 8
US-09-836-073-13
; Sequence 13, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Balidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mouse
US-09-836-073-13

Query Match
Best Local Similarity 81.2%; Score 84.5; DB 9; Length 17;
Matches 17; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 AALEAKICHQIEEYFGDF 19
Db 1 AALEAKICHQI-EYFGDF 17
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RESULT 9
US-09-836-073-11
; Sequence 11, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Balidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-11

Query Match
Best Local Similarity 80.3%; Score 83.5; DB 9; Length 18;
Matches 17; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 AALEAKICHQIEEYFGDF 19
Db 1 AALEAKICHQIEQ-YFGDF 18

RESULT 10
US-09-836-073-9
; Sequence 9, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Balidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-9

Query Match
Best Local Similarity 79.3%; Score 82.5; DB 9; Length 18;
Matches 17; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 AALEAKICHQIEEYFGD 18
Db 1 AALEAKICHQI-EYFGD 17

RESULT 11
US-09-836-073-12
; Sequence 12, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Balidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
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```

; APPLICANT: Balda, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-1

Query Match      85.1%; Score 88.5; DB 9; Length 18;
Best Local Similarity 94.7%; Pred. No. 5.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1 AALEAKICHQIEYYFGDF 19
        |||||||
        1 AALEAKICHQI-EYYFGDF 18

Db

RESULT 3
US-09-836-073-14
; Sequence 14, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Balda, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 14
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Bovine
US-09-836-073-14

Query Match      85.1%; Score 88.5; DB 9; Length 18;
Best Local Similarity 94.7%; Pred. No. 5.7e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1 AALEAKICHQIEYYFGDF 19
        |||||||
        1 AALEAKICHQI-EYYFGDF 18

Db

RESULT 4
US-10-170-385-477
; Sequence 477, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
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; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 477
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-477

Query Match      85.1%; Score 88.5; DB 12; Length 408;
Best Local Similarity 94.7%; Pred. No. 1.5e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1 AALEAKICHQIEYYFGDF 19
        |||||||
        11 AALEAKICHQI-EYYFGDF 28

Db

RESULT 5
US-09-925-298-695
; Sequence 695, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103
; CURRENT APPLICATION NUMBER: US/09/925,298
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 695
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-298-695

Query Match      85.1%; Score 88.5; DB 12; Length 460;
Best Local Similarity 94.7%; Pred. No. 1.7e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY      1 AALEAKICHQIEYYFGDF 19
        |||||||
        63 AALEAKICHQI-EYYFGDF 80

Db

RESULT 6
US-10-102-806-695
; Sequence 695, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 695
; LENGTH: 460
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OM protein - protein search, using sw model

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Title: US-09-836-073-16

Perfect score: 104
Sequence: 1 AALEAKICHOIEYFGDP 19

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Searched: 1335176 seqs, 320689617 residues

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Listing first 45 summaries

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17: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	104	100.0	19	9	US-09-836-073-16
2	88.5	85.1	18	9	US-09-836-073-1
3	88.5	85.1	18	9	US-09-836-073-14
4	88.5	85.1	408	12	US-10-170-385-477
5	88.5	85.1	460	12	US-09-925-298-695
6	88.5	85.1	460	14	US-10-102-806-695
7	88.5	85.1	460	15	US-10-264-049-2643
8	84.5	81.2	17	9	US-09-836-073-13
9	83.5	80.3	18	9	US-09-836-073-11
10	82.5	79.3	18	9	US-09-836-073-9
11	80.5	77.4	18	9	US-09-836-073-12
12	79.5	76.4	18	9	US-09-836-073-10
13	76.5	73.6	18	9	US-09-836-073-2
14	76.5	73.6	18	9	US-09-836-073-3
15	76.5	73.6	18	9	US-09-836-073-4

16	75.5	72.6	18	9	US-09-836-073-8	Sequence 8, Appli
17	73.5	70.7	18	9	US-09-836-073-7	Sequence 7, Appli
18	65.5	63.0	18	9	US-09-836-073-15	Sequence 15, Appli
19	64.5	62.0	18	9	US-09-836-073-5	Sequence 5, Appli
20	63	60.6	18	9	US-09-836-073-6	Sequence 6, Appli
21	62.5	60.1	21	15	US-10-376-121A-20	Sequence 20, Appli
22	58	55.8	37	9	US-09-843-676-24	Sequence 24, Appli
23	58	55.8	37	9	US-09-766-253-24	Sequence 24, Appli
24	58	55.8	37	10	US-09-438-486-24	Sequence 24, Appli
25	58	55.8	37	14	US-10-054-758-25	Sequence 24, Appli
26	58	55.8	37	14	US-10-054-295-24	Sequence 24, Appli
27	58	55.8	37	14	US-10-054-611-24	Sequence 24, Appli
28	57.5	55.3	38	12	US-10-325-810-214	Sequence 21, App
29	49	47.1	2169	9	US-09-738-626-5455	Sequence 5455, Ap
30	48.5	46.6	38	9	US-09-843-676-25	Sequence 25, Appli
31	48.5	46.6	38	10	US-09-766-253-25	Sequence 25, Appli
32	48.5	46.6	38	10	US-09-438-486-25	Sequence 25, Appli
33	48.5	46.6	38	12	US-10-325-810-215	Sequence 215, App
34	48.5	46.6	38	14	US-10-054-758-25	Sequence 25, Appli
35	48.5	46.6	38	14	US-10-054-295-25	Sequence 25, Appli
36	48.5	46.6	38	14	US-10-054-611-25	Sequence 25, Appli
37	47	45.2	456	9	US-09-861-400-6	Sequence 6, Appli
38	47	45.2	482	9	US-09-861-400-5	Sequence 5, Appli
39	46.5	44.7	16	9	US-09-836-073-19	Sequence 19, Appli
40	45.5	43.8	425	12	US-10-296-115-1146	Sequence 1146, Ap
41	45.5	43.8	643	9	US-09-736-968A-60	Sequence 60, Appli
42	45.5	43.8	675	10	US-09-978-244A-18	Sequence 18, Appli
43	45.5	43.8	2045	9	US-09-736-969A-95	Sequence 95, Appli
44	45.5	43.8	2045	9	US-09-736-960-92	Sequence 92, Appli
45	45.5	43.8	2045	9	US-09-736-968A-109	Sequence 109, App

ALIGNMENTS

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RESULT 1
US-09-836-073-16
; Sequence 16, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Rat
US-09-836-073-16

Query Match      100.0%; Score 104; DB 9; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.2e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AALEAKICHOIEYFGDP 19
Db      1 AALEAKICHOIEYFGDP 19

RESULT 2
US-09-836-073-1
; Sequence 1, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
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Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 7 ICHQIEEYYPGDP 19
| | | | | : | |
Db 147 IAHQIEGYFMGHP 159

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Query Match	43.38;	Score 45;	DB 2;	Length 100;
Best Local Similarity	61.58;	Pred. No. 18;		

Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 ICHQIEEYFGD 18
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Db 97 ICHELESWFLGD 108

RESULT 9

QEX37 PRELIMINARY; PRT; 301 AA.
ID QEX37;
AC QEX37;
DT 01-MAR-2003 (TRMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRMBLrel. 25, Last annotation update)
DE Pseudouridine synthase.
GN MYE130.
OS Mycoplasma penetrans.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NX NCBI_TaxID=28227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HF-2;
RA MEDLINE=22354719; PubMed=1246555;
RA Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,
RT Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.,
RT "The complete genomic sequence of Mycoplasma penetrans, an
RT intracellular bacterial pathogen in humans."
RL Nucleic Acids Res. 30:5293-5300(2002).
DR EMBL, AP004170; BAC43803.1;
DR GO: 0004730; F.pseudouridylylase synthase activity; IEA.
DR GO: 0003723; F.RNA binding; IEA.
DR InterPro; IPR006145; Pseudou_synth.
DR InterPro; IPR006225; Pseudou_synth.
DR InterPro; IPR006224; Rlu_synth.
DR Pfam; PF00849; Pseudou_synth_2; 1.
DR ProDom; PD001819; PSI_RLU; 1.
DR TIGRFAMs; TIGR00005; TUD_subfam; 1.
DR PROSITE; PS00889; S4; 1.
KM Complete proteome.
SQ SEQUENCE 301 AA; 35770 MW; 2961D557AB45B730 CRC64;

Query Match 45.2%; Score 47; DB 16; Length 301;
Best Local Similarity 46.7%; Pred. No. 15;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 LEAKICHOIEEYFG 17
|||:|:|
Db 131 LEANLCHRLDKYTTG 145

RESULT 10

Q8SC2 PRELIMINARY; PRT; 357 AA.
ID Q8SC2;
AC Q8SC2;
DT 01-OCT-2001 (TRMBLrel. 18, Created)
DT 01-OCT-2001 (TRMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TRMBLrel. 25, Last annotation update)
DE Hypothetical protein orf357 from chromosome 3.
GN ORF357.
OS Guillardia theta (Cryptomonas phi).
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
NX NCBI_TaxID=55529;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21223349; PubMed=11232671;
RA Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng L.T.,
RT Wu X., Reich M., Cavalier-Smith T., Maier U.G.,
RT "The highly reduced genome of an enslaved algal nucleus."
RL EMBL, AF083031; AAK39661.1; -.
DR PIR; H90120; H90120.
DR InterPro; IPR001680; WD40.

DR SMART; SM00320; WD40; 3.
KM Hypothetical protein; Repeat; WD repeat
SQ SEQUENCE 357 AA; 42401 MW; 71AB8F986A04C82 CRC64;

Query Match 45.2%; Score 47; DB 10; Length 357;
Best Local Similarity 50.0%; Pred. No. 18;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 LEAKICHOIEEYFGD 18
|||:|:|
Db 242 LKNVFSQMKRYFGD 257

RESULT 11

Q42907 PRELIMINARY; PRT; 448 AA.
ID Q42907;
AC Q42907;
DT 01-JUN-1998 (TRMBLrel. 06, Created)
DT 01-JUN-1998 (TRMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TRMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN SPBC119.16c.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
NX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97h-;
RA Wood V., Rajandream M.A., Barrell B.G., Skelton J., Churcher C.M.,
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL, AL022117; CA17931.1; -.
DR PIR; T39314; T39314.
DR GeneDB; SPombe; SPBC119.16c; -.
KM Hypothetical protein.
SQ SEQUENCE 448 AA; 51190 MW; 3856729F41A98DAB CRC64;

Query Match 45.2%; Score 47; DB 3; Length 448;
Best Local Similarity 47.4%; Pred. No. 23;
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 AALEAKICHOIEEYFGD 19
|||:|:|
Db 9 ATPDKKEGTVENYTPGDF 27

RESULT 12

Q04639 PRELIMINARY; PRT; 284 AA.
ID Q04639;
AC Q04639;
DT 01-NOV-1996 (TRMBLrel. 01, Created)
DT 01-NOV-1996 (TRMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TRMBLrel. 22, Last annotation update)
DE Chromosome XIII COSMID 9745.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NX NCBI_TaxID=49312;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB972;
RA Bowman S., Churcher C.,
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB972;
RA Barrell B., Rajandream M.A.,
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z38114; CAA86253.1; -.
SQ SEQUENCE 284 AA; 32882 MW; 200EB06A92A3CCF CRC64;

Query Match 44.2%; Score 46; DB 3; Length 284;

RESULT 5			
ID	067676	PRELIMINARY;	PRT; 135 AA.
AC	067676;		
DT	01-AUG-1998	(TREMBLrel. 07, Created)	
DT	01-AUG-1998	(TREMBLrel. 07, Last sequence update)	
DT	01-JUN-2003	(TREMBLrel. 24, Last annotation update)	
DE	Thioredoxin.		
DE	TRX2 OR A0.1811.		
OS	Aquifex aeolicus.		
OC	Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.		
OX	NCBI_TaxID=63363;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=VF5;		
RX	MEDLINE=98196666; PubMed=9537320;		
RA	Decker G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,		
RA	Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,		
RA	Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;		
RT	"The complete genome of the hyperthermophilic bacterium Aquifex		
RT	aeolicus";		
RL	Nature 392:353-358(1998).		
RL	EMBL; AE000757; AAC07635.1; -.		
DR	PIR; B70456; B70456.		
DR	GO; GO:0005489; F:electron transporter activity; IEA.		
DR	GO; GO:0006118; P:electron transport; IEA.		
DR	InterPro; IPR006653; ThioRedox_dom2.		
KW	Complete proteome.		
SQ	SEQUENCE 135 AA; 15746 MW; B9B8F51A91D7DD54 CRC64;		

Query Match	55;	Score	55;	DB	16;	length	155;
Beet Local Similarity	72.7%;	Pred. No.	0.31;				
Matches	8;	Conservative	2;	Mismatches	1;	Indels	0;
OY	8	CHOIEBRYFGD	18				
		:: ::					
Db	52	CHQVEEFVFGD	62				

RESULT 6	Q7ZT10	PRT;	401 AA.
ID	Q7ZT10	PRELIMINARY;	
AC	Q7ZT10;		
DT	01-JUN-2003 (TREMBLrel. 24, Created)		
DT	01-JUN-2003 (TREMBLrel. 25, last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 24, last annotation update)		
DE	Similar to sjogren syndrome antigen B (Auricanigen Ia).		
OS	Brachydanio rerio (Zebrafish) (Danio rerio).		
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostei		
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprin		
OC	Cyprinidae; Danio.		
NCBI	Taxid=7955;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Body;		
RA	Strausberg R.;		
RL	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.		
RL	EMBL; BC045392; AAH45392.1; -		
DR	GO; GO:0005634; C:nucleus; IEA.		
DR	GO; GO:0003723; F:RNA binding; IEA.		
DR	InterPro; IPR002344; Lupus Ia.		
DR	InterPro; IPR006630; Lupus Ia_dom.		
DR	InterPro; IPR000504; RNA_rec_mot.		
DR	Pfam; PF00076; rrm; 1.		
DR	PRINTS; PR00302; LUPUSIA.		
DR	SMART; SM00715; IA; 1.		
DR	SMART; SM00360; RRM; 1.		
DR	PROSITE; PSS0102; RRM; 1.		
DR	PROSITE; PSS00030; RRM_RNP_1; 1.		
SQ	SEQUENCE 401 AA; 46138 MW; 2EF032FDD3916291 CRC64;		

Best Local Similarity 68.8%; Pred. No. 3.7;
Matches 11; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

RESULT 7		
Q8NP6:		
ID	Q8NP6	PRELIMINARY; PRT; 2169 AA.
AC	Q8NP6	
DT	01-OCT-2002 (TrEMBLrel. 22, Created)	
DT	01-OCT-2002 (TrEMBLrel. 22, last sequence update)	
DT	01-JUN-2003 (TrEMBLrel. 24, last annotation update)	
DE	Hypothetical protein Cg11775.	
GN	Cg11775.	
OS	Corynebacterium glutamicum (Brevibacterium flavum).	
OC	Bacteria; Actinobacteria; Actinomycetales; Actinomycetaceae; Corynebacteriaceae; Corynebacterium.	
OC	Corynebacterineae; Corynebacteriaceae; Corynebacterium.	
OX	NCBI_TaxID=1718;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;	
RA	Nakagawa S.;	
RT	"Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";	
RL	Submitted (MAY-2002) to the EMBL/GenBank/DDJJ databases.	
DR	EMBL; AP005279; BAB99168.1; -	
DR	GO; GO:0006457; P:protein folding; IEA.	
DR	InterPro; IPR001179; FKBP foldase.	
DR	PROSITE; PS00453; FKBP_P1ASE.1; 1.	
KW	Hypothetical protein; Complete proteome.	
SQ	SEQUENCE 2169 AA; 240194 MW; 4AEB029B002C49A CRC64;	

Query Match Similarity	47.1%	Score 49;	DB 16;	Length 2169;
Best Local Similarity	43.8%	Pred. No. 57;		
Matches	7;	Conservative	7;	Mismatches 2;
				Indels 0;
				Gaps 0;
Qy	3	LEAKTCHQTEYYFGD	18	
		.: : : : : : : :		
Db	1291	LOAOECHEIMEHFN	1306	

RESULT 8				
ID	Q8YZF2	PRELIMINARY;	PRT;	187 AA.
AC	Q8YZF2;			
DT	01-MAR-2002 (TrEMBLrel. 20, Created)			
DT	01-MAR-2002 (TrEMBLrel. 20, last sequence update)			
DT	01-JUN-2003 (TrEMBLrel. 24, last annotation update)			
DE	Hypotheetical protein ALR0508.			
GN	ALR0508.			
OS	Anabaena sp. (strain PCC 7120).			
OC	Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.			
OX	NCBI_TaxID=103690;			
RN	[1]			
RA	SEQUENCE FROM N.A.			
RX	MEDLINE=21595285; PubMed=11759840;			
RA	Kaneo T., Nakamura Y., Wolk C.P., Kuritz T., Sasaemoto S.,			
RA	Watanabe A., Iiguchi M., Ishikawa A., Kawashima K., Kimura T			
RA	Kishida Y., Kohara M., Matsunoto M., Matsuno A., Muraki A.,			
RA	Nakazaki N., Shimoto S., Sugimoto M., Takazawa M., Yamada M.,			
RA	Yasuda N., Tabata S.;			
RT	"Complete genomic sequence of the filamentous nitrogen-fixing			
RT	Cyanobacterium Anabaena sp. strain PCC 7120.";			
RL	DNA Res. 8:205-213(2001).			
DR	EMBL; AF003582; BAB72466.1; -.			
DR	PIR; AC1870; AC1870.			
KW	Hypotheetical protein; Complete proteome.			
SQ	SEQUENCE 187 AA; 21553 MW; 77D82FC9DD03A53E CRC64;			
Query Match	45.2%;	Score 47;	DB 16;	Length 187;
Best Local Similarity	50.0%;	Pred. NO. 9.4;		

DR GO:0005634; C:nucleus; IDA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR00504; RNA_rec_mot.
DR Pfam; PF05383; LA; 1.
DR Pfam; PF00076; xrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
SQ SEQUENCE 381 AA; 43891 MW; 2E2DEF1452C0F0E9 CRC64;

Query Match 81.2%; Score 84.5; DB 11; Length 381;
Best Local Similarity 94.4%; Pred. No. 1; 1e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 2 ALEAKICHOIEEYFGDF 19
Db 12 ALEAKICHOI-EYFGDF 28

RESULT 2

Q8BTU4 PRELIMINARY; PRT; 415 AA.
AC Q8BTU4;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Sjogren syndrome antigen B.
GN SSB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NO; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT Nature 420:563-573 (2002).";
RL EMBL; AK088677; BAC40498.1; -.
DR MGD; MGI:98423; Seb.
DR GO:0005634; C:nucleus; IDA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR00504; RNA_rec_mot.
DR Pfam; PF05383; LA; 1.
DR Pfam; PF00076; xrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 415 AA; 47657 MW; A7545C7686AC6363 CRC64;

Query Match 81.2%; Score 84.5; DB 11; Length 415;
Best Local Similarity 94.4%; Pred. No. 1; 2e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 2 ALEAKICHOIEEYFGDF 19
Db 12 ALEAKICHOI-EYFGDF 28

RESULT 3

Q7ZTK2 PRELIMINARY; PRT; 427 AA.
AC Q7ZTK2;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Similar to lupus LA protein homolog B.

OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxId=8355;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Embryo.
RA Klein S., Strausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046654; AA046654.1; -.
DR GO:0005634; C:nucleus; IEA.
DR GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR00504; RNA_rec_mot.
DR Pfam; PF00076; xrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 2.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 427 AA; 48996 MW; 1E7CD82D8AB9C69A CRC64;

Query Match 57.2%; Score 59.5; DB 13; Length 427;
Best Local Similarity 75.0%; Pred. No. 0.19;
Matches 12; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 3 LEAKICHOIEEYFGD 18
Db 12 LDTKICEGI-EYFGD 26

RESULT 4

Q8OHI5 PRELIMINARY; PRT; 206 AA.
AC Q8OHI5;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Untranslated region binding-protein.
GN UBP.

OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxId=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA L'Ecuuyer T.J., Fang H.-L.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF467897; AAL76269.1; -.
DR GO:0005634; C:nucleus; IEA.
DR GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR00504; RNA_rec_mot.
DR Pfam; PF05383; LA; 1.
DR Pfam; PF00076; xrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 206 AA; 23992 MW; 965B62FDFFB90E9 CRC64;

Query Match 56.2%; Score 58.5; DB 13; Length 206;
Best Local Similarity 75.0%; Pred. No. 0.13;
Matches 12; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Qy 3 LEAKICHOIEEYFGD 18
Db 13 LESKICQOI-EYFGN 27

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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:29:01; Search time 43.5196 Seconds
(without alignments)
137.751 Million cell updates/sec

Title: US-09-836-073-16

Perfect score: 104
Sequence: 1 AALEAKICHQIEHYFGDP 19

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL, 25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertibrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriophage: *
17: sp_archaeal: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	84.5	81.2	381	11	Q9CXB9 mus musculus
2	84.5	81.2	415	11	Q8BTU4 Q8btu4 mus musculus
3	59.5	57.2	427	13	Q7ZTK2 xenopus lae
4	58.5	56.2	206	13	Q8OH15 Q8oh15 gallus gall
5	55	52.9	135	16	Q67676 aquifex aeo
6	51.5	49.5	401	13	Q7ZT10 brachydanio
7	49	47.1	2169	16	Q8NPN6 Q8npn6 corynebacte
8	47	45.2	187	16	Q8YZF2 Q8yzf2 anabaena sp
9	47	45.2	301	16	Q8EX37 Q8ex37 mycoplasma
10	47	45.2	357	10	Q98SC2 Q98sc2 guillardia
11	47	45.2	448	3	Q42907 Q42907 schizosacch
12	46	44.2	284	3	Q04639 Q04639 saccharomyc
13	46	44.2	456	17	Q29131 Q29131 archaeoglob
14	45.5	43.8	509	4	Q7Z7P4 Q7z7p4 homo sapien
15	45	43.3	166	2	Q8GK02 Q8gk02 helicobacte
16	45	43.3	184	2	Q7X5D8 Q7x5d8 helicobacte

17	45	43.3	231	2	Q7X5E0 Q7x5e0 helicobacte
18	45	43.3	409	8	Q98RP4 Q98rp4 guillardia
19	45	43.3	748	16	Q8AXX3 Q8axx3 bacteroides
20	45	43.3	928	10	Q9LJ02 Q9lj02 oryza sativ
21	45	43.3	1156	12	Q57230 Q57230 vaccinia vi
22	45	43.3	1164	12	Q90027 Q90027 variola maj
23	45	43.3	1164	12	Q9JF79 Q9jf79 vaccinia vi
24	45	43.3	1164	12	Q90031 Q90031 variola vir
25	45	43.3	1164	12	Q8L190 Q8l190 ectromella
26	45	43.3	1164	12	Q8V4V3 Q8v4v3 monkeypox v
27	45	43.3	1164	12	Q8V2N1 Q8v2n1 camelpox vi
28	45	43.3	1164	12	Q8DVL1 Q8dvl1 cowpox viru
29	45	43.3	1676	8	Q85FR6 Q85fr6 cyanidiosch
30	44	42.3	281	11	Q9COK3 Q9cok3 mus musculu
31	44	42.3	284	4	Q8NG50 Q8ng50 homo sapien
32	44	42.3	505	8	Q8SV94 Q8sv94 elaeagnus u
33	44	42.3	592	5	Q9VN01 Q9vn01 dreosiphila
34	44	42.3	627	5	Q81EX1 Q81ex1 trypanosoma
35	44	42.3	627	5	Q86MC2 Q86mc2 trypanosoma
36	44	42.3	627	5	Q7YU26 Q7yu26 trypanosoma
37	44	42.3	658	5	Q86BB2 Q86bb2 dreosiphila
38	44	42.3	888	3	Q873B9 Q873b9 neurospora
39	43.5	41.8	119	10	Q9ZPB9 Q9zpb9 neurotheca
40	43	41.3	185	5	Q9UAF3 Q9uaf3 polyantheca
41	43	41.3	297	4	Q9H1U9 Q9h1u9 homo sapien
42	43	41.3	427	16	Q05874 Q05874 mycobacteri
43	43	41.3	427	16	Q7TWY2 Q7twy2 mycobacteri
44	43	41.3	447	10	Q93V61 Q93v61 arabidopsis
45	43	41.3	510	10	Q43819 Q43819 pisum sativ

ALIGNMENTS

RESULT 1

ID Q9CXB9 PRELIMINARY; PRT; 381 AA.
AC Q9CXB9; 01-JUN-2001 (T-REMBLrel. 17, Created)
DT 01-JUN-2001 (T-REMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (T-REMBLrel. 25, Last annotation update)
DE Sjogren syndrome antigen B.
OS SSB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=1117851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishi Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana S.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadora K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giesi C., King B., Kociba H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Maehio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bartsch G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohesuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK017822; BAB30957.1; -.
DR MGD; MGI:98423; Ssd.

DR Pfam; PF00562; RNA_pol_Rpb2_6; 1.
 DR Pfam; PF04560; RNA_pol_Rpb2_7; 1.
 DR PROSITE; PS01166; RNA_POL_BETA; 1.
 KW Transferase; DNA-directed RNA polymerase; Transcription; Zinc;
 KW Zinc-finger.
 FT ZN PING 1087 1106 C4-TYPE (POTENTIAL).
 SQ SEQUENCE 1164 AA; 133329 MW; 0452B84ED810CD53 CRC64;

Query Match 43.3%; Score 45; DB 1; Length 1164;
 Best local Similarity 56.2%; Pred. NO. 22;
 Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 3 LEAKTCHQIEHYFGD 18
 |||||
 Db 505 LEKKICEYIRSYKDD 520

Search completed: September 10, 2004, 17:53:09
 Job time : 9.64246 secs

FT INIT MET 9 9 POLYPEPTIDE, ISOFORM 2.
 FT ZN FING 1087 1106 C4-TYPE (POTENTIAL).
 FT SEQUENCE 1164 AA, 133363 MW, 2200D68F5238DB7 CRC64;
 SQ
 Query Match 43.3%; Score 45; DB 1; Length 1164;
 Best Local Similarity 56.2%; Pred. No. 22;
 Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 3 LEAKICHOIEEYFGD 18
 DB 505 LEKICIEYIRSYKXD 520
 RESULT 14
 ID RPO2 VACCV STANDARD; PRT; 1164 AA.
 AC P19798;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DNA-directed RNA polymerase 132 kDa polypeptide (EC 2.7.7.6).
 GN RPO132 OR A24R.
 OS Vaccinia virus (strain WR), and
 OS Vaccinia virus (strain Copenhagen).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 NCBI_TaxID=10254, 10249;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WR;
 RX MEDLINE=91082452; PubMed=1824607;
 RA Amegdadze B.Y., Holmes M.H., Cole N.B., Jones E.V., Earl P.L.,
 RA Moss B.;
 RT "Identification, sequence, and expression of the gene encoding the
 RT second-largest subunit of the vaccinia virus DNA-dependent RNA
 RT polymerase.";
 RT Virology 180:88-96(1991).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Copenhagen;
 RX MEDLINE=91021027; PubMed=2219722;
 RA Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P.,
 RA Paolletti E.;
 RT "The complete DNA sequence of vaccinia virus.";
 RT Virology 179:247-266(1990).
 RL [3]
 RP COMPLETE GENOME.
 RC STRAIN=Copenhagen;
 RA Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P.,
 RA Paolletti E.;
 RT "Appendix to 'The complete DNA sequence of vaccinia virus.'";
 RT Virology 179:517-563(1990).
 RL -1- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
 of DNA into RNA using the four ribonucleoside triphosphates as
 CC substrates.
 CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC {RNA}(N).
 CC -1- SUBUNIT: This enzyme consists of at least eight subunits.
 CC -1- SIMILARITY: Belongs to the RNA polymerase beta chain family.
 CC
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 CC
 CC EMBL: M37415; AAA72882.1; -
 CC EMBL: M35027; AAA48148.1; -
 CC PIR: H42519; RNZ8T.
 CC InterPro: IPR007121; RNA_pol_B.

DR InterPro: IPR007645; RNA_pol_Rpb2_3.
 DR InterPro: IPR007646; RNA_pol_Rpb2_4.
 DR InterPro: IPR007647; RNA_pol_Rpb2_5.
 DR InterPro: IPR007120; RNA_pol_Rpb2_6.
 DR InterPro: IPR007641; RNA_pol_Rpb2_7.
 DR Pfam: PF04565; RNA_pol_Rpb2_3; 1.
 DR Pfam: PF04566; RNA_pol_Rpb2_4; 1.
 DR Pfam: PF04567; RNA_pol_Rpb2_5; 1.
 DR Pfam: PF04568; RNA_pol_Rpb2_6; 1.
 DR Pfam: PF04569; RNA_pol_Rpb2_7; 1.
 DR PROSITE: PS01166; RNA_Pol_BETA.1.
 DR Transferrase; DNA-directed RNA polymerase; Transcription; Zinc;
 KW Zinc-finger.
 FT ZN FING 1087 1106 C4-TYPE (POTENTIAL).
 FT SEQUENCE 1164 AA, 133363 MW, 2200D68F5238DB7 CRC64;
 SQ
 Query Match 43.3%; Score 45; DB 1; Length 1164;
 Best Local Similarity 56.2%; Pred. No. 22;
 Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 3 LEAKICHOIEEYFGD 18
 DB 505 LEKICIEYIRSYKXD 520
 RESULT 15
 ID RPO2 VARV STANDARD; PRT; 1164 AA.
 AC P33811;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE DNA-directed RNA polymerase 132 kDa polypeptide (EC 2.7.7.6).
 GN RPO132 OR A24R.
 OS Variola virus.
 OS Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 NCBI_TaxID=10255;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=India-1967 / Isolate Ind3;
 RX MEDLINE=93202281; PubMed=8384129;
 RA Shchelkinov S.N., Blinov V.M., Sandakhchiev L.S.;
 RT "Genes of variola and vaccinia viruses necessary to overcome the host
 RT protective mechanisms.";
 RT FEBS Lett. 319:80-83(1993).
 RL -1- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
 of DNA into RNA using the four ribonucleoside triphosphates as
 CC substrates.
 CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC {RNA}(N).
 CC -1- SUBUNIT: This enzyme consists of at least eight subunits.
 CC -1- SIMILARITY: Belongs to the RNA polymerase beta chain family.
 CC
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 CC
 CC EMBL: X69198; CAA49069.1; -
 CC PIR: G36850; G36850.
 CC InterPro: IPR007121; RNA_pol_B.
 CC InterPro: IPR007645; RNA_pol_Rpb2_3.
 CC InterPro: IPR007646; RNA_pol_Rpb2_4.
 CC InterPro: IPR007647; RNA_pol_Rpb2_5.
 CC InterPro: IPR007120; RNA_pol_Rpb2_6.
 CC InterPro: IPR007641; RNA_pol_Rpb2_7.
 CC Pfam: PF04565; RNA_pol_Rpb2_3; 1.
 CC Pfam: PF04566; RNA_pol_Rpb2_4; 1.
 CC Pfam: PF04567; RNA_pol_Rpb2_5; 1.
 CC Pfam: PF04568; RNA_pol_Rpb2_6; 1.
 CC Pfam: PF04569; RNA_pol_Rpb2_7; 1.

AC P38433: 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Acetylcholinesterase 1 precursor (EC 3.1.1.7) (ACHE 1).
 GN ACB-1 OR W09812.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP STRAIN-Bristol N2;
 RC MEDLINE=94193691; PubMed=8144590;
 RX Arpagaus M., Fedon Y., Cousin X., Chatonnet A., Berge J.-B.,
 RA Fournier D., Toulant J.-P.;
 RT "cDNA sequence, gene structure, and in vitro expression of ace-1, the
 RT gene encoding acetylcholinesterase of class A in the nematode
 RT Caenorhabditis elegans.";
 RL J. Biol. Chem. 269:9957-9965 (1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Mu X., Le T.T.;
 RL Submitted (May-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: RAPIDLY HYDROLYZES CHOLINE RELEASED INTO THE SYNAPSE.
 CC IT CAN HYDROLYZE BUTYRYLTHIOCHOLINE.
 CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
 CC -1- SUBUNIT: Oligomer composed of disulfide-linked homodimers (by
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: MAY BE SECRETED OR MEMBRANE ASSOCIATED VIA
 CC A NON-CATALYTIC SUBUNIT.
 CC -1- DEVELOPMENTAL STAGE: DETECTED AT ALL STAGES. FOUND TO BE MORE
 CC ABUNDANT IN LARVAL STAGES THAN IN EMBRYOS OR ADULTS.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X7531; CA53080.1; -;
 CC EMBL: U58731; AAB00593.1; -;
 CC PIR: A54413; A54413.
 CC HSSP: P21836; IMAA.
 CC WormPep: W09812.1; CE07569.
 DR InterPro: IPR002018; Carboxylesterase.
 DR InterPro: IPR000997; Cholinesterase.
 DR InterPro: IPR000379; Ser esters.
 DR Pfam: PF00135; Coesterase; 1.
 DR PRINTS: PR00878; CHOLINESTERASE.
 DR PROSITE: PS00122; CARBOXYL-ESTERASE B_1; 1.
 DR PROSITE: PS00941; CARBOXYL-ESTERASE B_2; 1.
 DR Hydrolase; Serine esterase; Synapse; Membrane; Nerve; Signal;
 KW Neurotransmitter degradation; Multigene family.
 FT SIGNAL 1 31
 FT CHAIN 1 620
 FT ACT_SITE 216 620
 FT ACT_SITE 346 346
 FT ACT_SITE 468 468
 FT DISULFID 82 109
 FT DISULFID 270 286
 FT DISULFID 430 558
 FT DISULFID 618 618
 FT CARBOXHD 74 74
 FT CARBOXHD 272 272
 FT CARBOXHD 466 466
 FT CARBOXHD 536 536
 FT SEQUENCE 620 AA; 71433 MW; 61D78C4899F55C65 CRC64;

Query Match 43.3%; Score 45; DB 1; Length 620;
 Best Local Similarity 66.7%; Pred. No. 11;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 8 CHOIEEYFGDF 19
 DB 82 CIOSEDTYFGDF 93
 RESULT 13
 RPO2 COMPLEX STANDARD; PRT; 1164 AA.
 AC P17474; Q90025;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE DNA-directed RNA polymerase 132 kDa polypeptide (EC 2.7.7.6).
 GN RPO132.
 OS Compo virus (CPV).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=10243;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Brighton red;
 RX MEDLINE=89125698; PubMed=2915377;
 RA Patel D.D., Pickup D.V.;
 RT "The second-largest subunit of the poxvirus RNA polymerase is similar
 RT to the corresponding subunits of procaryotic and eucaryotic RNA
 RT polymerases.";
 RL J. Virol. 63:1076-1086 (1989).
 CC -1- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
 CC of DNA into RNA using the four ribonucleoside triphosphates as
 CC substrates.
 CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC {RNA} (N).
 CC -1- SUBUNIT: This enzyme consists of at least eight subunits.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event:Alternative initiation;
 CC Comment=2 isoforms, 1/late specific (shown here) and 2/early and
 CC late, are produced by alternative initiation. One
 CC transcriptional start site is operative at late times only and
 CC the other is operative both at early and late times;
 CC -1- SIMILARITY: Belongs to the RNA polymerase beta chain family.
 CC -----
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 CC -----
 CC EMBL: M26173; AAA42919.1; -;
 CC EMBL: M26173; AAA42920.1; -;
 CC PIR: A31879; RNZCP.
 DR InterPro: IPR007121; RNA_pol_B.
 DR InterPro: IPR007645; RNA_pol_Rpb2_3.
 DR InterPro: IPR007646; RNA_pol_Rpb2_4.
 DR InterPro: IPR007647; RNA_pol_Rpb2_5.
 DR InterPro: IPR007120; RNA_pol_Rpb2_6.
 DR InterPro: IPR007641; RNA_pol_Rpb2_7.
 DR Pfam: PF04565; RNA_pol_Rpb2_3; 1.
 DR Pfam: PF04566; RNA_pol_Rpb2_4; 1.
 DR Pfam: PF04567; RNA_pol_Rpb2_5; 1.
 DR Pfam: PF00562; RNA_pol_Rpb2_6; 1.
 DR Pfam: PF04560; RNA_pol_Rpb2_7; 1.
 DR PROSITE: PS01166; RNA_POL_BETA_1.
 DR Transferase; DNA-directed RNA polymerase; Transcription; Zinc;
 KW Zinc-finger; Alternative initiation.
 FT CHAIN 1 1164
 FT CHAIN 9 1164
 FT SEQUENCE 1164 AA; 12644 MW; 61D78C4899F55C65 CRC64;

RT "Construction of expression-ready cDNA clones for KIAA genes: manual
RT curation of 330 KIAA cDNA clones."
RL DNA Res. 9:99-106(2002).
RN [3]
RP SEQUENCE OF 1188-2047 FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=2238257; PubMed=12477932;
RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schler G.D.,
RA Altchul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mollahy S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Maria M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP NOMENCLATURE.
RX MEDLINE=22319137; PubMed=12432077;
RT Cote J.-F., Vuori K.;
RT "Identification of an evolutionarily conserved superfamily of DOK180-
RT related proteins with guanine nucleotide exchange activity."
RL J. Cell Sci. 115:4901-4913(2002).
CC -1- FUNCTION: Potential guanine nucleotide exchange factor (GEF). GEF
CC proteins activate some small GTPases by exchanging bound GDP for
CC free GTP (By similarity).
CC -1- TISSUE SPECIFICITY: Widely expressed. Expressed at low level in
CC spleen, cerebellum, hippocampus and in substantia nigra.
CC -1- DOMAIN: The DHR-2 domain may mediate some GEF activity (By
CC similarity).
CC -1- SIMILARITY: Belongs to the DOK family.
CC -1- SIMILARITY: Contains 1 DHR-1 (CZH-1) domain.
CC -1- SIMILARITY: Contains 1 DHR-2 (CZH-2) domain.
CC -----
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CC -----
CC EMBL; AB037816; BAA92633.2; ALT_INIT.
DR EMBL; BC008335; AA083335.1; -
DR Genew; HGNC:19189; DOK6.
DR InterPro; IPR002016; Peroxidase.
KW Guanine-nucleotide releasing factor.
FT DOMAIN 548 786 DHR-1.
FT FT 1489 2012 DHR-2.
SQ SEQUENCE 2047 AA; 229655 MW; 55F4BDDAB1E60F31 CRC64;

QY 5 AKICHOIEEY---FGD 18
Db 1780 AETSHRLREYTERFGD 1796

Query Match 43.8%; Score 45.5; DB 1; Length 2047;
Best Local Similarity 52.9%; Pred. No. 33;
Matches 9; Conservative 4; Mismatches 1; Indels 3; Gaps 1;

RESULT 11
ACEL_CAEER
ID AC1_CAEER STANDARD; PRT; 620 AA.
AC 027459;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acetylcholinesterase 1 precursor (EC 3.1.1.7) (ACHe 1).
GN ACE-1.
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_Taxid=6238;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97069944; PubMed=8912924;
RA Grauso M., Culetto E., Borge J.B., Toulant J.-P., Arpaug M.;
RT "Sequence comparison of ACE-1, the gene encoding acetylcholinesterase
RT of class A, in the two nematodes Caenorhabditis elegans and
RT Caenorhabditis briggsae."
RL DNA Seq. 6:217-227(1996).
CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -1- SUBUNIT: oligomer composed of disulfide-linked homodimers (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: MAY BE SECRETED OR MEMBRANE ASSOCIATED VIA
CC A NON-CATALYTIC SUBUNIT (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
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CC -----
CC EMBL; U41846; AAB41269.1; -
DR HSSP; P21836; IMAA.
DR InterPro; IPR002018; Carboxylesterase.
DR InterPro; IPR000997; Carboxylesterase.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PRO0878; CHOLINESTERASE.
DR PROSITE; PS00122; CARBOXYLSTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLSTERASE_B_2; 1.
KW Hydrolyase; Serine esterase; Synapse; Membrane; Signal; Glycoprotein;
KW Neurotransmitter degradation; Multigene family.
FT SIGNAL 1 31
FT CHAIN 32 620
FT ACT SITE 216 216
FT ACT SITE 346 346
FT ACT SITE 468 468
FT DISULFID 82 109
FT DISULFID 270 286
FT DISULFID 430 558
FT DISULFID 618 618
FT CARBOHYD 74 74
FT CARBOHYD 272 272
FT CARBOHYD 486 486
FT CARBOHYD 536 536
SQ SEQUENCE 620 AA; 71501 MW; 69D73CD3996E11FC CRC64;

QY 8 CHQIEEYFGDF 19
Db 82 CIGSEDTYFGDF 93

Query Match 43.3%; Score 45; DB 1; Length 620;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

RESULT 12
ACEL_CAEEL
ID AC1_CAEEL STANDARD; PRT; 620 AA.
AC 027459;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acetylcholinesterase 1 precursor (EC 3.1.1.7) (ACHe 1).
GN ACE-1.
OS Caenorhabditis briggsae.
OC Eukaryota; Metazoa; Nematoda; Rhabditida; Rhabditioidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_Taxid=6238;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97069944; PubMed=8912924;
RA Grauso M., Culetto E., Borge J.B., Toulant J.-P., Arpaug M.;
RT "Sequence comparison of ACE-1, the gene encoding acetylcholinesterase
RT of class A, in the two nematodes Caenorhabditis elegans and
RT Caenorhabditis briggsae."
RL DNA Seq. 6:217-227(1996).
CC -1- FUNCTION: Rapidly hydrolyzes choline released into the synapse.
CC -1- CATALYTIC ACTIVITY: Acetylcholine + H(2)O = choline + acetate.
CC -1- SUBUNIT: oligomer composed of disulfide-linked homodimers (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: MAY BE SECRETED OR MEMBRANE ASSOCIATED VIA
CC A NON-CATALYTIC SUBUNIT (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
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CC -----
CC EMBL; U41846; AAB41269.1; -
DR HSSP; P21836; IMAA.
DR InterPro; IPR002018; Carboxylesterase.
DR InterPro; IPR000997; Carboxylesterase.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00135; Coesterase; 1.
DR PRINTS; PRO0878; CHOLINESTERASE.
DR PROSITE; PS00122; CARBOXYLSTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLSTERASE_B_2; 1.
KW Hydrolyase; Serine esterase; Synapse; Membrane; Signal; Glycoprotein;
KW Neurotransmitter degradation; Multigene family.
FT SIGNAL 1 31
FT CHAIN 32 620
FT ACT SITE 216 216
FT ACT SITE 346 346
FT ACT SITE 468 468
FT DISULFID 82 109
FT DISULFID 270 286
FT DISULFID 430 558
FT DISULFID 618 618
FT CARBOHYD 74 74
FT CARBOHYD 272 272
FT CARBOHYD 486 486
FT CARBOHYD 536 536
SQ SEQUENCE 620 AA; 71501 MW; 69D73CD3996E11FC CRC64;

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KW Hypothetical protein: Transmembrane.
PT TRANSMEM 24 44 POTENTIAL.
PT TRANSMEM 290 310 POTENTIAL.
FT TRANSMEM 312 332 POTENTIAL.
SQ SEQUENCE 352 AA; 40705 MW; A9P002FEB9766501 CRC64;

Query Match
Query Local Similarity 56.2%; Pred. No. 4.2; Length 352;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Cy 4 BAKICHOIEEYFGDF 19
196 ELKFMHVINERFSGDF 211

RESULT 9
DOC6_MOUSE STANDARD; PRT; 849 AA.
AC 08VDR9; 09P461;
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Dedicator of cytokinesis protein 6 (Fragment).
GN DOCK6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain, and Breast tumor;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Scheffen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein W.J., Uebli B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Gilmwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE OF 640-849 FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22554683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nishida I., Oatso N., Saito R., Suzuki H., Yamahaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotojori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schiml L.M., Kanapi A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J., Brad T., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grumond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kongave A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Malais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Petosa G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Rungwald M.,
RA Sanelin A., Schneider C., Sempé C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

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RA Verardo R., Wagner L., Maniested C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazune N., Sato K.,
RA Shitaka T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
CC -I- FUNCTION: Potential guanine nucleotide exchange factor (GEF). GEF
CC proteins activate some small GTPases by exchanging bound GDP for
CC free GTP (By similarity).
CC -I- DOMAIN: The DHR-2 domain may mediate some GEF activity (By
CC similarity).
CC -I- SIMILARITY: Belongs to the DOCK family.
CC -I- SIMILARITY: Contains 1 DHR-2 (CZH-2) domain.
CC -----
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CC -----
DR EMBL, BC021414; AAH21414.1; ALT_INIT.
DR EMBL, BC043042; AAH43042.1; -.
DR EMBL, AK016777; BAB30423.2; -.
DR MGI: 1914789; 4931431C02R1K.
KW Guanine-nucleotide releasing factor.
FT N-TER 1
FT DOMAIN 1 814 DHR-2.
SQ SEQUENCE 849 AA; 95975 MW; 5374B30CB97265CE CRC64;

Query Match
Query Local Similarity 52.9%; Pred. No. 13; Length 849;
Matches 9; Conservative 4; Mismatches 1; Indels 3; Gaps 1;

Cy 5 AKICHOIEEY---FGD 18
582 AHSIRLRFETTERGCD 598

Db 582 AHSIRLRFETTERGCD 598

RESULT 10
DOC6_HUMAN STANDARD; PRT; 2047 AA.
AC 096H0; 09P2F2;
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Dedicator of cytokinesis protein 6.
GN DOCK6 OR KIAA1395.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Brain;
RX MEDLINE=2018126; PubMed=10718198;
RA Nagase T., Kikuno R., Ishikawa K.-I., Hirogawa M., Ohara O.,
RT "Prediction of the coding sequences of unidentified human genes. XVI.
RT The complete sequences of 150 new cDNA clones from brain which code
RT for large proteins in vitro."
RL DNA Res. 7:65-73(2000).
RN [2]
RP REVISIONS.
RC TISSUE=Brain;
RX MEDLINE=22158633; PubMed=12168954;
RA Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;

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CC -----
DR EMBL, X68817, CAA48715.1;
DR PIR, S33818, S33818.
DR InterPro, IPR002344, Lupus_La.
DR InterPro, IPR006630, Lupus_La_dom.
DR InterPro, IPR000504, RNA_rec_mot.
DR Pfam, PF05383, La; 1.
DR Pfam, PF00076, xrm; 1.
DR PRINTS, PR00302, LUPUSLA.
DR SMART, SM00715, LA; 1.
DR SMART, SM00360, RRM; 1.
DR PROSITE, PS50102, RRM; 1.
DR PROSITE, PS00030, RRM_RNP_1; 1.
DR RNA-binding; Nuclear protein; Phosphorylation.
FT DOMAIN 111 203 RNA-BINDING (RRM).
FT FT 196 212 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT FT 316 332 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
SQ SEQUENCE 428 AA; 48864 MW; AEB3A3B7D2E3EC3 CRC64;

Query Match 53.4%; Score 55.5; DB 1; Length 428;
Best Local Similarity 73.3%; Pred. No. 0.14;
Matches 11; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

OY 4 EAKICHOIEEYFGD 18
Db 14 DTKICEQI-EYVFGD 27

RESULT 7
LBP RABIT STANDARD; PRT; 482 AA.
AC P17454;
DT 01-APR-1990 (Rel. 15, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE L1popolysaccharide-binding protein precursor. (LBP).
GN LBP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90385281; PubMed=2402617;
RA Schumann R.R., Leong S.R., Flags G.W., Gray P.W., Wright S.D.,
RA Wachsmann J.C., Tobias P.S., Ulevitch R.J.,
RT "Structure and function of l1popolysaccharide binding protein.";
RL Science 249:1429-1431(1990).
RN [2]
RP SEQUENCE OF 27-66.
RC TISSUE=serum;
RX MEDLINE=86306528; PubMed=2427635;
RA Tobias P.S., Soldau K., Ulevitch R.J.;
RT "Isolation of a l1popolysaccharide-binding acute phase reactant from
RT rabbit serum.";
RL J. Exp. Med. 164:777-793(1986).
CC -!- FUNCTION: Binds to the lipid a moiety of bacterial
CC l1popolysaccharides (LPS), a glycolipid present in the outer
CC membrane of all Gram-negative bacteria. The LBP/LPS complex seems
CC to interact with the CD14 receptor.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP
CC family.
CC -----
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CC      -----
DR      EMBL, M35534; AAA99235.1; -.
DR      PIR, B35843; B35843.
DR      HSSP, P17213; 1BP1.
DR      InterPro, IPR001124; LBP_BPI_CERP.
DR      Pfam, PF01273; LBP_BPI_CERP, 1.
DR      Pfam, PF02866; LBP_BPI_CERP_c, 1.
DR      SMART, SM00328; BPI1; 1.
DR      SMART, SM00329; BPI2; 1.
DR      PROSITE, PS00400; LBP_BPI_CERP, 1.
KM      lipid transport; Antibiotic; Transmembrane; Glycoprotein; Signal.
FT      SIGNAL
FT      CHAIN
FT      CARBOHYD
FT      CARBOHYD
FT      CARBOHYD
FT      CONFLICT
FT      CONFLICT
SQ      SEQUENCE
      482 AA; 54001 MM; 628A6E0A647200C2 CRC64;

Query Match
Best Local Similarity
Matches 9; Conservative
      45.2%; Score 47; DB 1; Length 482;
      81.8%; Pred. No. 4;
      1; Mismatches 1; Indels 0; Gaps 0;

Qy      3 LEAKCHOIEE 13
      ||:|||||
Db      194 LESKICROIEE 204

RESULT 8
YMG7_YEAST
ID_YMG7_YEAST STANDARD; PRT; 352 AA.
AC Q04651;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical 40.7 kDa protein in DAK1-ORC1 intergenic region.
GN YML067C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=97313268; PubMed=9169872;
RA Bowman S., Churcher C.M., Baddock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Ragsdale K., Lyne G., Moule S., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S., Whitehead S., Barrett B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
RT XII."
RT Nature 387:90-93 (1997).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: TO YEAST YAL042W AND S.POMBE SPAC24B11.08C.
CC -----
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CC -----
DR EMBL, Z38114; CA8A6254.1; -.
DR PIR, S48331; S48331.
DR GERMOnline, I42598; -.
DR SGD, S0004532; ERV41.
DR GO, GO:0030138; C:COPII-coated vesicle; IDA.
DR GO, GO:0030176; C:integral to endoplasmic reticulum membrane; IDA.
DR GO, GO:0030173; C:integral to Golgi membrane; IDA.
DR GO, GO:0006886; P:ER to Golgi transport; ITI.

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DR EMBL; L00993; AAA39415.1; -
 DR EMBL; BC003820; AAH03820.1; -
 DR EMBL; Y07951; CA69249.1; -
 DR MGD; MGI:98423; Ssb.
 DR GO; GO:0005634; C:nucleus; IDA.
 DR InterPro; IPR002344; Lupus_La_dom.
 DR InterPro; IPR006630; Lupus_La.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF05383; La; 1.
 DR Pfam; PF00076; xrm; 1.
 DR SMART; SM00715; LA; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PS0102; RRM; 1.
 DR PROSITE; PS0030; RRM_RNP_1; 1.
 DR RNA-binding; Nuclear protein; Phosphorylation.
 DR RNA-binding; Nuclear protein; Phosphorylation.
 FT DOMAIN 111 187
 SQ SEQUENCE 415 AA; 47756 MW; 2D75197692FDC933 CRC64;

Query Match 81.2%; Score 84.5; DB 1; Length 415;
 Best Local Similarity 94.4%; Pred. No. 2.1e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 2 ALEAKICHOIEEYFGDF 19
 Db 12 ALEAKICHOI-EYFGDF 28

RESULT 5
 LAB_XENLA STANDARD; PRT; 427 AA.
 ID LAB_XENLA
 AC P28049; 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Lupus La protein homolog B (La ribonucleoprotein B) (La autoantigen
 DE homolog B).
 GN LAB1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Oocyte;
 RX MEDLINE=93287095; PubMed=8510143;
 RA Scherly D., Stutz F., Lin-Marg N., Clarkson S.G.;
 RT "La proteins from Xenopus laevis. cDNA cloning and developmental
 RT expression.";
 RL J. Mol. Biol. 231:196-204(1993).
 CC -1- FUNCTION: La protein plays a role in the transcription of RNA
 CC polymerase III. It is most probably a transcription termination
 CC factor. Binds to the 3' terminus of virtually all nascent
 CC polymerase III transcripts (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- DEVELOPMENTAL STAGE: Barely detectable in stage I/II oocytes,
 CC accumulate in stage III/IV oocytes, then exhibit a roughly
 CC constant steady state level in mature oocytes, eggs, and early
 CC embryos.
 CC -1- PTM: Phosphorylated (Probable).
 CC -1- MISCELLANEOUS: There are two forms of La, Laa and Lab, in xenopus.
 CC -1- SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN.
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
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DR EMBL; X68818; CAA48716.1; -
 DR PIR; S33817; S33817.
 DR InterPro; IPR002344; Lupus_La.
 DR InterPro; IPR006630; Lupus_La_dom.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF05383; La; 1.
 DR Pfam; PF00076; xrm; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PS0102; RRM; 1.
 DR PROSITE; PS0030; RRM_RNP_1; FALSE NEG.
 DR RNA-binding; Nuclear protein; Phosphorylation.
 DR RNA-binding; Nuclear protein; Phosphorylation.
 FT DOMAIN 110 202
 FT DOMAIN 315 331
 SQ SEQUENCE 427 AA; 48995 MW; 45F3146F934A355 CRC64;

Query Match 57.2%; Score 59.5; DB 1; Length 427;
 Best Local Similarity 75.0%; Pred. No. 0.03;
 Matches 12; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 3 LEAKICHOIEEYFGD 18
 Db 12 LDTKICEQI-EYFGD 26

RESULT 6
 LAB_XENLA STANDARD; PRT; 428 AA.
 ID LAB_XENLA
 AC P28048; 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Lupus La protein homolog A (La ribonucleoprotein A) (La autoantigen
 DE homolog A).
 GN LAB1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Oocyte;
 RX MEDLINE=93287095; PubMed=8510143;
 RA Scherly D., Stutz F., Lin-Marg N., Clarkson S.G.;
 RT "La proteins from Xenopus laevis. cDNA cloning and developmental
 RT expression.";
 RL J. Mol. Biol. 231:196-204(1993).
 CC -1- FUNCTION: La protein plays a role in the transcription of RNA
 CC polymerase III. It is most probably a transcription termination
 CC factor. Binds to the 3' terminus of virtually all nascent
 CC polymerase III transcripts (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- DEVELOPMENTAL STAGE: Barely detectable in stage I/II oocytes,
 CC accumulate in stage III/IV oocytes, then exhibit a roughly
 CC constant steady state level in mature oocytes, eggs, and early
 CC embryos.
 CC -1- PTM: Phosphorylated (Probable).
 CC -1- MISCELLANEOUS: There are two forms of La, Laa and Lab, in xenopus.
 CC -1- SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN.
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
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DR PROSITE: PS00030; RRM_RNP_1; 1.
 KW Systemic lupus erythematosus; RNA-binding; Phosphorylation;
 KM Nuclear protein.
 FT DOMAIN 111 187 RNA-BINDING (RRM).
 FT MOD RES 366 366 PHOSPHORYLATION (BY CK2).
 SQ SEQUENCE 408 AA; 46837 MW; EC153C15F9187FC4 CRC64;

Query Match 85.1%; Score 88.5; DB 1; Length 408;
 Best Local Similarity 94.7%; Pred. No. 4.5e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 AALEAKICHQIEYYEGDF 19
 DB 11 AALEAKICHQI-EYYEGDF 28

RESULT 3

LA RAT STANDARD; PRT; 415 AA.

AC P3856; 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lupus La protein homolog (La ribonucleoprotein) (La autoantigen
 homolog).
 GN SSB OR SS-B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN (1)

SEQUENCE FROM N.A.
 MEDLINE=9324625; PubMed=7916708;
 RA Semel I., Trosset H., Bartsch H., Schwemmle M., Igloi G.L.,
 RA Bachmann M.;
 RT "Isolation of rat cDNA clones coding for the autoantigen SS-B/La:
 RT detection of species-specific variations.";
 RL Gene 126:265-268(1993).

CC -1- FUNCTION: La protein plays a role in the transcription of RNA
 CC polymerase III. It is most probably a transcription termination
 CC factor. Binds to the 3' terminus of virtually all nascent
 CC polymerase III transcripts. It is associated with precursor forms
 CC of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S,
 CC and 7-2 RNAs.

CC -1- SUBUNIT: Interacts with DDX15 (By similarity).

CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).

CC -1- PTM: Phosphorylated (By similarity).

CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.

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CC -----
 CC EMBL: X67859; CAA48043.1; -.
 DR PIR: JCI1494; JCI1494.
 DR InterPro: IPR002344; Lupus_La.
 DR InterPro: IPR006630; Lupus_La_dom.
 DR InterPro: IPR000504; RNA_rec_mot.
 DR Pfam: PF00383; La; 1.
 DR Pfam: PF00076; rrm; 1.
 DR PRINTS: PR00302; LUPUSLA.
 DR SMART: SMO0715; La; 1.
 DR SMART: SMO0360; RRM; 1.
 DR PROSITE: PS0102; RRM; 1.
 DR PROSITE: PS0030; RRM_RNP_1; 1.
 DR RNA-Binding; Nuclear protein; Phosphorylation.
 FT DOMAIN 111 187 RNA-BINDING (RRM).
 SQ SEQUENCE 415 AA; 47777 MW; 033FD9CC18A75F98 CRC64;

Query Match 85.1%; Score 88.5; DB 1; Length 415;
 Best Local Similarity 94.7%; Pred. No. 4.6e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 AALEAKICHQIEYYEGDF 19
 DB 11 AALEAKICHQI-EYYEGDF 28

RESULT 4

LA MOUSE STANDARD; PRT; 415 AA.

AC P32067; 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Lupus La protein homolog (La ribonucleoprotein) (La autoantigen
 homolog).
 GN SSB OR SS-B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN (1)

SEQUENCE FROM N.A.
 MEDLINE=93203630; PubMed=8454877;
 RA Topfer F., Gordon T., McCluskey J.;
 RT "Characterization of the mouse autoantigen La (SS-B). Identification
 RT of conserved RNA-binding motifs, a putative ATP binding site and
 RT reactivity of recombinant protein with poly(U) and human
 RT autoantibodies.";
 RL J. Immunol. 150:3091-3100(1993).

CC -----
 CC SEQUENCE FROM N.A.
 CC STRAIN=FVB/N; TISUB=Mammary gland;
 CC MEDLINE=22388257; PubMed=12477932;
 CC Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 CC Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 CC Altshuler S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 CC Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 CC Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 CC Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 CC Brownstein M.D., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 CC Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
 CC Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 CC Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 CC Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
 CC Fahey J., Helton E., Kettelman M., Madan A., Rodtighes S., Sanchez A.,
 CC Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 CC Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 CC Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 CC Scherch A., Schein J.E., Jones S.J.M., Maita M.A.;
 CC "Generation and initial analysis of more than 15,000 full-length
 CC human and mouse cDNA sequences.";
 CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -----
 CC SEQUENCE OF 1-11 FROM N.A.
 RP Groelz D., Bachmann M.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: La protein plays a role in the transcription of RNA
 CC polymerase III. It is most probably a transcription termination
 CC factor. Binds to the 3' terminus of virtually all nascent
 CC polymerase III transcripts. It is associated with precursor forms
 CC of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S,
 CC and 7-2 RNAs.
 CC -1- SUBUNIT: Interacts with DDX15 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- PTM: Phosphorylated (By similarity).
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
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FT DOMAIN 111 187 RNA-BINDING (RBM).
 SQ SEQUENCE 404 AA; 46534 MW; 4EE30B5C262AD6A1 CRC64;
 Query Match 85.1%; Score 88.5; DB 1; Length 404;
 Best Local Similarity 94.7%; Pred. No. 4.5e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 CQ 1 AALEAKICHQIEEYFGDF 19
 DB 11 AALEAKICHQI-EYFGDF 28
 RESULT 2
 ID LA_HUMAN STANDARD; PRT; 408 AA.
 ID P05455;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Lupus La protein (Sjogren syndrome type B antigen) (SS-B) (La ribonucleoprotein) (La autoantigen).
 GN SSB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 CX NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=89202037; PubMed=2468131;
 RT Chan E.K.L., Sullivan K.F., Tan E.M.;
 RT "Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences for RNA-binding.";
 RT Nucleic Acids Res. 17:2233-2244 (1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=89053970; PubMed=3192525;
 RT Chambers J.C., Kenan D., Martin B.J., Keene J.D.;
 RT "Genomic structure and amino acid sequence domains of the human La autoantigen.";
 RT J. Biol. Chem. 263:18043-18051 (1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA TISSUE=Placenta, and Skeletal muscle;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Umed T.B., Toshiyuki S., Carrinci P., Prange C., Rata S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vittalal D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [4]
 RP SEQUENCE OF 54-408 FROM N.A.
 RX MEDLINE=88199081; PubMed=2452201;
 RA Sturgees A.D., Peterson M.G., McNeillage L.J., Whittingham S., Coppel R.S.;
 RT "Characteristics and epitope mapping of a cloned human autoantigen La.";
 RT J. Immunol. 140:3212-3218 (1988).
 RN [5]

RP SEQUENCE OF 54-97 FROM N.A.
 RX MEDLINE=8516283; PubMed=385688;
 RA Chambers J.C., Keene J.D.;
 RT "Isolation and analysis of cDNA clones expressing human lupus La antigen.";
 RT Proc. Natl. Acad. Sci. U.S.A. 82:2115-2119 (1985).
 RN [6]
 RP FUNCTION.
 RX MEDLINE=89251617; PubMed=2470590;
 RA Gottlieb E., Steltz J.A.;
 RT "Function of the mammalian La protein: evidence for its action in transcription termination by RNA polymerase III.";
 RT EMBO J. 8:851-861 (1989).
 RN [7]
 RP PHOSPHORYLATION.
 RX MEDLINE=97207017; PubMed=9054510;
 RA Fan H., Sakulich A.L., Goodier J.L., Zhang X., Qin J., Marate R.J.;
 RT "Phosphorylation of the human La antigen on serine 366 can regulate recycling of RNA polymerase III transcription complexes.";
 RT Cell 88:707-715 (1997).
 RN [8]
 RP INTERACTION WITH DDX15.
 RX MEDLINE=22346609; PubMed=12458796;
 RA Fouraux M.A., Kolkman M.J.M., Van der Heijden A., De Jong A.S., Van Venrooij W.J., Pruijn G.J.M.;
 RT "The human La (SS-B) autoantigen interacts with DDX15/hPrp43, a putative DEAD-box RNA helicase.";
 RT RNA 8:1428-1443 (2002).
 CC -1- FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor forms of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S, and 7-2 RNAs.
 CC -1- SUBUNIT: Interacts with DDX15.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- PTM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES ARE AT THE C-TERMINAL PART OF THE PROTEIN.
 CC -1- PTM: The N-terminus is blocked.
 CC -1- DISEASE: Sera from patients with systemic lupus erythematosus often contain antibodies that react with the normal cellular La protein as if this antigen was foreign.
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RBM) domain.
 CC -----
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 CC -----
 CC EMBL: X13697; CAA31985.1; -;
 CC EMBL: J04205; AAA51885.1; -;
 CC EMBL: BC001289; AAH01289.1; -;
 CC EMBL: BC020818; AAH20818.1; -;
 CC PIR: A31888; A31888.
 CC GeneW: HGNC:11316; SSB.
 CC MIM: 109090; -;
 CC GO: GO:0030529; C:ribonucleoprotein complex; TAS.
 CC GO: GO:0003729; F:mRNA binding; TAS.
 CC GO: GO:0000049; F:tRNA binding; TAS.
 CC GO: GO:0008334; P:histone mRNA metabolism; TAS.
 CC GO: GO:0006400; P:tRNA modification; TAS.
 CC InterPro: IPR002344; Lupus La.
 CC InterPro: IPR006630; Lupus La dom.
 CC InterPro: IPR00504; RNA_rec_mot.
 CC Pfam: PF05383; La; 1.
 CC Pfam: PF00076; rim; 1.
 CC PRINTS: PR00302; LUPUSLA.
 CC SMART: SM00715; LA; 1.
 CC SMART: SM00360; RBM; 1.
 CC PROSITE: PS50102; RBM; 1.

GenCore version 5.1.6
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OM protein - protein search, using sw model

```
Run on:      September 10, 2004, 17:01:41 ; Search time 7.6s246 Seconds
              (without alignments)
              129.452 Million cell updates/second
```

Title: US-09-836-073-16

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Perfect score: 104
Sequence:      1 AALEAKICHQIEEYFGDF 199
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	88.5	85.1	404	1	LA_BOVIN	P10861 bos taurus
2	88.5	85.1	408	1	LA_HUMAN	P05455 homo sapiens
3	88.5	85.1	415	1	LA_RAT	P38656 rattus norvegicus
4	84.5	81.2	415	1	LA_MOUSE	P32067 mus musculus
5	59.5	57.2	427	1	LA_XENLA	P28049 xenopus laevis
6	55.5	53.4	428	1	LA_XENLA	P28048 xenopus laevis
7	47	45.2	482	1	LBP_RABIT	P17454 oryctolagus cuniculus
8	46	44.2	352	1	YMG7_YEAST	P04651 saccharomyces cerevisiae
9	45.5	43.8	849	1	DOC6_MOUSE	O8vd69 mus musculus
10	45.5	43.8	2047	1	DOC6_HUMAN	O96hd0 homo sapiens
11	45	43.3	620	1	ACE1_CAER	O27459 caenorhabditis elegans
12	45	43.3	620	1	ACE1_CAERL	P38433 caenorhabditis elegans
13	45	43.3	1164	1	RPO2_COMPLEX	P17474 complexin 1
14	45	43.3	1164	1	RPO2_COMPLEX	P19798 vaccinia virus
15	45	43.3	1164	1	RPO2_VACCV	P33811 variola virus
16	44.5	42.8	383	1	LA_ADAL	O26457 aedes albopictus
17	44	42.3	487	1	GATB_CHICK	O82346 chlamydomonas reinhardtii
18	44	42.3	552	1	ESTE_MYDPE	P35501 myzus persicae
19	44	42.3	564	1	ESTE_MYDPE	P35502 myzus persicae
20	43	41.3	88	1	V419_NEITMA	O9jqd5 neisseria meningitidis
21	43	41.3	297	1	MNT1_HUMAN	O9h1q5 homo sapiens
22	43	41.3	609	1	V458_METUA	O58482 methanococcus jannaschii
23	42	40.4	421	1	HMDH_AERRE	O9ya44 aeryopyrum ferox
24	42	40.4	428	1	V813_TREPA	O83759 treponema pallidum
25	42	40.4	512	1	MATK_GINBI	O8me22 ginkgo biloba
26	42	40.4	1037	1	ACRD_ECOLI	P24177 escherichia coli
27	41	39.4	263	1	MTX2_MOUSE	O88441 mus musculus
28	41	39.4	926	1	ME19_DROME	O24087 drosophila melanogaster
29	40.5	38.9	390	1	LA_DROME	P40767 drosophila melanogaster
30	40.5	38.9	773	1	PNK4_HUMAN	O9hv57 homo sapiens
31	40	38.5	263	1	MTX2_HUMAN	O75431 homo sapiens
32	40	38.5	271	1	VY46_COEHI	O8ep44 oceanobacillus anophageus
33	40	38.5	320	1	PLA0_SOEBH	P50346 glycerol max

45	39.5	37.5	35	33.8	1	HEN1_CHLVC	Q82441	chlamydomon
44	39.5	37.5	35	35.2	1	DATA_STANA	P54684	staphylococ
43	39.5	38.0	40	77.3	1	PNK4_STAT	Q92368	ratulus norv
42	40	38.5	41	1505	1	AT7B_SHEEP	O93500	ovis aries
41	40	38.5	41	1253	1	POLS_SFV	P03315	semliki for
40	40	38.5	41	919	1	RP02_CAPVK	P16716	capripoxviri
39	40	38.5	41	812	1	MCW3_MOUSE	P25026	mus muscucu
38	40	38.5	40	670	1	SYR_BIFLO	Q69472	bifidobacter
37	40	38.5	40	557	1	SYR_RHOCA	Q69472	bifidobacter
36	40	38.5	40	571	1	MBH1_CHLNP	P19524	rhodobacter
35	40	38.5	40	509	1	STR_HYDAP	Q92963	chlamydia p
34	40	38.5	40	484	1	TH11_PSEBK	O88734	pseudomonas
33	40	38.5	40	509	1	STR_HYDAP	P17713	hydra attenu

ALIGNMENTS

RESULT 1	LA BOVIN	STANDARD;	PRT;	404 AA.
ID	LA BOVIN			
AC	P10881;			
DT	01-JUL-1989 (Rel. 11, Created)			
DT	01-JUL-1989 (Rel. 11, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Lupus la protein homolog (la ribonucleoprotein) (la autoantigen homolog).			
GN	SSB.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
KN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Pituitary;			
RX	MEDLINE=89202037; PubMed=2468131;			
RA	Chan E.K.L., Sullivan K.F., Tan E.M.;			
RT	"Ribonucleoprotein SS-/La belongs to a protein family with consensus sequences for RNA-binding.";			
RL	Nucleic Acids Res. 17:2233-2244(1989).			
CC	-1- FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor forms of RNA polymerase III transcripts including rRNA and 4.5S, 5S, 7S, and 7-2 rRNAs.			
CC	-1- SUBUNIT: Interacts with DDX15 (By similarity).			
CC	-1- SUBCELLULAR LOCATION: Nuclear (Probable).			
CC	-1- PM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES ARE AT THE C-TERMINAL PART OF THE PROTEIN.			
CC	-1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; X13598; CAA31986.1; -.			
DR	PIR; S03849; S03849.			
DR	InterPro; IPR002344; Lupus_La.			
DR	InterPro; IPR006630; Lupus_La.dom.			
DR	InterPro; IPR005054; RNA_rec_mot.			
DR	Pfam; PF05383; La; 1.			
DR	Pfam; PF00076; Rtm; 1.			
DR	PRINTS; PR00302; LUPUSLA.			
DR	SMART; SM00715; LA; 1.			
DR	SMART; SM00360; RRM; 1.			
DR	PROSITE; PS50102; RRM; 1.			
DR	PROSITE; PS00030; RRM_RNP_1; 1.			
KW	RNA-binding; Nuclear protein; Phosphorylation.			

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A:Reference number: Z20693
 A:Accession: T29824
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-620 <WUX>
 A:Cross-references: EMBL:U58731; PIDN:AAB00593.1; GSPDB:GN00028
 A:Experimental source: strain Bristol N2; clone W09B12
 C:Genetics:
 A:Gene: CESP:ace-1
 A:Map position: X
 A:Introns: 13/3; 59/2; 154/2; 236/3; 296/2; 454/2; 509/2; 573/1; 606/2
 C:Superfamily: cholinesterase; cholinesterase homology
 C:Keywords: carboxylic ester hydrolase
 F:45-567/Domain: cholinesterase homology <CHB>

Query Match 43.3%; Score 45; DB 2; Length 620;
 Best Local Similarity 66.7%; Pred. No. 37;
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 CHQIEHYFGDF 19
 | | | | |
 Db 82 CIQSEDTYFGDF 93

RESULT 15
 T37411
 RNA polymerase subunit rpo132 - vaccinia virus (strain Ankara)
 C:Species: vaccinia virus
 A:Variety: strain Ankara
 C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
 C:Accession: T37411
 R:Antoine, G.; Schefflinger, F.; Falkner, F.G.; Dorner, F.
 submitted to the EMBL Data Library, March 1997
 A:Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strain
 A:Reference number: Z20877
 A:Accession: T37411
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1156 <ANT>
 A:Cross-references: EMBL:U94848; PIDN:AAB96526.1
 A:Experimental source: strain Ankara
 C:Genetics:
 A:Note: MVA135R
 C:Superfamily: DNA-directed RNA polymerase 132k polypeptide

Query Match 43.3%; Score 45; DB 2; Length 1156;
 Best Local Similarity 56.2%; Pred. No. 66;
 Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 3 LEAKICHQIEHYFGD 18
 | | | | |
 Db 497 LEKKICEYIRSYKDD 512

Search completed: September 10, 2004, 18:02:35
 Job time : 16.8603 secs

lipopolysaccharide-binding protein - rabbit
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 20-Aug-1999
 C:Accession: B35843; A46553
 R:Schumann, R.R.; Leong, S.R.; Flaegge, G.W.; Gray, P.W.; Wright, S.D.; Mathison, J.C.; J
 Science 249, 1429-1431, 1990
 A>Title: Structure and function of lipopolysaccharide binding protein.
 A:Reference number: A35843; MUID:90385281; PMID:2402637
 A:Accession: B35843
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-482 <SCH>
 A:Cross-references: GB:M35534; NID:G165467; PIDN:AAA99235.1; PID:G165468
 R:Tobias, P.S.; Soldau, K.; Ulevitch, R.J.
 J Exp. Med. 164, 777-793, 1986
 A>Title: Isolation of a lipopolysaccharide-binding acute phase reactant from rabbit seru
 A:Reference number: A46553; MUID:86306528; PMID:2427635
 A:Accession: A46553
 A:Molecule type: protein
 A:Residues: 27-55, 'XG', 58-62, 'F', 64-65 <TOB>
 C:Superfamily: lipopolysaccharide-binding protein
 C:Keywords: acute phase

Query Match 45.2%; Score 47; DB 2; Length 482;
 Best Local Similarity 81.8%; Pred. No. 14;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 LEAKICHOIEE 13
 ||:|||||
 Db 194 LESKICRQIEE 204

RESULT 11
 S48331
 probable membrane protein YML067C - yeast (Saccharomyces cerevisiae)
 C:Species: Saccharomyces cerevisiae
 C:Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 19-Apr-2002
 C:Accession: S48331; S48330
 R:Bowman, S.; Churcher, C.
 submitted to the EMBL Data Library, August 1994
 A:Reference number: S48326
 A:Accession: S48331
 A:Molecule type: DNA
 A:Residues: 1-352 <BOW>
 A:Cross-references: EMBL:Z38114; NID:G558402; PID:G558408; GSPDB:GN00013; MIPS:YML067C
 A:Accession: S48330
 A:Molecule type: DNA
 A:Residues: 69-352 <BOF>
 A:Cross-references: EMBL:Z38114; NID:G558402; PID:G558407
 C:Genetics:
 A:Gene: SGD:ERV41; MIPS:YML067C
 A:Cross-references: SGD:S0004532
 A:Map position: 13L
 A:Introns: 11/1
 C:Keywords: transmembrane protein
 F:230-246/Domain: transmembrane #status predicted <TM1>
 F:248-264/Domain: transmembrane #status predicted <TM2>

Query Match 44.2%; Score 46; DB 2; Length 352;
 Best Local Similarity 56.2%; Pred. No. 15;
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

OY 4 EAKICHOIEEYFGDF 19
 ||:|||||
 Db 196 ELKFNHVINERFSGDF 211

RESULT 12
 E69391
 hypothetical protein AF1134 - Archaeoglobus fulgidus
 C:Species: Archaeoglobus fulgidus
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
 C:Accession: E69391

R:Klink, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
 . Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirschner, E.F.
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 366-370, 1997
 A:Authors: Overbeek, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Sykes, S.;
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A>Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon
 A:Reference number: A69250; MUID:98049343; PMID:9389475
 A:Accession: E69391
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-456 <KLE>
 A:Cross-references: GB:AE001026; GB:AE000782; NID:G2689349; PIDN:AB90123.1; PID:G264946

Query Match 44.2%; Score 46; DB 2; Length 456;
 Best Local Similarity 61.5%; Pred. No. 19;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 3 LEAKICHOIEEY 15
 ||:|||||
 Db 405 WEAKIPHOIEEY 417

RESULT 13
 H90096
 eukaryotic release factor 1 homolog [imported] - Galliardia theta nucleomorph
 C:Species: nucleomorph Galliardia theta
 A>Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 15-Jun-2001
 C:Accession: H90096
 R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rel
 Nature 410, 1091-1096, 2001
 A>Title: The highly reduced genome of an enslaved algal nucleus.
 A:Reference number: A99082; MUID:11323671; PMID:11323671
 A:Accession: H90096
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-409 <DOU>
 A:Cross-references: GB:AF165818; NID:G13794528; PIDN:AAK39903.1; GSPDB:GN00150
 C:Genetics:
 A:Gene: erf1
 A:Map position: 1
 A:Genome: nucleomorph
 C:Superfamily: translation releasing factor eRF-1
 C:Keywords: nucleomorph

Query Match 43.3%; Score 45; DB 2; Length 409;
 Best Local Similarity 50.0%; Pred. No. 25;
 Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 6 KICHOIEEYFGDF 19
 ||:|||||
 Db 200 KICEADQYLSDF 213

RESULT 14
 A54413
 acetylcholinesterase (EC 3.1.1.7) A precursor - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 21-Jul-2000
 C:Accession: A54413; T29824
 R:Arpagaus, M.; Pedon, Y.; Cousin, X.; Chatonnet, A.; Berge, J.B.; Fournier, D.; Toutant
 J. Biol. Chem. 269, 9957-9965, 1994
 A>Title: cDNA sequence, gene structure, and in vitro expression of ace-1, the gene encod
 A:Reference number: A54413; MUID:94193691; PMID:8144590
 A:Accession: A54413
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-620 <ARP>
 A:Cross-references: GB:X7531; NID:G475060; PIDN:CAA3080.1; PID:G671831
 R:Wu, X.; Le, T.T.
 submitted to the EMBL Data Library, May 1996
 A:Description: The sequence of C. elegans cosmid W09B12.

R.Scherly, D.; Stutz, F.; Lin-Marg, N.; Clarkson, S.G.

J. Mol. Biol. 231, 196-204, 1993

A>Title: La proteins from *Xenopus laevis*. cDNA cloning and developmental expression.

A/Reference number: S33817; MUID:93287095; PMID:8510143

A/Accession: S33818

A/Molecule type: mRNA

A/Residues: 1-428 <SCH>

A/Cross-references: EMBL:X68817; NID:g64873; PIDN:CAA48715.1; PID:g64874

C/Comment: This protein associates with a variety of small RNA molecules, most of which

act as a transcription termination factor.

C/Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology

C/Keywords: phosphoprotein; RNA binding

F.112-178/Domain: ribonucleoprotein repeat homology <RRM>

F.113-118/Region: RNA-binding RNP motif

F.151-158/Region: RNA-binding RNP motif

F.228-428/Domain: phosphorylated #status predicted <PHY>

Query Match 53.4%; Score 55.5; DB 1; Length 428;

Best Local Similarity 73.3%; Pred. No. 0.57;

Matches 11; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 4 EAKICHOIEEYFGD 18

Db 14 DFKICEQI-EYFGD 27

RESULT 6

B70456

thioredoxin - Aquifex aeolicus

C/Species: Aquifex aeolicus

C/Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999

C/Accession: B70456

R/Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Oy

V.

Nature 392, 353-358, 1998

A>Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.

A/Reference number: A70300; MUID:9819666; PMID:9537320

A/Accession: B70456

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-135 <NOF>

A/Cross-references: GB:AE000757; NID:g2984092; PIDN:AAC07635.1; PID:g2984097; GB:AE00065

A/Experimental source: strain VFS

C/Genetics: trxA2

Query Match 52.9%; Score 55; DB 2; Length 135;

Best Local Similarity 72.7%; Pred. No. 0.23;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 CHOIEEYFGD 18

Db 52 CHOIEEYFGD 62

RESULT 7

AC1870

hypothetical protein alr0508 [imported] - Nostoc sp. (strain PCC 7120)

C/Species: Nostoc sp. PCC 7120

A/Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120

C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C/Accession: AC1870

R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S

DNA Res. 9, 205-213, 2001

A>Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*

A/Reference number: AB1807; MUID:21595285; PMID:11759840

A/Accession: AC1870

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-187 <KUR>

A/Cross-references: GB:BA000019; PIDN:BA072466.1; PID:g17129853; GSPDB:GN00179

A/Experimental source: strain PCC 7120

C/Genetics: alr0508

Query Match 45.2%; Score 47; DB 2; Length 187;

Best Local Similarity 50.0%; Pred. No. 5.6;

Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 ICHOIEEYFGD 18

Db 97 ICHOIEEYFGD 108

RESULT 8

H90120

hypothetical protein orf357 [imported] - *Guillardia theta* nucleomorph

C/Species: nucleomorph *Guillardia theta*

A/Note: A nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont

C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001

C/Accession: H90120

R/Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Re

Nature 410, 1091-1096, 2001

A>Title: The highly reduced genome of an enslaved algal nucleus.

A/Reference number: A99082; MUID:11323671; PMID:11323671

A/Accession: H90120

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-357 <DOU>

A/Cross-references: GB:AF083031; NID:g13794284; PIDN:AAK39661.1; GSPDB:GN00152

C/Genetics: orf357

A/Map position: 3

A/Keywords: nucleomorph

Query Match 45.2%; Score 47; DB 2; Length 357;

Best Local Similarity 50.0%; Pred. No. 10;

Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 LEAKICHOIEEYFGD 18

Db 242 LKXKVFQNMKXYFGD 257

RESULT 9

T39314

hypothetical protein SPBC119.16c - fission yeast (*Schizosaccharomyces pombe*)

C/Species: *Schizosaccharomyces pombe*

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C/Accession: T39314

R/Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.

submitted to the EMBL Data Library, March 1998

A/Reference number: Z21843

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: DNA

A/Residues: 1-448 <WOO>

A/Cross-references: EMBL:AL022117; PIDN:CAA17931.1; GSPDB:GN00067; SPDB:SPBC119.16c

A/Experimental source: strain 972n-; cosmid c119

C/Genetics:

A/Map position: 2

Query Match 45.2%; Score 47; DB 2; Length 448;

Best Local Similarity 47.4%; Pred. No. 13;

Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 ALEAKICHOIEEYFGD 19

Db 9 ATFDAKEGVNENYRDF 27

RESULT 10

B35843

A:Reference number: S03848; MUID:89202037; PMID:2468131
 A:Accession: S03848
 A:Molecule type: mRNA
 A:Residues: 1-408 <CH2>
 A:Cross-references: EMBL:X13697; NID:g36414; PIDN:CAA31985.1; PID:g36415
 R:Chambers, J.C.; Keene, J.D.
 Proc. Natl. Acad. Sci. U.S.A. 82, 2115-2119, 1985
 A>Title: Isolation and analysis of cDNA clones expressing human lupus La antigen.
 A:Reference number: A22956; MUID:85166283; PMID:3856888
 A:Accession: A22956
 A:Molecule type: mRNA
 A:Residues: 45-97, 'LK' <CH3>
 A:Cross-references: GB:J06205
 A>Note: This sequence has been revised in reference A31888
 R:NYman, U.; Ringertz, N.R.; Petersson, I.
 Immunol. Lett. 22, 65-72, 1989
 A>Title: Demonstration of an amino terminal La epitope recognized by human anti-La sera.
 A:Reference number: A61051; MUID:89379261; PMID:2476379
 A:Accession: A61051
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-19, 'E', '21-47 <NYM>
 R:Sturges, A.D.; Peterson, M.G.; McNeillage, L.J.; Whittingham, S.; Coppel, R.L.
 J. Immunol. 140, 3212-3218, 1988
 A>Title: Characteristics and epitope mapping of a cloned human autoantigen La.
 A:Reference number: S11013; MUID:88199081; PMID:2452201
 A:Accession: S11013
 A:Molecule type: mRNA
 A:Residues: 'E', '55-287', 'V', '289-408 <STU>
 A:Cross-references: EMBL:M20328; NID:g337456; PIDN:AAA36577.1; PID:g337457
 R:Kobayashi, H.; Yamamoto, K.; Fujii, H.; Mura, H.; Miyasaka, N.; Nishio, K.; Miyamoto, U.
 Clin. Invest. 85, 1566-1574, 1990
 A>Title: Fine epitope mapping the human SS-B/La protein. Identification of a distinct La
 A:Reference number: I55553; MUID:90237237; PMID:1692037
 A:Accession: I55553
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 81-107 <RES>
 A:Cross-references: GB:M35261; NID:g338491; PIDN:AAA36652.1; PID:g338495
 A:Accession: I70205
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 174-224 <RE2>
 A:Cross-references: GB:M35263; NID:g338492; PIDN:AAA36653.1; PID:g338496
 A:Accession: I70206
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 279-342 <RE3>
 A:Cross-references: GB:M35262; NID:g338493; PIDN:AAA36654.1; PID:g338497
 C:Comment: This protein associates with a variety of small RNA molecules, most of which
 act as a transcription termination factor.
 C:Keywords: phosphoprotein; RNA binding
 F:112-176/Domain: ribonucleoprotein repeat homology <RPM>
 F:113-118/Region: RNA-binding RNP2 motif
 F:151-158/Region: RNA-binding RNP1 motif
 F:228-408/Domain: phosphotyrlated #status experimental <PHY>

Query Match 85.1%; Score 88.5; DB 1; Length 408;
 Best Local Similarity 94.7%; Pred. No. 3.5e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 AALEAKICHOIEYYFGDF 19
 |||||
 Db 11 AALEAKICHOI-EYYFGDF 28

RESULT 3

JC1494
 ribonucleoprotein La - rat
 N:Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 24-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
 C:Accession: JC1494; S25145
 R:Semsei, I.; Troester, H.; Bartsch, H.; Schlemme, M.; Idol, G.L.; Bachmann, M.
 Gene 126, 265-268, 1993
 A>Title: Isolation of rat cDNA clones coding for the autoantigen SS-B/La: Detection of B
 A:Reference number: JC1494; MUID:93246255; PMID:7916708
 A:Accession: JC1494
 A:Molecule type: mRNA
 A:Residues: 1-415 <SEM>
 A:Cross-references: GB:X67859; NID:g55778; PIDN:CAA48043.1; PID:g55779
 A:Experimental source: liver
 C:Comment: This protein associates with a variety of small RNA molecules, most of which
 act as a transcription termination factor.
 C:Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
 C:Keywords: phosphoprotein; RNA binding
 F:112-178/Domain: ribonucleoprotein repeat homology <RPM>
 F:113-118/Region: RNA-binding RNP2 motif
 F:151-158/Region: RNA-binding RNP1 motif
 F:227-415/Domain: phosphotyrlated #status predicted <PHY>

Query Match 85.1%; Score 88.5; DB 1; Length 415;
 Best Local Similarity 94.7%; Pred. No. 3.6e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 AALEAKICHOIEYYFGDF 19
 |||||
 Db 11 AALEAKICHOI-EYYFGDF 28

RESULT 4

S33817
 ribonucleoprotein La-B - African clawed frog
 N:Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
 C:Accession: S33817; S28544
 R:Schery, D.; Stutz, F.; Lin-Marg, N.; Clarkson, S.G.
 J. Mol. Biol. 231, 196-204, 1993
 A>Title: La proteins from Xenopus laevis. cDNA cloning and developmental expression.
 A:Reference number: S33817; MUID:93287095; PMID:8510143
 A:Accession: S33817
 A:Molecule type: mRNA
 A:Residues: 1-427 <SCH>
 A:Cross-references: EMBL:X68818; NID:g64875; PIDN:CAA48716.1; PID:g64876
 C:Comment: This protein associates with a variety of small RNA molecules, most of which
 act as a transcription termination factor.
 C:Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
 C:Keywords: phosphoprotein; RNA binding
 F:111-177/Domain: ribonucleoprotein repeat homology <RPM>
 F:112-117/Region: RNA-binding RNP2 motif
 F:150-157/Region: RNA-binding RNP1 motif
 F:227-427/Domain: phosphotyrlated #status predicted <PHY>

Query Match 57.2%; Score 59.5; DB 1; Length 427;
 Best Local Similarity 75.0%; Pred. No. 0.13;
 Matches 12; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 3 LEAKICHOIEYYFGD 18
 |||||
 Db 12 LDTKICEQI-EYYFGD 26

RESULT 5

S33818
 ribonucleoprotein La-A - African clawed frog
 N:Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
 C:Accession: S33818; S28545

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:33:11 ; Search time 14.8603 Seconds
(without alignments)
122.988 Million cell updates/sec

Title: US-09-836-073-16

Perfect score: 104

Sequence: 1 AALEAKICHQIEHYFGDF 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

1: PIR 78: *
2: p1r1: *
3: p1r2: *
4: p1r3: *
5: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88.5	85.1	404	1 S03849	ribonucleoprotein
2	88.5	85.1	408	1 A31888	ribonucleoprotein
3	88.5	85.1	415	1 UC1494	ribonucleoprotein
4	59.5	57.2	427	1 S33817	ribonucleoprotein
5	55.5	53.4	428	1 S33818	ribonucleoprotein
6	55	52.9	135	2 B70456	thioredoxin - Aqu
7	47	45.2	187	2 AC1870	hypothetical prote
8	47	45.2	357	2 H90120	hypothetical prote
9	47	45.2	448	2 T39314	hypothetical prote
10	47	45.2	482	2 B35843	lipopolysaccharide
11	46	44.2	352	2 S48331	probable membrane
12	46	44.2	456	2 E69391	hypothetical prote
13	45	43.3	409	2 H90086	eukaryotic release
14	45	43.3	620	2 A54413	acetylcholinestera
15	45	43.3	1156	2 T37411	DNA-directed RNA p
16	45	43.3	1164	1 RNWZ8T	DNA-directed RNA p
17	45	43.3	1164	1 RNWZ8T	DNA-directed RNA p
18	45	43.3	1164	2 T28566	DNA-directed RNA p
19	45	43.3	1164	2 F72166	A25R protein - var
20	45	43.3	1164	2 S36786	A24R protein - var
21	44	42.3	552	2 S36786	carboxylesterase (
22	44	42.3	552	2 S36786	carboxylesterase (
23	43	41.3	88	2 H81014	conserved hypochet
24	43	41.3	427	2 G70590	probable dead3 pro
25	43	41.3	510	2 T06495	glucose-1-phosphat
26	43	41.3	609	2 A64432	modulation factor
27	42	40.4	386	2 H86870	hypothetical prote
28	42	40.4	421	2 E72573	probable 3-hydroxy
29	42	40.4	428	2 B71278	hypothetical prote

30	42	40.4	468	2 T21535	hypothetical prote
31	42	40.4	541	2 H71887	hypothetical prote
32	42	40.4	542	2 G64627	hypothetical prote
33	42	40.4	905	2 T38314	probable vacuolar
34	42	40.4	969	2 A75634	McR-related prote
35	42	40.4	1037	2 E65022	acetylflavin resist
36	42	40.4	1037	2 D91045	aminoglycoside eff
37	42	40.4	1037	2 G85889	hypothetical prote
38	42	40.4	1069	2 AF1930	hypothetical prote
39	41.5	39.9	463	2 T39004	probable histone a
40	41	39.4	153	2 T19054	hypothetical prote
41	41	39.4	203	2 T28352	ORF MSV191 MFG mot
42	41	39.4	528	2 T02972	SRP protein homol
43	41	39.4	650	2 C69678	involved in polyke
44	41	39.4	771	2 T43612	transposase - Yers
45	41	39.4	926	2 S58936	meiotic recombinat

ALIGNMENTS

RESULT 1
S03849
ribonucleoprotein la - bovine
N:Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
C:Species: Bos primigenius taurus (cattle)
C>Date: 31-Dec-1990 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C/Accession: S03849
R/Chan, E.K.L.; Sullivan, K.F.; Tan, E.M.
Nucleic Acids Res. 17, 2233-2244, 1989
A>Title: Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences
A/Reference number: S03848; MWID:89202037; PMID:2468131
A/Accession: S03849
A/Molecule type: mRNA
A/Residues: 1-404 <CHA>
A/Cross-references: EMBL:X13698; NID:g755; PIDN:CAA31986.1; PID:g756
A/Note: part of this sequence was confirmed by protein sequencing
C/Comment: This protein associates with a variety of small RNA molecules, most of which
ay act as a transcription termination factor.
C/Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology
C/Keywords: blocked amino end; phosphoprotein; RNA binding
F/112-178/Domain: ribonucleoprotein repeat homology <RKM>
F/113-118/Region: RNA-binding RNP2 motif
F/151-158/Region: RNA-binding RNP1 motif
F/228-404/Domain: phosphorylated #statue predicted <PHY>

Query Match 85.1%; Score 88.5; DB 1; Length 404;
Best Local Similarity 94.7%; Pred. No. 3.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 AALEAKICHQIEHYFGDF 19
DB 11 AALEAKICHQI-EYFGDF 28

RESULT 2
A31888
ribonucleoprotein la - human
N:Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B; Sjogren syndrome antigen
C:Species: Homo sapiens (man)
C/Date: 21-May-1990 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C/Accession: A31888; S03848; A22956; A61051; S11013; I55553; I70205; I70206; A31273
R/Chambers, J.C.; Kenan, D.; Martin, B.J.; Keene, J.D.
J. Biol. Chem. 263, 18043-18051, 1988
A>Title: Genomic structure and amino acid sequence domains of the human la autoantigen.
A/Reference number: A31888; MWID:89053970; PMID:3192525
A/Accession: A31888
A/Molecule type: mRNA
A/Residues: 1-408 <CHA>
A/Cross-references: GB:004205; NID:g178686; PIDN:AAA51885.1; PID:g178687
R/Chan, E.K.L.; Sullivan, K.F.; Tan, E.M.
Nucleic Acids Res. 17, 2233-2244, 1989
A>Title: Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences

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Job time : 41.424 secs

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FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-9
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Query Match          70.0%; Score 70; DB 9; Length 18;
Best Local Similarity 80.0%; Pred. No. 0.0075;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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```
Qy      3 LDTKICEQIEYFGDF 17
        ||| ||| ||| ||| |||
Db      3 LEAKICHQIEYFGDF 17
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```
RESULT 12
US-09-836-073-11
; Sequence 11, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-11
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Query Match          68.0%; Score 68; DB 9; Length 18;
Best Local Similarity 75.0%; Pred. No. 0.0015;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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```
Qy      3 LDTKICEQIEYFGDF 18
        ||| ||| ||| ||| |||
Db      3 LEAKICHQIEYFGDF 18
```

```
RESULT 13
US-09-836-073-12
; Sequence 12, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
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```
US-09-836-073-12
```

```
Query Match          68.0%; Score 68; DB 9; Length 18;
Best Local Similarity 75.0%; Pred. No. 0.0015;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      3 LDTKICEQIEYFGDF 18
        ||| ||| ||| ||| |||
Db      3 LEAKICHQIEYFGDF 18
```

```
RESULT 14
US-09-836-073-10
; Sequence 10, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-10
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Query Match          67.0%; Score 67; DB 9; Length 18;
Best Local Similarity 75.0%; Pred. No. 0.0022;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      3 LDTKICEQIEYFGDF 18
        ||| ||| ||| ||| |||
Db      3 LEAKICHQIEYFGDF 18
```

```
RESULT 15
US-09-836-073-16
; Sequence 16, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Rat
US-09-836-073-16
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Query Match          65.5%; Score 65.5; DB 9; Length 19;
Best Local Similarity 76.5%; Pred. No. 0.0039;
Matches 13; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
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Qy      3 LDTKICEQI-EYFGDF 18
        ||| ||| ||| ||| |||
Db      3 LEAKICHQIEYFGDF 19
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US-09-925-298-695

Query Match	76.0%	Score 76;	DB 12;	Length 460;
Best Local Similarity	81.2%	Pred. No. 0.0025;		
Matches 13;	Conservative 1;	Mismatches 2;	Indels 0;	Gaps 0;

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QY      3 LDTKICEQIEYYFGDF 18
        | : ||| ||| ||| |||
Db      65 LEAKICHQIEYYFGDF 80
```

RESULT 7
US-10-102-806-695

```

; Sequence 695: Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103P1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 695
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-102-806-695

```

Query Match	76.0%	Score 76;	DB 14;	Length 460;
Best Local Similarity	81.2%;	Pred. No. 0.0026;		
Matches 13; Conservative	1;	Mismatches 2;	Indels 0;	Gaps 0

```
QY      3 LDTKICEQIEYYFGDF 18
        | : ||| ||||| |||
Db      65 LEAKICHQIEYYFGDF 80
```

RESULT 8
US-10-264-049-264

```

Sequence 2643: Application US/10264049
Publication No. US20040005579A1
GENERAL INFORMATION:
APPLICANT: Bixse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P133P1
CURRENT APPLICATION NUMBER: US/10/264,049
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 2643
LENGTH: 460
TYPE: PRT
ORGANISM: Homo sapiens
US-10-264-049-2643

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Query Match	76.0%	Score 76;	DB 15;	Length 460;
Best Local Similarity	81.2%	Pred. No. 0.0026;		
Matches 13; Conservative	1;	Mismatches 2;	Indels 0;	Gaps 0

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QY      3 LDTKICEQIEYFGDF 18
        | : ||| ||||| |||
Db      65 LEAKICHQIEYFGDF 80
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RESULT 9
US-09-836-073-2

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; Sequence 2, Application US/098350/3
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baliga, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: prt
; ORGANISM: Homo Sapiens
US-09-836-073-2

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Query Match	74.0%;	Score 74;	DB 9;	Length 18;
Best Local Similarity	75.0%;	Pred. No. 0.00018;		
Matches	12;	Conservative	3;	Mismatches 1;
				Indels 0;
				Gaps 0;

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QY      3 LDTKICEQIEYYFGDF 18
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Db      3 LEAQICQIEYYFGDF 18
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RESULT 10
US-09-836-073-4

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? Sequence 4, Application US/09836073
? Patent No. US20020173475A1
? GENERAL INFORMATION:
? APPLICANT: Dasgupta, Asim
? APPLICANT: Das, S.
? APPLICANT: Baidya, Narayan
? TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
? FILE REFERENCE: 220002054822
? CURRENT APPLICATION NUMBER: US/09/836,073
? CURRENT FILING DATE: 2002-10-24
? PRIOR APPLICATION NUMBER: 09/316,630
? PRIOR FILING DATE: 1999-05-21
? NUMBER OF SEQ ID NOS: 19
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 4
? LENGTH: 18
? TYPE: prt
? ORGANISM: Homo Sapiens
US-09-836-073-4

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Query Match	72.0%;	Score 72;	DB 9;	Length 18;
Best Local Similarity	80.0%;	Pred. No. 0.00037;		
Matches	12;	Conservative	1;	Mismatches 2;
			Indels	0;
			Gaps	0;

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QY      4 DTKICEQIEYFGDF 18
Db      : ||| ||||| |||
         4 EAKICHQIEYFGDF 18
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RESULT 11
US-09-836-073-9

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: Sequence 9, Application US/09836073
: Patent No. US20020173475A1
: GENERAL INFORMATION:
: APPLICANT: Dasgupta, Asim
: APPLICANT: Das, S.
: APPLICANT: Baidya, Narayan
: TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION

```

```
APPLICANT: Baldeva, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mouse
US-09-836-073-13
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Best Local Similarity 81.2%; Pred. No. 8,6e-05;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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        |:|||||
Db      2 LEAKICQIEYFGDF 17
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RESULT 3
US-09-836-073-1
; Sequence 1, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-1
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Query Match          76.0%; Score 76; DB 9; Length 18;
Best Local Similarity 81.2%; Pred. No. 9,1e-05;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy      3 LDTKICQIEYFGDF 18
        |:|||||
Db      3 LEAKICQIEYFGDF 18
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RESULT 4
US-09-836-073-14
; Sequence 14, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 18
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; TYPE: PRT
; ORGANISM: Bovine
US-09-836-073-14
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Query Match          76.0%; Score 76; DB 9; Length 18;
Best Local Similarity 81.2%; Pred. No. 9,1e-05;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy      3 LDTKICQIEYFGDF 18
        |:|||||
Db      3 LEAKICQIEYFGDF 18
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RESULT 5
US-10-170-385-477
; Sequence 477, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 477
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-477
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Query Match          76.0%; Score 76; DB 12; Length 408;
Best Local Similarity 81.2%; Pred. No. 0.0023;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy      3 LDTKICQIEYFGDF 18
        |:|||||
Db      13 LEAKICQIEYFGDF 28
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RESULT 6
US-09-925-298-695
; Sequence 695, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103
; CURRENT APPLICATION NUMBER: US/09/925,298
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 695
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo sapiens
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:52:06 ; Search time 40.324 Seconds
(without alignments)
143.151 Million cell updates/sec

Title: US-09-836-073-15

Sequence: 1 LDLDTRICEQIERYFGDF 18

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Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*
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2: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB.pep:*
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8: /cgn2_6/prodata/1/pubppa/US08_PUBCOMB.pep:*
9: /cgn2_6/prodata/1/pubppa/US09_PUBCOMB.pep:*
10: /cgn2_6/prodata/1/pubppa/US09C_PUBCOMB.pep:*
11: /cgn2_6/prodata/1/pubppa/US09C_NEW_PUB.pep:*
12: /cgn2_6/prodata/1/pubppa/US10_PUBCOMB.pep:*
13: /cgn2_6/prodata/1/pubppa/US10C_PUBCOMB.pep:*
14: /cgn2_6/prodata/1/pubppa/US10C_PUBCOMB.pep:*
15: /cgn2_6/prodata/1/pubppa/US10C_PUBCOMB.pep:*
16: /cgn2_6/prodata/1/pubppa/US10_NEW_PUB.pep:*
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18: /cgn2_6/prodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	100.0	100.0	18	US-09-836-073-15	Sequence 15, Appl
2	76.0	76.0	17	US-09-836-073-13	Sequence 13, Appl
3	76.0	76.0	18	US-09-836-073-1	Sequence 1, Appl
4	76.0	76.0	18	US-09-836-073-14	Sequence 14, Appl
5	76.0	76.0	408	US-10-170-385-477	Sequence 477, App
6	76.0	76.0	460	US-09-925-298-695	Sequence 695, App
7	76.0	76.0	460	US-10-102-806-695	Sequence 695, App
8	76.0	76.0	460	US-10-264-049-2643	Sequence 2643, App
9	74.0	74.0	18	US-09-836-073-2	Sequence 2, Appl
10	72.0	72.0	18	US-09-836-073-4	Sequence 4, Appl
11	70.0	70.0	18	US-09-836-073-9	Sequence 9, Appl
12	68.0	68.0	18	US-09-836-073-11	Sequence 11, Appl
13	68.0	68.0	18	US-09-836-073-12	Sequence 12, Appl
14	67.0	67.0	18	US-09-836-073-10	Sequence 10, Appl
15	65.5	65.5	19	US-09-836-073-16	Sequence 16, Appl

16	65.0	18	9	US-09-836-073-3	Sequence 3, Appl
17	65.0	21	15	US-10-376-121A-20	Sequence 20, Appl
18	64.0	18	9	US-09-836-073-5	Sequence 5, Appl
19	64.0	38	9	US-09-843-676-25	Sequence 25, Appl
20	64.0	38	9	US-09-766-253-25	Sequence 25, Appl
21	64.0	38	10	US-09-438-466-25	Sequence 25, Appl
22	64.0	38	12	US-10-325-810-215	Sequence 215, App
23	64.0	38	14	US-10-053-758-25	Sequence 25, Appl
24	64.0	38	14	US-10-054-295-25	Sequence 25, Appl
25	64.0	38	14	US-10-054-611-25	Sequence 25, Appl
26	61.0	18	9	US-09-836-073-7	Sequence 7, Appl
27	60.0	18	9	US-09-836-073-8	Sequence 8, Appl
28	60.0	38	12	US-10-325-810-214	Sequence 214, App
29	56.0	143	12	US-10-424-599-254661	Sequence 254661, Sequence 254664, Sequence 17, Appl
30	56.0	395	12	US-10-424-599-254664	Sequence 17, Appl
31	55.0	18	9	US-09-836-073-17	Sequence 17, Appl
32	54.0	16	9	US-09-836-073-19	Sequence 19, Appl
33	53.0	411	14	US-10-177-478-8	Sequence 8, Appl
34	52.0	303	12	US-10-425-114-45759	Sequence 45759, A
35	52.0	401	12	US-10-424-599-254663	Sequence 254663, A
36	51.0	377	12	US-10-282-1322A-71434	Sequence 71434, A
37	51.0	488	12	US-10-424-599-272690	Sequence 272690, A
38	50.5	37	9	US-09-843-676-24	Sequence 24, Appl
39	50.5	37	9	US-09-766-253-24	Sequence 24, Appl
40	50.5	37	10	US-09-438-466-24	Sequence 24, Appl
41	50.5	37	14	US-10-054-758-24	Sequence 24, Appl
42	50.5	37	14	US-10-054-295-24	Sequence 24, Appl
43	50.5	37	14	US-10-054-611-24	Sequence 24, Appl
44	50.0	922	16	US-10-437-963-125036	Sequence 125036, A
45	49.0	329	12	US-10-425-114-49433	Sequence 49433, A

ALIGNMENTS

RESULT 1
US-09-836-073-15
; Sequence 15, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Xenopus
US-09-836-073-15

Query Match 100.0%; Score 100; DB 9; Length 18;

Best Local Similarity 100.0%; Pred. No. 2e-08; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDLDTRICEQIERYFGDF 18
Db 1 LDLDTRICEQIERYFGDF 18

RESULT 2
US-09-836-073-13
; Sequence 13, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-854-050-24

Query Match 50.5%; Score 50.5; DB 3; Length 37;
Best Local Similarity 83.3%; Pred. No. 0.21;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 7 ICEQIEYYFGDF 18
||| |||||
Db 1 ICHQ-EYFYGDF 11

RESULT 15
US-09-430-323-24
Sequence 24, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. 6309867e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-430-323-24

Query Match 50.5%; Score 50.5; DB 4; Length 37;
Best Local Similarity 83.3%; Pred. No. 0.21;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 7 ICEQIEYYFGDF 18
||| |||||
Db 1 ICHQ-EYFYGDF 11

Search completed: September 10, 2004, 18:05:10
Job time : 16.8883 secs

FILED DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-721-456-214

Query Match 60.0%; Score 60; DB 4; Length 38;
Best Local Similarity 83.3%; Pred. No. 0.0063;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 ICQIEYFGDF 18
DB 1 ICQIEYFGDF 12

RESULT 13
US-08-851-843A-24
Sequence 24, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017

FILED DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-851-843A-24

Query Match 50.5%; Score 50.5; DB 3; Length 37;
Best Local Similarity 83.3%; Pred. No. 0.21;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 7 ICQIEYFGDF 18
DB 1 ICQIEYFGDF 11

RESULT 14
US-08-854-050-24
Sequence 24, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536

APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-214

Query Match 60.0%; Score 60; DB 3; Length 38;
Best Local Similarity 83.3%; Pred. No. 0.0063;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 ICEQIEYFGDF 18
Db 1 ICHQXEYFGDF 12

RESULT 11
US-09-402-181B-214
Sequence 214, Application US/09402181B
Patent No. 6610839
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhu, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-402-181B-214

Query Match 60.0%; Score 60; DB 4; Length 38;
Best Local Similarity 83.3%; Pred. No. 0.0063;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 ICEQIEYFGDF 18
Db 1 ICHQXEYFGDF 12

RESULT 12
US-09-721-456-214
Sequence 214, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-NOV-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017

STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 215:
US-09-402-181B-215

Query Match 64.0%; Score 64; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ICEQIEYFQD 17
DB 1 ICEQIEYFQD 11

RESULT 9
US-09-721-456-215
Sequence 215, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-NOV-1997
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 215:
US-09-721-456-215

Query Match 64.0%; Score 64; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ICEQIEYFQD 17
DB 1 ICEQIEYFQD 11

RESULT 10
US-08-974-549A-214
Sequence 214, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:

TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 25;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-08-854-050-25

Query Match 64.0%; Score 64; DB 3; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ICEQIEYFFGD 17
Db 1 ICEQIEYFFGD 11

RESULT 7

US-09-430-323-25
; Sequence 25, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:

APPLICANT: Cecch, Thomas R.

lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: No. 6309867el Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/430,323

FILING DATE: 29-Oct-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002930US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 25;
; US-09-430-323-25

Query Match 64.0%; Score 64; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ICEQIEYFFGD 17
Db 1 ICEQIEYFFGD 11

RESULT 8

US-09-402-181B-215
; Sequence 215, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:

APPLICANT: Cecch, Thomas R.

lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 633

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/402,181B

FILING DATE: 29-Sep-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ausenhus, Scott L.

REGISTRATION NUMBER: 42,271

REFERENCE/DOCKET NUMBER: 015389-002620US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 215:

SEQUENCE CHARACTERISTICS:

LENGTH: 38 amino acids

TYPE: amino acid

Query Match 64.0%; Score 64; DB 3; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ICEQIEYFGD 17
DB 1 ICEQIEYFGD 11

RESULT 5
US-08-974-549A-215

; Sequence 215, Application US/08974549A
; Patent No. 6166178

; GENERAL INFORMATION:

; APPLICANT: Cecch, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin B.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 215:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-974-549A-215

Query Match 64.0%; Score 64; DB 3; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ICEQIEYFGD 17
DB 1 ICEQIEYFGD 11

RESULT 6
US-08-854-050-25

; Sequence 25, Application US/08854050
; Patent No. 6261836

; GENERAL INFORMATION:

; APPLICANT: Cecch, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

PRIOR FILING DATE: 1997-10-06
PRIOR APPLICATION NUMBER: 08/321,427
PRIOR FILING DATE: 1994-10-11
PRIOR APPLICATION NUMBER: 60/086,527
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 4
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: B-LAP
OTHER INFORMATION: this peptide is biotinylated
US-09-316-630-4

Query Match 76.0%; Score 76; DB 3; Length 18;
Best Local Similarity 81.2%; Pred. No. 7.4e-06;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 LDTKCEQIEYFGDF 18
Db 3 LEAKICHQIEYFGDF 18

RESULT 3
US-08-475-955-20
Sequence 20, Application US/08475955
Patent No. 6641813
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
TITLE OF INVENTION: AUTOANTIBODIES
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patricia L. Pabst
STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,955
FILING DATE: June 7, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patricia L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMF114CIP(2)DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Binding-site
LOCATION: 8..15
US-08-475-955-20

Query Match 65.0%; Score 65; DB 4; Length 21;
Best Local Similarity 91.7%; Pred. No. 0.00051;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ICEQIEYFGDF 18
Db 1 ICHQIEYFGDF 12

RESULT 4
US-08-851-843A-25
Sequence 25, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.

APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California

COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/851,843A

FILING DATE: 06-MAY-1997

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 015369-002930US

FILING DATE: 01-OCT-1996

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015369-002930US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-851-843A-25

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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:43:01; Search time 15.8883 Seconds
(without alignments)
58.488 Million cell updates/sec

Title: US-09-836-073-15

Perfect score: 100

Sequence: 1 LDDPKICEQIEYFGDF 18

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*
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5: /cgn2_6/prodata/2/1aa/6C_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfillseq1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	76.0	76.0	18	US-09-316-630-4	Sequence 4, Appl1
3	65.0	65.0	21	US-08-475-955-20	Sequence 20, Appl1
4	64.0	64.0	38	US-08-851-843A-25	Sequence 25, Appl1
5	64.0	64.0	38	US-08-974-549A-215	Sequence 25, Appl1
6	64.0	64.0	38	US-08-854-050-25	Sequence 25, Appl1
7	64.0	64.0	38	US-09-430-323-25	Sequence 25, Appl1
8	64.0	64.0	38	US-09-402-181B-215	Sequence 25, Appl1
9	64.0	64.0	38	US-09-721-456-215	Sequence 25, Appl1
10	60.0	60.0	38	US-08-974-549A-214	Sequence 214, Appl1
11	60.0	60.0	38	US-09-402-181B-214	Sequence 214, Appl1
12	60.0	60.0	38	US-09-721-456-214	Sequence 214, Appl1
13	50.5	50.5	37	US-08-851-843A-24	Sequence 24, Appl1
14	50.5	50.5	37	US-08-854-050-24	Sequence 24, Appl1
15	50.5	50.5	37	US-09-430-323-24	Sequence 24, Appl1
16	48.0	48.0	39	US-08-851-843A-26	Sequence 26, Appl1
17	48.0	48.0	39	US-08-974-549A-216	Sequence 26, Appl1
18	48.0	48.0	39	US-08-854-050-26	Sequence 26, Appl1
19	48.0	48.0	39	US-09-430-323-26	Sequence 26, Appl1
20	48.0	48.0	39	US-09-402-181B-216	Sequence 26, Appl1
21	48.0	48.0	39	US-09-721-456-216	Sequence 26, Appl1
22	44.5	44.5	178	US-09-107-532A-5800	Sequence 800, Appl1
23	40.0	40.0	590	US-08-448-196A-9	Sequence 9, Appl1
24	40.0	40.0	754	US-08-941-262-1	Sequence 1, Appl1
25	40.0	40.0	755	US-08-941-262-3	Sequence 4, Appl1
26	40.0	40.0	775	US-08-966-388-4	Sequence 4, Appl1
27	40.0	40.0	775	US-09-188-403-4	Sequence 4, Appl1

23	40	40.0	775	3	US-09-188-404-4	Sequence 4, Appl1
29	40	40.0	775	3	US-09-281-259-4	Sequence 4, Appl1
30	40	40.0	1956	3	US-08-843-417-2	Sequence 2, Appl1
31	40	40.0	1956	3	US-08-843-417-10	Sequence 10, Appl1
32	40	40.0	1956	4	US-09-527-013-2	Sequence 2, Appl1
33	40	40.0	1956	4	US-09-527-013-10	Sequence 10, Appl1
34	39	39.0	83	3	US-08-851-843A-9	Sequence 9, Appl1
35	39	39.0	83	3	US-08-851-843A-191	Sequence 191, Appl1
36	39	39.0	83	3	US-08-854-050-9	Sequence 9, Appl1
37	39	39.0	83	4	US-09-430-323-9	Sequence 9, Appl1
38	39	39.0	83	4	US-09-402-181B-191	Sequence 191, Appl1
39	39	39.0	83	4	US-09-721-456-191	Sequence 191, Appl1
40	39	39.0	85	3	US-08-851-843A-11	Sequence 11, Appl1
41	39	39.0	85	3	US-08-974-549A-193	Sequence 193, Appl1
42	39	39.0	85	3	US-08-854-050-11	Sequence 11, Appl1
43	39	39.0	85	4	US-09-430-323-11	Sequence 11, Appl1
44	39	39.0	85	4	US-09-402-181B-193	Sequence 193, Appl1
45	39	39.0	85	4	US-09-721-456-193	Sequence 193, Appl1

ALIGNMENTS

RESULT 1
US-09-316-630-3
; Sequence 3, Application US/09316630
; Patent No. 6291637
; GENERAL INFORMATION:
; APPLICANT: Das, Saumitra
; APPLICANT: Dasgupta, Asim
; TITLE OF INVENTION: INTERFERENCE WITH VIRAL IRES-MEDIATED TRANSLATION BY A
; FILE REFERENCE: 22000-20548.21
; CURRENT APPLICATION NUMBER: US/09/316,630
; CURRENT FILING DATE: 1999-05-21
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 08/817,953
; PRIOR FILING DATE: 1994-10-11
; PRIOR APPLICATION NUMBER: 60/086,527
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LAP
US-09-316-630-3
Query Match 76.0%; Score 76; DB 3; Length 18;
Best local similarity 81.2%; Pred. No. 7.4e-06;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
DB 3 LDDPKICEQIEYFGDF 18
QY 3 LDDPKICEQIEYFGDF 18
US-09-316-630-4
; Sequence 4, Application US/09316630
; Patent No. 6291637
; GENERAL INFORMATION:
; APPLICANT: Das, Saumitra
; APPLICANT: Dasgupta, Asim
; TITLE OF INVENTION: INTERFERENCE WITH VIRAL IRES-MEDIATED TRANSLATION BY A
; FILE REFERENCE: 22000-20548.21
; CURRENT APPLICATION NUMBER: US/09/316,630
; CURRENT FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 08/817,953

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OY 1 LDIDTRICQREYFPGD 17
|||:||||| | :|
DB 503 LDLEKKICBYIRSYKXD 519

Search completed: September 10, 2004, 18:00:09
Job time : 43.229 secs

[2]
 RN SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Shim P., Bowser L., Carninci P.,
 RA Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,
 RA Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
 RA Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,
 RA Soutchick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
 RA Yamada K., Yu G., Yuan S., Shinzaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis ORF clones."
 RL Submitted (SEP-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY050403; AAK91419.1; -;
 DR EMBL; BT000588; AAN18157.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR InterPro; IPR002344; Lupus La.
 DR InterPro; IPR006630; Lupus La. dom.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF05383; La; 1.
 DR Pfam; PF00076; xtm; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RM; 1.
 DR PROSITE; PS0102; RM; 1.
 SO SEQUENCE 422 AA; 46842 MW; 4EC4BBBF1E068F0E CRC64;

Query Match 53.0%; Score 53; DB 10; Length 422;
 Best Local Similarity 56.2%; Pred. No. 4.3;
 Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 LDLTKECEIYFEGD 17
 Db 102 ELNOKIRQVEYFSD 117

RESULT 14
 OS 057230 PRELIMINARY; PRT; 1156 AA.
 AC 057230;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE RNA polymerase subunit rpol32 (EC 2.7.7.6) (DNA-directed RNA
 DE polymerase beta chain).
 GN MVA135R.
 OS Vaccinia virus (strain Ankara).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OC NCB1_TaxID=126794;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Ankara;
 RA Antoine G., Schefflinger F., Falkner F.G., Dörner F.;
 RT "The complete genomic sequence of the Modified Vaccinia Ankara (MVA)
 RL strain."
 RL Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N DIPHOSPHATE +
 CC {RNA} (N).
 DR EMBL; U94848; AAB96526.1; -;
 DR PIR; T37411; T37411.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0003899; F:DNA-directed RNA polymerase activity; IEA.
 DR GO; GO:0003900; F:DNA-directed RNA polymerase I activity; IEA.
 DR GO; GO:0003901; F:DNA-directed RNA polymerase II activity; IEA.
 DR GO; GO:0003902; F:DNA-directed RNA polymerase III activity; IEA.
 DR GO; GO:0016740; F:transcriptase activity; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR InterPro; IPR007121; RNA_pol_B.
 DR InterPro; IPR007645; RNA_pol_Rpb2_3.
 DR InterPro; IPR007646; RNA_pol_Rpb2_4.
 DR InterPro; IPR007647; RNA_pol_Rpb2_5.
 DR InterPro; IPR007120; RNA_pol_Rpb2_6.
 DR InterPro; IPR007641; RNA_pol_Rpb2_7.
 DR Pfam; PF04565; RNA_pol_Rpb2_3; 1.
 DR Pfam; PF04566; RNA_pol_Rpb2_4; 1.
 DR Pfam; PF04567; RNA_pol_Rpb2_5; 1.
 DR Pfam; PF04568; RNA_pol_Rpb2_6; 1.
 DR Pfam; PF04569; RNA_pol_Rpb2_7; 1.
 DR PROSITE; PS01166; RNA_POL_BETA; 1.
 KW DNA-directed RNA polymerase; Transcription; Transferase.
 SO SEQUENCE 1164 AA; 133401 MW; D28A83F6EBDB810B CRC64;

DR InterPro; IPR007641; RNA_pol_Rpb2_7.
 DR Pfam; PF04565; RNA_pol_Rpb2_3; 1.
 DR Pfam; PF04566; RNA_pol_Rpb2_4; 1.
 DR Pfam; PF04567; RNA_pol_Rpb2_5; 1.
 DR Pfam; PF04568; RNA_pol_Rpb2_6; 1.
 DR Pfam; PF04569; RNA_pol_Rpb2_7; 1.
 DR PROSITE; PS01166; RNA_POL_BETA; 1.
 KW DNA-directed RNA polymerase; Transcription; Transferase.
 SO SEQUENCE 1156 AA; 132425 MW; F6657C8AF5E22BC3 CRC64;

Query Match 53.0%; Score 53; DB 12; Length 1156;
 Best Local Similarity 58.8%; Pred. No. 11;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LDLTKECEIYFEGD 17
 Db 495 LDLEKICEYIRSYKD 511

RESULT 15
 OS 090027 PRELIMINARY; PRT; 1164 AA.
 AC 090027;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE A25R (EC 2.7.7.6) (DNA-directed RNA polymerase beta chain).
 GN A25R.
 OS Variola major virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OC NCB1_TaxID=12870;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bangladesh-1975;
 RX MEDLINE=94088747; PubMed=8264798;
 RA Masung R.F., Esposito J.J., Liu L., Qi J., Utechtack T.R.,
 RA Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,
 RA Selivanov N.A., Cavaliaro K.F., Kerlavage A.R., Mahy B.W.J.,
 RA Venter C.J.;
 RT "Potential virulence determinants in terminal regions of variola
 RT smallpox virus genome."
 RL Nature 366:748-751(1993).
 CC -1- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N DIPHOSPHATE +
 CC {RNA} (N).
 DR EMBL; U2579; AAA60876.1; -;
 DR PIR; T28566; T28566.
 DR GO; GO:0003677; F:DNA binding; IEA.
 DR GO; GO:0003899; F:DNA-directed RNA polymerase activity; IEA.
 DR GO; GO:0003900; F:DNA-directed RNA polymerase I activity; IEA.
 DR GO; GO:0003901; F:DNA-directed RNA polymerase II activity; IEA.
 DR GO; GO:0003902; F:DNA-directed RNA polymerase III activity; IEA.
 DR GO; GO:0016740; F:transcriptase activity; IEA.
 DR GO; GO:0006350; P:transcription; IEA.
 DR InterPro; IPR007121; RNA_pol_B.
 DR InterPro; IPR007645; RNA_pol_Rpb2_3.
 DR InterPro; IPR007646; RNA_pol_Rpb2_4.
 DR InterPro; IPR007647; RNA_pol_Rpb2_5.
 DR InterPro; IPR007120; RNA_pol_Rpb2_6.
 DR InterPro; IPR007641; RNA_pol_Rpb2_7.
 DR Pfam; PF04565; RNA_pol_Rpb2_3; 1.
 DR Pfam; PF04566; RNA_pol_Rpb2_4; 1.
 DR Pfam; PF04567; RNA_pol_Rpb2_5; 1.
 DR Pfam; PF04568; RNA_pol_Rpb2_6; 1.
 DR Pfam; PF04569; RNA_pol_Rpb2_7; 1.
 DR PROSITE; PS01166; RNA_POL_BETA; 1.
 KW DNA-directed RNA polymerase; Transcription; Transferase.
 SO SEQUENCE 1164 AA; 133401 MW; D28A83F6EBDB810B CRC64;

Query Match 53.0%; Score 53; DB 12; Length 1164;
 Best Local Similarity 58.8%; Pred. No. 11;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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RT Staphylococcus aureus type 5 capsular polysaccharide."
RL Mol. Microbiol. 27:9-21(1998).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Reynolds and Newman;
RA Baggia N., Mann E.R., Foster T.J., Lee J.C.;
RU Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81973; AAC66099.1; -.
DR HSP; P27828; I16D.
DR GO; GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity; IEA.
DR GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
DR GO; GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.
DR InterPro; IPR003331; Epimerase_2.
DR Pfam; PF02350; Epimerase_2; 1.
DR TIGRFAMs; TIGR00236; wecB; 1.
SQ SEQUENCE 391 AA; 4432 MW; B0105F690B7CF1D CRC64;

Query Match 54.0%; Score 54; DB 2; Length 391;
Best Local Similarity 81.8%; Pred. No. 2.8;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 KICEQIEYFG 16
Db 366 RICEAIEYFG 376

RESULT 11
Q99X57 PRELIMINARY; PRT; 391 AA.
ID 099X57
AC 099X57;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Capsular polysaccharide synthesis enzyme CapsB.
GN CAP OR SAV0164 OR SA0159.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OC Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878; 158879;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952; PubMed=11418146;
RA Koroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kubara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshira K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003358; BAB56326.1; -.
DR EMBL; AP003329; BAB41379.1; -.
DR FUR; H89777; H89777.
DR HSP; P27828; I16D.
DR GO; GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity; IEA.
DR GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
DR GO; GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.
DR InterPro; IPR003331; Epimerase_2.
DR Pfam; PF02350; Epimerase_2; 1.
DR TIGRFAMs; TIGR00236; wecB; 1.
KM Complete proteome.
SQ SEQUENCE 391 AA; 44372 MW; D0DF5FA715BCCECC CRC64;

Query Match 54.0%; Score 54; DB 16; Length 391;
Best Local Similarity 81.8%; Pred. No. 2.8;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 KICEQIEYFG 16
Db 366 RICEAIEYFG 376

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RESULT 12
Q9FL36 PRELIMINARY; PRT; 411 AA.
ID Q9FL36
AC Q9FL36;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similarity to RNA-binding protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=98344145; PubMed=9679202;
RA Kaneo T., Korani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence
RT features of the regions of 1,381,565 bp covered by twenty one
RT DNA Res. 5:131-145(1998)."
RL EMBL; AB010698; BAB1080.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PRO0302; LUPUSLA.
DR SMART; SM00715; La; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PSS0102; RRM; 1.
SQ SEQUENCE 411 AA; 45655 MW; A2EF62EB588B099 CRC64;

Query Match 53.0%; Score 53; DB 10; Length 411;
Best Local Similarity 56.2%; Pred. No. 4.2;
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 DLDPTKICEQIEYFG 17
Db 91 ELNQLIRQVEYFSD 106

RESULT 13
Q94A38 PRELIMINARY; PRT; 422 AA.
ID Q94A38
AC Q94A38;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE AT5G46250/MPL12.3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Col-0;
RA Shum P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
RA Banb J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamita A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen M., Onda C.S., Palm C.J.,
RA Pham P.K., Quach H.L., Sakurai T., Saito M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

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DR EMBL: AY052365; AAK96556.1; -.
DR EMBL: AY139801; AAM98107.1; -.
DR EMBL: AC140977; AAO73903.1; -.
DR GO: GO:0003743; F:translational initiation factor activity; IEA.
DR GO: GO:0006413; P:translational initiation; IEA.
DR InterPro: IPR002965; P:rich_extensin.
DR InterPro: IPR001950; TIF_SUI1.
DR Pfam: PF05383; Ia; 1.
DR PRINTS: PR01217; PRICHEXTENSIN.
DR PROSITE: PS01118; SUI1.1; 1.
SQ SEQUENCE 826 AA; 91377 MW; 8D41922E5B609D9A CRC64;

Query Match 55.0%; Score 55; DB 10; Length 826;
Best Local Similarity 52.9%; Pred. No. 4;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LDLDTRICEQIEYFGD 17
Db 276 LDLDTRVLKQVEYFGD 292

RESULT 8
O8NYN8 PRELIMINARY; PRT; 381 AA.
AC O8NYN8;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Capsular polysaccharide synthesis enzyme Cap8P.
GN CAP8P OR MW0139.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramoto K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL: AP004822; BAB94004.1; -.
DR GO: GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity; IEA.
DR GO: GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
DR GO: GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.
DR InterPro: IPR003331; Epimerase_2.
DR Pfam: PF02350; Epimerase_2; 1.
DR TIGRFAMs: TIGR00236; wecB; 1.
KW Complete proteome.
SQ SEQUENCE 381 AA; 43106 MW; 125E4D5D1904779C CRC64;

Query Match 54.0%; Score 54; DB 16; Length 381;
Best Local Similarity 81.8%; Pred. No. 2.7;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 KICEQIEYFG 16
Db 356 RICEAIEYFG 366

RESULT 9
P72382 PRELIMINARY; PRT; 391 AA.
AC P72382;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Cap8P.
GN CAP8P.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
RT

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OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Becker;
RX MEDLINE=96178981; PubMed=8606192;
RA Sau S., Lee C.Y.;
RT "Cloning of type 8 capsule genes and analysis of gene clusters for the
RT production of different capsular polysaccharides in Staphylococcus
RT aureus.";
RL J. Bacteriol. 178:2118-2126(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Becker;
RX MEDLINE=97197525;
RA Sau S., Sun J., Lee C.Y.;
RT "Molecular characterization and transcriptional analysis of type 8
RT capsule genes in Staphylococcus aureus.";
RL J. Bacteriol. 179:1614-1621(1997).
DR EMBL: U73374; AAB49445.1; -.
DR HSP: P27828; IRED.
DR GO: GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity; IEA.
DR GO: GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
DR GO: GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.
DR InterPro: IPR003331; Epimerase_2.
DR Pfam: PF02350; Epimerase_2; 1.
DR TIGRFAMs: TIGR00236; wecB; 1.
SQ SEQUENCE 391 AA; 44247 MW; 1B8D9FA9BCT6F0D CRC64;

Query Match 54.0%; Score 54; DB 2; Length 391;
Best Local Similarity 81.8%; Pred. No. 2.8;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 KICEQIEYFG 16
Db 366 RICEAIEYFG 376

RESULT 10
P95709 PRELIMINARY; PRT; 391 AA.
AC P95709;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Cap8P.
GN CAP8P.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Reynolds and Newman;
RX MEDLINE=97388587; PubMed=9245821;
RA Sau S., Basian N., Wann E.R., Lee J.C., Foster T.J., Lee C.Y.;
RT "The Staphylococcus aureus allelic genetic loci for serotype 5 and 8
RT capsule expression contain the type-specific genes flanked by common
RT genes.";
RL Microbiology 143:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Reynolds and Newman;
RX MEDLINE=98101481; PubMed=9440531;
RA Kiser K.B., Lee J.C.;
RT "Staphylococcus aureus cap50 and cap8P genes functionally complement
RT mutations affecting enterobacterial common-antigen biosynthesis in
RT Escherichia coli.";
RL J. Bacteriol. 180:403-406(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Reynolds and Newman;
RX MEDLINE=98125727; PubMed=9466251;
RA Basian N., Albus A., Michon F., Livolsi P.J., Park J.-S., Lee J.C.;
RT "Identification of a gene essential for O-acetylation of the

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RESULT 5
Q72T10 ID Q72T10 PRELIMINARY; PRT; 401 AA.
AC 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)
DE Similar to sjgren syndrome antigen B (Autoantigen Ia).
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002344; Lupa La.
DR InterPro; IPR006630; Lupa La. dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 401 AA; 46138 MW; 2EF032PDD3916291 CRC64;

Query Match
Best Local Similarity 64.0%; Score 64; DB 13; Length 401;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 LDKTKCEQIEYFGD 17
DB 10 LERKVAQIEYFGD 24

RESULT 6
001806 ID 001806 PRELIMINARY; PRT; 396 AA.
AC 001806;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)
DE C44B4.4 protein.
OS Caenorhabditis elegans.
OC Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodermidae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RA "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RT Science 282:2012-2018(1998).
RL [2]
RN SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RC Sammons L., Wohlmann P., Gillam B.;
RT "The sequence of C. elegans cosmid C44B4.";
RN Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RP STRAIN=Bristol N2;
RC Waterston R.;

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RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003140; AAB54169.1; -.
DR PIR; T30953; T30953.
DR WormRep; C44B4.4; CE08718.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002344; Lupa La.
DR InterPro; IPR006630; Lupa La. dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; Lef; 1.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; FALSE NEG.
SQ SEQUENCE 396 AA; 43631 MW; A2D828A4AA3C34 CRC64;

Query Match
Best Local Similarity 58.0%; Score 58; DB 5; Length 396;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 LDKTKCEQIEYFGD 17
DB 11 DADQIKIQIEYFGN 26

RESULT 7
Q940X9 ID Q940X9 PRELIMINARY; PRT; 826 AA.
AC Q940X9;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)
DE A15G21160/T10F18_190 (Prolin-rich protein family).
GN A15G21160.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shin P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
RA Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinzaki K., Davis R.W., Theologis A., Becker J.R.;
RT "Arabidopsis cDNA clones.";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP Shin P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P.,
RA Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,
RA Heuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,
RA Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C.,
RA Yamada K., Yu G., Yuan S., Shinzaki K., Davis R.W., Theologis A.,
RA Becker J.R.;
RT "Arabidopsis ORF clones.";
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia;
RC Town C.D., Haas B.J., Maiti R., Hannick L.I., Chan A.P., Renning C.M.,
RA Smith Jr R.K., Arbogast T., Tallon L.J., Utterback T.R., Vanaken S.E.,
RA Feldblum T.V., Yu C., Wortman J.R., White O., Fraser C.M.;
RT "Arabidopsis thaliana chromosome 5 BAC F13M1 genomic sequence.";
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

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RESULT 2
Q9CYB9 PRELIMINARY; PRT; 381 AA.
ID Q9CYB9;
AC Q9CYB9;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Sjogren syndrome antigen B.
GN SSB.
OS Mus musculus (Mouse).
OC Eukaryota; Euteleostomi; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi U., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
RA Fleischnann W., Lewis S., Matsumoto Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Saeki H., Sato K., Schoedach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:688-690(2001).
RL EMBL; AK017822; BAB30957.1; -.
DR MGD; MGI:98423; Ssb.
DR GO; GO:0005634; C:nucleus; IDA.
DR InterPro; IPR002344; LupaLa_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; itm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00715; LA; 1.
SQ SEQUENCE 381 AA; 43891 MW; 2E2DE1452C0F0E9 CRC64;

Query Match
Best Local Similarity 76.0%; Score 76; DB 11; Length 381;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LDTKCEQIEYFGDF 18
DB 13 LEAKICQIEYFGDF 28

RESULT 3
Q8BTU4 PRELIMINARY; PRT; 415 AA.
ID Q8BTU4;
AC Q8BTU4;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Sjogren syndrome antigen B.
GN SSB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=ND; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK088677; BAC40498.1; -.
DR MGD; MGI:98423; Ssb.
DR GO; GO:0005634; C:nucleus; IDA.
DR InterPro; IPR002344; LupaLa_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; itm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 415 AA; 47657 MW; A7545C7686AC8363 CRC64;

Query Match
Best Local Similarity 76.0%; Score 76; DB 11; Length 415;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LDTKCEQIEYFGDF 18
DB 13 LEAKICQIEYFGDF 28

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RESULT 4
Q8OH15 PRELIMINARY; PRT; 206 AA.
ID Q8OH15;
AC Q8OH15;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Untranslated region binding-protein.
GN UBP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxId=9031;
RN [1]
RP SEQUENCE FROM N.A.
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF467897; AL76269.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002344; LupaLa_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; itm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 206 AA; 23992 MW; 965B62F7DFFB90E9 CRC64;

Query Match
Best Local Similarity 68.0%; Score 68; DB 13; Length 206;
Matches 11; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 LDTKCEQIEYFGDF 17
DB 13 LEAKICQIEYFGDF 27

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:29:01; Search time 41.229 Seconds
(without alignments)
137.751 Million cell updates/sec

Title: US-09-836-073-15

Perfect score: 100
Sequence: 1 LDLTKICQIEYFGDF 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL.25:*
1: sp archaea:*
2: sp bacteria:*
3: sp fungi:*
4: sp human:*
5: sp invertebrate:*
6: sp mammal:*
7: sp mhc:*
8: sp organelle:*
9: sp phage:*
10: sp plant:*
11: sp rodent:*
12: sp virus:*
13: sp vertebrate:*
14: sp unclassified:*
15: sp virus:*
16: sp bacteriaph:*
17: sp archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94	94.0	427	13	Q7ZTK2 xenopus lae
2	76	76.0	381	11	Q9CYB9 mus musculu
3	76	76.0	415	11	Q8BRT4 mus musculu
4	68	68.0	206	13	Q8OHT5 gallus galli
5	64	64.0	401	13	Q7ZT10 brachydanio
6	58	58.0	396	5	001806 caenorhabdi
7	55	55.0	826	10	Q940X9 arabidopsis
8	54	54.0	381	16	Q8NNT8 staphylococ
9	54	54.0	391	2	P72382 staphylococ
10	54	54.0	391	2	P95709 staphylococ
11	53	53.0	411	10	Q9FX57 staphylococ
12	53	53.0	422	10	Q9FX36 arabidopsis
13	53	53.0	422	10	Q94A38 arabidopsis
14	53	53.0	1164	12	Q57230 vaccinia vi
15	53	53.0	1164	12	Q90027 variola ma
16	53	53.0	1164	12	Q9JF79 vaccinia vi

17	53	53.0	1164	12	Q90031 variola vir
18	53	53.0	1164	12	Q8JL90 ectromelia
19	53	53.0	1164	12	Q8V4V3 monkeypox v
20	53	53.0	1164	12	Q8V2N1 camel痘x vi
21	53	53.0	1164	12	Q80DV1 cowpox viru
22	51	51.0	116	16	Q7VLE1 haemophilus
23	51	51.0	1221	12	Q8B9G3 rachioplusia
24	49	49.0	411	2	Q8GDD9 rhodospirill
25	48	48.0	190	12	Q90149 bombyx mori
26	48	48.0	337	2	Q8RK98 mycoplasma
27	48	48.0	390	5	Q8TRV5 dirosophila
28	48	48.0	571	5	Q7ZIR8 plasmodium
29	48	48.0	1222	12	Q7ZIR8 plasmodium
30	48	48.0	1222	12	P90691 bombyx mori
31	47	47.0	91	5	Q92455 bombyx mori
32	47	47.0	91	5	Q44678 caenorhabdi
33	47	47.0	389	10	Q8S0T8 oryza sativ
34	47	47.0	545	10	Q80567 arabidopsis
35	46.5	46.5	462	5	Q8ER84 dermatophag
36	46	46.0	122	13	Q8AW27 brachydanio
37	46	46.0	296	11	Q9CTN3 mus musculu
38	46	46.0	491	4	Q9BR58 mus musculu
39	46	46.0	492	11	Q8CA51 mus musculu
40	46	46.0	492	11	Q8C9A3 mus musculu
41	46	46.0	492	11	Q8BN59 mus musculu
42	46	46.0	501	4	Q8N3N2 mus musculu
43	46	46.0	551	13	Q7ZZ53 human sapien
44	46	46.0	652	13	Q7ZZ77 brachydanio
45	46	46.0	657	13	Q8AW24 brachydanio

ALIGNMENTS

RESULT 1
Q7ZTK2 PRELIMINARY; PRT; 427 AA.

AC Q7ZTK2;
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to lupus LA protein homolog B.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxId=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.,
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046654; AA46654.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002344; Lupus La.
DR InterPro; IPR006630; Lupus La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rtm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 2.
DR PROSITE; PSS0102; RRM; 1.
SQ SSQUNCE 427 AA; 4896 MM; 1E7CD82D8AB9C69A CRC64;

Query Match 94.0%; Score 94; DB 13; Length 427;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LDLTKICQIEYFGDF 17
Db 10 LDLTKICQIEYFGDF 26

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RX MEDLINE=95320184; PubMed=7597051;
RA Logemann E., Partridge M., Hahlbrock K.;
RT "Modes of expression and common structural features of the complete
  phenylalanine ammonia-lyase gene family in parsley.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:5995-5999(1995)
CC -1- FUNCTION: Controls carbon flux to pigments essential for
  pollination or UV protection, to numerous pycocauloxins synthesized
  by plants when challenged by pathogens, and to lignins.
CC -1- CATALYTIC ACTIVITY: Trans-cinnamate + NADPH + O(2) = 4-
  hydroxycinnamate + NADP(+) + H(2)O.
CC -1- PATHWAY: Lignin biosynthesis.
CC -1- PATHWAY: Phenylpropanoid metabolism; second step.
CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
  modified and this statement is not removed. Usage by and for commercial
  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L38898; AAC41660.1; -.
DR PIR; T14907; T14907.
DR InterPro; IPR001128; Cytochrome_P450.
DR Pfam; PF00067; P450; 1.
DR PRINTS; PR00385; P450.
DR PROSITE; PS00086; CYTOCHROME_P450; 1.
DR Oxidoreductase; Monooxygenase; Heme; NADP.
DR METAL 448 448 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 506 AA; 58047 MW; 32F00BE959D69CCF CRC64;
OY 5 TKICEQIEYYFGDF 18
  :: : ||: |||
Db 215 SRLAQSFYRHGDF 228

Query Match 45.0%; Score 45; DB 1; Length 506;
Best Local Similarity 42.9%; Pred. No. 9.3;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0.

Search completed: September 10, 2004, 17:53:07
Job time : 8.24022 secs

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DR PROSITE: PS00030: RRM RNP 1: FALSE NEG.
 KM RNA-binding; Nuclear protein; DNA-binding.
 FT DOMAIN 141 228
 SQ SEQUENCE 383 AA; 44430 MW; 4E5C8F21C40F452 CRC64;
 Query Match: 48.0%; Score 48; DB 1; Length 383;
 Best Local Similarity 53.3%; Pred. No. 2.2;
 Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 LDTKICBQIEVYFGD 17
 | : |||||
 Db 43 LEASTIRQLRYVFGD 57

RESULT 13
 LA DROME STANDARD; PRT; 390 AA.
 AC P40796; Q24375; Q9VIN2;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE La protein homolog (la ribonucleoprotein) (la autoantigen homolog).
 GN LA OR CG10922.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OK NCBI_TaxID=7227;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Canton-S; TISSUE=Ovary;
 RX MEDLINE=94309632; PubMed=8035794;
 RA Bai C., Li Z., Tolias P.P.;
 RT "Developmental characterization of a Drosophila RNA-binding protein
 RT homologous to the human systemic lupus erythematosus-associated
 RT La/SS-B autoantigen.";
 RL Mol. Cell. Biol. 14:5123-5129 (1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94309661; PubMed=8035818;
 RA Yoo C.J., Molin S.L.;
 RT "La proteins from Drosophila melanogaster and Saccharomyces
 RT cerevisiae: a yeast homolog of the la autoantigen is dispensable for
 RT growth.";
 RL Mol. Cell. Biol. 14:5412-5424 (1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chame M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.W., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K.J., Doull L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostel C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jaiswal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
 RA Laake P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milne N.V., Modarres C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pacלב J.M.,
 RA Palazzolo M., Plittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svrlkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J., Yao Q.A.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195 (2000).
 CC -1- FUNCTION: May be involved in transcription termination by RNA
 CC polymerase III. Binds RNA and DNA. Binds to precursors of RNA
 CC polymerase III transcripts. May play a specialized role during fly
 CC development.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- DEVELOPMENTAL STAGE: Expressed throughout embryonic, larval,
 CC pupal, and adult development. Expression throughout the embryo is
 CC followed by a restricted pattern of mesodermal expression that is
 CC later confined to the visceral mesoderm, gonads, gut, and salivary
 CC glands.
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
 CC -1- SIMILARITY: TO VERTEBRATE PROTEIN LA.
 CC -----
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC DR EMBL: U07652; AAA20518.1; -;
 CC DR EMBL: L32988; AAA21776.1; -;
 CC DR EMBL: AE003666; AA053885.1; -;
 CC DR PIR: A53773; A53773.
 CC DR PIR: A53781; A53781.
 CC DR FLYBASE: FBgn0011638; la.
 CC DR GO: GO:0008098; F:5S rRNA primary transcript binding; IDA.
 CC DR GO: GO:0003723; F:RNA binding; NAS.
 CC DR InterPro: IPR002344; Lupus_La.
 CC DR InterPro: IPR006630; Lupus_La_dom.
 CC DR InterPro: IPR00504; RNA_rec_mot.
 CC DR Pfam: PF05383; La; 1.
 CC DR Pfam: PF00076; rtm; 1.
 CC DR PRINTS: PR00302; LUPUSLA.
 CC DR SMART: SM00715; LA; 1.
 CC DR SMART: SM00360; RRM; 1.
 CC DR PROSITE: PS5102; RRM; 1.
 CC DR PROSITE: PS00030; RRM RNP 1; 1.
 CC DR RNA-binding; Nuclear protein; DNA-binding.
 CC KW DOMAIN 149 234
 CC FT CONFLICT 169 169 A -> T (IN REF. 1).
 CC FT CONFLICT 182 183 KH -> NS (IN REF. 1).
 CC FT CONFLICT 283 283 A -> R (IN REF. 1).
 CC FT CONFLICT 329 329 K -> N (IN REF. 1).
 CC SQ SEQUENCE 390 AA; 44884 MW; A80992889044655 CRC64;

Query Match: 48.0%; Score 48; DB 1; Length 390;
 Best Local Similarity 72.7%; Pred. No. 2.2;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 ICBOIEVYFGD 17
 | : |||||
 Db 54 IIRQVRYFGD 64

RESULT 14
 THIC_LBPIN STANDARD; PRT; 495 AA.

CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
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 CC -----
 CC DR EMBL; M57687; AAA67907.1; -
 CC DR EMBL; L22858; AAA6725.1; -
 CC DR PIR; A38499; HUNNAV.
 CC DR InterPro; IPR006824; Baculo_helicase.
 CC Pfam; PF04735; Baculo_helicase.1.
 CC Helicase; DNA replication; ATP-binding; DNA-binding; Nuclear protein;
 CC Early protein.
 CC FT DOMAIN 692 701 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 CC FT NP_BIND 917 924 ATP (BY SIMILARITY).
 CC FT DNA_BIND 967 981 H-T-H MOTIF (BY SIMILARITY).
 CC FT MUTAGEN 934 934 V->M: DEFECTIVE IN THE SYNTHESIS OF VIRAL
 CC SHUTOFF OF HOST PROTEIN SYNTHESIS AND THE
 CC NONPERMISSIVE TEMPERATURE (MUTANT T58).
 CC FT CONFLICT 126 126 F -> S (IN REF. 1).
 CC FT CONFLICT 1149 1149 F -> L (IN REF. 1).
 CC SQ SEQUENCE 1221 AA; 143213 MW; 090E19985862D1B CRC64;
 CC -----
 CC Query Match 51.0%; Score 51; DB 1; Length 1221;
 CC Best Local Similarity 61.5%; Pred. No. 2.4;
 CC Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 CC -----
 CC Qy 4 DTKICEQIEYRFG 16
 CC Db 440 DTKICVSLGTYRFG 452
 CC -----
 CC RESULT 11
 CC IPR MYCPU STANDARD; PRT; 183 AA.
 CC AC 098096;
 CC DT 28-FEB-2003 (Rel. 41, Created)
 CC DT 28-FEB-2003 (Rel. 41, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
 CC hydrolase) (Ppase).
 CC GN PPA OR MYPU 4700.
 CC OS Mycoplasma pulmonis.
 CC NCBI_TaxId=2107;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=21267165; PubMed=11353084;
 CC RA Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
 CC Moszer I., Dybvis K., Wroblewski H., Viari A., Rocha E.P.C.,
 CC Blanchard A.;
 CC RT "The complete genome sequence of the murine respiratory pathogen
 CC Mycoplasma pulmonis."
 CC RL Nucleic Acids Res. 29:2145-2153(2001).
 CC CC CATALYTIC ACTIVITY: diphosphate + H(2)O = 2 phosphate.
 CC -1- COFACTOR: Binds 4 magnesium ions per subunit. Other metal ions can
 CC support activity, but at a lower rate. Two magnesium ions are
 CC required for the activation of the enzyme and are present before
 CC substrate binds, two additional magnesium ions form complexes with
 CC substrate and product (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the Ppase family.
 CC -----
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 CC -----
 CC DR EMBL; AL445564; CAC13643.1; -
 CC DR PIR; F90570; F90570.
 CC DR MyPulIat; MYPU_4700; -
 CC DR HAMAP; MF_00209; -; 1.
 CC DR InterPro; IPR008163; Inorg_ppnaph.
 CC DR InterPro; IPR008162; Pyrophosphatase.
 CC Pfam; PF00719; Pyrophosphatase.1.
 CC DR PRODOM; PD002014; Inorg_ppnaph.1.
 CC DR PROSITE; PS00387; PPASE.1.
 CC KM Hydrolyase; Metal-binding; Magnesium; Complete proteome.
 CC FT METAL 53 53 MAGNESIUM 1 (BY SIMILARITY).
 CC FT METAL 58 58 MAGNESIUM 1 AND 2 (BY SIMILARITY).
 CC FT METAL 90 90 MAGNESIUM 1 (BY SIMILARITY).
 CC SQ SEQUENCE 183 AA; 21715 MW; 65AF81A063AAAD3 CRC64;
 CC -----
 CC Query Match 50.0%; Score 50; DB 1; Length 183;
 CC Best Local Similarity 47.1%; Pred. No. 0.47;
 CC Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 CC -----
 CC Qy 2 DDTKICEQIEYRFGDF 18
 CC Db 111 DDDSKMLEIKYFSGNY 127
 CC -----
 CC RESULT 12
 CC LA AEDAL STANDARD; PRT; 383 AA.
 CC ID 026457;
 CC DT 15-JUL-1998 (Rel. 36, Created)
 CC DT 15-JUL-1998 (Rel. 36, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE A protein homolog (La ribonucleoprotein) (La autoantigen homolog).
 CC Aedes albopictus (Forest day mosquito).
 CC OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes.
 CC NCBI_TaxId=7160;
 CC RN [1]
 CC RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 CC RX MEDLINE=96135233; PubMed=8551578;
 CC RA Parignon N., Strauss J.H.;
 CC RT "Mosquito homolog of the La autoantigen binds to Sindbis virus RNA.",
 CC RL J. Virol. 70:1173-1181(1996).
 CC CC -1- FUNCTION: May be involved in transcription termination by RNA
 CC polymerase III. Binds RNA and DNA. Binds to the 3' end of the
 CC minus strand of Sindbis virus RNA. This may be significant for
 CC Sindbis virus RNA replication.
 CC -1- SUBCELLULAR LOCATION: Nuclear. Primarily nuclear, but significant
 CC amounts are present in the cytoplasm.
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
 CC -1- SIMILARITY: TO VERTEBRATE PROTEIN LA.
 CC -----
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 CC -----
 CC DR EMBL; S80954; AAB35931.1; -
 CC DR InterPro; IPR002344; LupaLa.
 CC DR InterPro; IPR006630; LupaLa_dom.
 CC DR InterPro; IPR000504; RNA_rec_mot.
 CC Pfam; PF05383; La; 1.
 CC DR PIR; P00076; Irm; 1.
 CC DR PRINTS; PR00302; LUPUSLA.
 CC DR SMART; SM00715; LA; 1.
 CC DR SMART; SM00360; RRM; 1.
 CC DR PROSITE; PS50102; RRM; 1.

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CC -|- SUBUNIT: This enzyme consists of at least eight subunits.
CC -|- SIMILARITY: Belongs to the RNA polymerase beta chain family.
CC -----
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CC -----
CC EMBL; X69198; CAA49069.1; -.
CC
CC DR PIR; G36850.
CC DR InterPro; IPR007121; RNA_pol_B.
CC DR InterPro; IPR007645; RNA_pol_Rpb2_3.
CC DR InterPro; IPR007646; RNA_pol_Rpb2_4.
CC DR InterPro; IPR007647; RNA_pol_Rpb2_5.
CC DR InterPro; IPR007120; RNA_pol_Rpb2_6.
CC DR InterPro; IPR007641; RNA_pol_Rpb2_7.
CC DR Pfam; PF04565; RNA_pol_Rpb2_3_1.
CC DR Pfam; PF04566; RNA_pol_Rpb2_4_1.
CC DR Pfam; PF04567; RNA_pol_Rpb2_5_1.
CC DR Pfam; PF00562; RNA_pol_Rpb2_6_1.
CC DR Pfam; PF04560; RNA_pol_Rpb2_7_1.
CC DR PROSITE; PS01166; RNA_POL_BETA; 1.
CC
CC DR Translasease; DNA-directed RNA polymerase; Transcription; Zinc;
CC Zinc-finger.
CC
CC KW ZN FING
CC FT SEQUENCE
CC
CC SQ SEQUENCE 1164 AA; 133329 MW; 0452B84ED810CD53 CRC64;
CC
CC
CC Query Match 53.0%; Score 53; DB 1; Length 1164;
CC Best Local Similarity 58.8%; Pred. No. 1.1;
CC Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
CC
CC QY 1 LDLPXICEQIEYYFGD 17
CC ||| ||||| |||
CC Db 503 LDLEKICICEYIRSYKD 519
CC
CC RESULT 10
CC V143 NPVAC
CC ID V143 NPVAC STANDARD; PRT; 1221 AA.
CC AC P24307;
CC DT 01-MAR-1992 (Rel. 21, Created)
CC DT 01-NOV-1995 (Rel. 32, Last sequence update)
CC DT 01-NOV-1997 (Rel. 35, Last annotation update)
CC DE Helicase.
CC GN P143.
CC OS Autographa californica nuclear polyhedrosis virus (AcMNPV).
CC OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
CC OC Nucleopolyhedrovirus.
CC OX NCBI_TaxID=46015;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=HR3;
CC RX MEDLINE=91134998; PubMed=1994581;
CC RA Lu A., Carstens E.B.;
CC RT "Nucleotide sequence of a gene essential for viral DNA replication in
CC the baculovirus Autographa californica nuclear polyhedrosis virus.";
CC RL Virology 181:336-347(1991).
CC RN [2]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=C6;
CC RX MEDLINE=94303173; PubMed=8030224;
CC RA Ayres M.D., Howard S.C., Kuzio J., Loper-Ferber M., Possee R.D.;
CC RT "The complete DNA sequence of Autographa californica nuclear
CC polyhedrosis virus.";
CC RL Virology 202:586-605(1994).
CC -| FUNCTION: Essential for the initiation of viral DNA replication,
CC it may contribute to other functions such as controlling the
CC switch to the late phase and leading to the inhibition of host
CC protein synthesis. Required for late and very late gene
CC expression.
CC

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CC -----
CC EMBL: X67859; CAA48043.1; -
CC PIR: JCI1494; JCI1494.
CC InterPro: IPR002344; Lupus_La.
CC InterPro: IPR006630; Lupus_La_dom.
CC InterPro: IPR00504; RNA_rec_mot.
CC Pfam: PF05383; La; 1.
CC Pfam: PF00076; rrm; 1.
CC PRINTS: PR00302; LUPUSLA.
CC SMART: SM00715; LA; 1.
CC SMART: SM00360; RRM; 1.
CC PROSITE: PS50102; RRM; 1.
CC PROSITE: PS00030; RRM_RNP_1; 1.
CC RNA-binding; Nuclear protein; Phosphorylation.
CC DOMAIN 111 187
CC SEQUENCE 415 AA; 47777 MW; 033FD9C1E475F98 CRC64;

Query Match 76.0%; Score 76; DB 1; Length 415;
Best Local Similarity 81.2%; Pred. No. 5.7e-05;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 LDTKICEQIEYFGDF 18
DB 13 LEAKICHQIEYFGDF 28

RESULT 7
RPO2_COMPX ID RPO2_COMPX STANDARD; PRT; 1164 AA.

AC P17474; Q90025;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE DNA-directed RNA polymerase 132-kDa polypeptide (EC 2.7.7.6).
GN RPO132.

OS Compox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10243;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Brighton red;
RX MEDLINE=89125698; PubMed=2915377;
RA Patel D.D., Pickup D.J.;

RT "The second-largest subunit of the poxvirus RNA polymerase is similar
RT to the corresponding subunits of procaryotic and eucaryotic RNA
RT polymerases.";
RL J. Virol. 63:1076-1086(1989).

CC -1- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
CC of DNA into RNA using the four ribonucleoside triphosphates as
CC substrates.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC {RNA} (N).

CC -1- SUBUNIT: This enzyme consists of at least eight subunits.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative initiation;
CC Comment=2 isoforms, 1/late specific (shown here) and 2/early and
CC Late, are produced by alternative initiation. One
CC transcripional start site is operative at late times only and
CC the other is operative both at early and late times;

CC -1- SIMILARITY: Belongs to the RNA polymerase beta chain family.
CC -----
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CC -----
CC EMBL: M26173; AAA42919.1; -
CC EMBL: M26173; AAA42920.1; -
CC PIR: A1879; RNVP.1.
CC InterPro: IPR007121; RNA_pol_B.
CC InterPro: IPR007645; RNA_pol_Rpb2_3.
CC InterPro: IPR007646; RNA_pol_Rpb2_4.
CC InterPro: IPR007647; RNA_pol_Rpb2_5.
CC InterPro: IPR007120; RNA_pol_Rpb2_6.
CC InterPro: IPR007641; RNA_pol_Rpb2_7.
CC Pfam: PF04565; RNA_pol_Rpb2_3; 1.
CC Pfam: PF04566; RNA_pol_Rpb2_4; 1.
CC Pfam: PF04567; RNA_pol_Rpb2_5; 1.
CC Pfam: PF00562; RNA_pol_Rpb2_6; 1.
CC Pfam: PF04560; RNA_pol_Rpb2_7; 1.
CC PROSITE: PS01166; RNA_POL_BETA_1.
CC -transferase; DNA-directed RNA polymerase; Transcription; Zinc;
CC Zinc-finger; Alternative initiation.
CC CHAIN 1 1164
CC FT CHAIN 9 1164
FT INIT MET 9 1106
FT ZN FING 1087 1106
FT SEQUENCE 1164 AA; 133323 MW; 220D6EF5238DBE7 CRC64;

Query Match 53.0%; Score 53; DB 1; Length 1164;
Best Local Similarity 58.8%; Pred. No. 1.1;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 LDTKICEQIEYFGDF 17
DB 503 LDKKICQIEYFGDF 519

RESULT 8
RPO2_VACCV ID RPO2_VACCV STANDARD; PRT; 1164 AA.

AC P19758;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE DNA-directed RNA polymerase 132 kDa polypeptide (EC 2.7.7.6).
GN RPO132 OR A24R.

OS Vaccinia virus (strain WR), and
OS Vaccinia virus (strain Copenhagen).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10254; 10249;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WR;
RX MEDLINE=91082452; PubMed=1824607;
RA Amesgazi B.Y., Holmes M.H., Cole N.B., Jones E.V., Earl P.L.,
RA Moss B.;

RT "Identification, sequence, and expression of the gene encoding the
RT second-largest subunit of the vaccinia virus DNA-dependent RNA
RT polymerase.";
RL Virology 180:88-98(1991).

CC [2]
CC SEQUENCE FROM N.A.
CC STRAIN=Copenhagen;
CC MEDLINE=91021027; PubMed=2219722;
CC Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P.,
CC Paoletti E.;

CC "The complete DNA sequence of vaccinia virus.";
CC Virology 179:247-266(1990).
CC [3]
CC COMPLETE GENOME.

CC STRAIN=Copenhagen;
CC STRAIN=Copenhagen;
CC Goebel S.J., Johnson G.P., Perkins M.E., Davis S.W., Winslow J.P.,
CC Paoletti E.;

```

FT DOMAIN 111 187 RNA-BINDING (RRM).
SQ MOD RES 366 366 PHOSPHORYLATION (BY CK2).
SQ SEQUENCE 408 AA; 46837 MW; EC153C15F9187FC4 CRC64;

Query Match
Best Local Similarity 81.2%; Score 76; DB 1; Length 408;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 LDTKCEQIEYFGDF 18
Db 13 LEAKICHQIEYFGDF 28

RESULT 5
LA_MOUSE STANDARD; PRT; 415 AA.
ID LA_MOUSE
AC P32067;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Lupus La protein homolog (La ribonucleoprotein) (La autoantigen
homolog).
DE SSB OR SS-B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
(1)
RP SEQUENCE FROM N.A.
RX MEDLINE=93203630; PubMed=8454877;
RA Topfer F., Gordon T., McCluskey J.;
RT "Characterization of the mouse autoantigen La (SS-B). Identification
of conserved RNA-binding motifs, a putative ATP binding site and
RT reactivity of recombinant protein with poly(U) and human
RT autoantibodies."
RT J. Immunol. 150:3091-3100(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=FVB/N; TISSUE=Mammary gland;
MEDLINE=22388257; PubMed=1247932;
RA Klausner R.L., Feigold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan T., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stopleon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rabe S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boeak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.U., Lu X., Gibbs R.A.,
RA Fahy J., Helton B., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.T., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE OF 1-11 FROM N.A.
RA Grodz D., Bachmann M.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: La protein plays a role in the transcription of RNA
CC polymerase III. It is most probably a transcription termination
CC factor. Binds to the 3' terminus of virtually all nascent
CC of RNA polymerase III transcripts. It is associated with precursor forms
CC and 7-2 RNAs.
CC -1- SUBUNIT: Interacts with DDX15 (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- PTM: Phosphorylated (By similarity).

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CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announce/
CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; L00993; AAA3945.1; -
CC EMBL; BC003820; AA03820.1; -
CC EMBL; Y07951; CA69249.1; -
CC MGD; MGI:98423; Ssb.
CC GO; GO:0005634; C:nucleus; IDA.
CC InterPro; IPR002344; Lupus_La.
CC InterPro; IPR006630; Lupus_La_dom.
CC InterPro; IPR000504; RNA_rec_mot.
CC Pfam; PF05383; La; 1.
CC Pfam; PF00076; rrm; 1.
CC PRINTS; PR00302; LUPUSLA.
CC SMART; SM00715; LA; 1.
CC SMART; SM00360; RRM; 1.
CC PROSITE; PS50102; RRM; 1.
CC PROSITE; PS00300; RRM_RNP_1; 1.
CC RNA-binding; Nuclear protein; Phosphorylation.
CC DOMAIN 111 187
SQ SEQUENCE 415 AA; 47756 MW; 2D75197692FDC933 CRC64;

Query Match
Best Local Similarity 81.2%; Score 76; DB 1; Length 415;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 LDTKCEQIEYFGDF 18
Db 13 LEAKICHQIEYFGDF 28

RESULT 6
LA_RAT STANDARD; PRT; 415 AA.
ID LA_RAT
AC P36656;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lupus La protein homolog (La ribonucleoprotein) (La autoantigen
homolog).
DE SSB OR SS-B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
(1)
RP SEQUENCE FROM N.A.
RX MEDLINE=93246255; PubMed=7916708;
RA Seneel I., Troester H., Bartsch H., Schemmle M., Igloi G.L.,
RA Bachmann M.;
RL "Isolation of rat cDNA clones coding for the autoantigen SS-B/La:
RT detection of species-specific variations."
RT Gene 126:265-268(1993).
RN [2]
RP SEQUENCE OF 1-11 FROM N.A.
RA Grodz D., Bachmann M.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: La protein plays a role in the transcription of RNA
CC polymerase III. It is most probably a transcription termination
CC factor. Binds to the 3' terminus of virtually all nascent
CC of RNA polymerase III transcripts. It is associated with precursor forms
CC and 7-2 RNAs.
CC -1- SUBUNIT: Interacts with DDX15 (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- PTM: Phosphorylated (By similarity).
CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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Query Match 76.0%; Score 76; DB 1; Length 404;
Best Local Similarity 81.2%; Pred. No. 5.5e-05;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LDTKICEQIEYFGDF 18
|: ||| ||||| |||
DB 13 LEAKICHQIEYFGDF 28

RESULT 4
LA_HUMAN STANDARD; PRT; 408 AA.
ID P05455;
AC 01-NOV-1988 (Rel. 09, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Lupus La protein (Sjogren syndrome type B antigen) (SS-B) (La
ribonucleoprotein) (La autoantigen).
GN SSB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=89202037; PubMed=2468131;
RT Chan E.K.L., Sullivan K.F., Tan E.M.;
RT "Ribonucleoprotein SS-B/La belongs to a protein family with consensus
sequences for RNA-binding.";
RT Nucleic Acids Res. 17:2233-2244(1989).
[2]
SEQUENCE FROM N.A.
RX MEDLINE=89053970; PubMed=3192525;
RT Chambers U.C., Keman D., Martin B.J., Keene J.D.;
RT "Genomic structure and amino acid sequence domains of the human La
autoantigen.";
RT J. Biol. Chem. 263:18043-18051(1988).
[3]
SEQUENCE FROM N.A.
RC TISSUE=Placenta, and Skeletal muscle;
RX MEDLINE=22388257; PubMed=1247932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Ziegler B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzyzinski M.I., Skalska U., Smalins D.E.,
RA Scheraga A., Schein U.E., Jones S.U.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
SEQUENCE OF 54-408 FROM N.A.
RX MEDLINE=88199081; PubMed=2452201;
RA Sturge S.A.D., Peterson M.G., McNeillage L.J., Whittingham S.,
RA Coppel R.S.;
RT "Characteristics and epitope mapping of a cloned human autoantigen
La.";
RL J. Immunol. 140:3212-3218(1988).
[5]
SEQUENCE OF 54-97 FROM N.A.
RX MEDLINE=8516283; PubMed=8556886;
RA Chambers J.C., Keene J.D.;

RT "Isolation and analysis of cDNA clones expressing human lupus La
antigen.";
RT Proc. Natl. Acad. Sci. U.S.A. 82:2115-2119(1985).
RL
RN [6]
RX MEDLINE=89251617; PubMed=2470590;
RA Gottlieb E., Steitz J.A.;
RT "Function of the mammalian La protein: evidence for its action in
transcription termination by RNA polymerase III.";
RL EMBO J. 8:851-861(1989).
RN [7]
RX MEDLINE=97207017; PubMed=9054510;
RA Fan H., Sakulich A.L., Goodier J.L., Zhang X., Qin J., Marais R.J.;
RT "Phosphorylation of the human La antigen on serine 366 can regulate
recycling of RNA polymerase III transcription complexes.";
RL Cell 88:707-715(1997).
RN [8]
RX MEDLINE=22346609; PubMed=12458796;
RA Fournaux M.A., Kolman M.J.M., Van der Heijden A., De Jong A.S.,
RA Van Venrooij W.J., Pruijn G.J.M.;
RT "The human La (SS-B) autoantigen interacts with DDX15/hPrp43, a
putative DEAD-box RNA helicase.";
RL RNA 8:1428-1443(2002).
CC -1- FUNCTION: La protein plays a role in the transcription of RNA
polymerase III. It is most probably a transcription termination
factor. Binds to the 3' terminus of virtually all nascent
polymerase III transcripts. It is associated with precursor forms
of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S,
and 7-2 RNAs.
CC -1- SUBUNIT: Interacts with DDX15.
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- PTM: PHOSPHORYLATION. THE PHOSPHORYLATION SITES ARE AT THE
C-TERMINAL PART OF THE PROTEIN.
CC -1- PTM: The N-terminus is blocked.
CC -1- DISBASE: Sera from patients with systemic lupus erythematosus
often contain antibodies that react with the normal cellular
La protein as if this antigen was foreign.
CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
CC
CC -----
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CC
CC EMBL; X13697; CAA31985.1; -
CC EMBL; J04205; AAA51885.1; -
CC EMBL; BC001289; AAH01289.1; -
CC EMBL; BC020818; AAH20818.1; -
CC PIR; A13888; A13888.
CC Genew; HGNC:11316; SSB.
CC MIM; 109090; -
CC GO; GO:0030529; C:ribonucleoprotein complex; TAS.
CC GO; GO:0003729; F:RNA binding; TAS.
CC GO; GO:0000049; F:RNA binding; TAS.
CC GO; GO:0008334; P:histone mRNA metabolism; TAS.
CC GO; GO:0006400; P:RNA modification; TAS.
CC InterPro; IPR002344; Lupus_La.
CC InterPro; IPR006630; Lupus_La_dom.
CC InterPro; IPR000504; RNA_rec_mot.
CC Pfam; PF00383; La; 1.
CC Pfam; PF0076; rtm; 1.
CC PRINTS; PR00302; LUPUSLA.
CC SMART; SM00715; La; 1.
CC SMART; SM00360; RRM; 1.
CC PROSITE; PS50102; RRM; 1.
CC PROSITE; PS00030; RRM_RNP_1; 1.
CC Systemic lupus erythematosus; RNA-binding; Phosphorylation;
KW Nuclear protein.

DR PROSITE: PS00030; RRM_RNP_1; FALSE NEG.
 KM RNA-binding; Nuclear protein; Phosphorylation.
 FT DOMAIN 110 202 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 315 331 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 SQ SEQUENCE 427 AA; 48995 MW; 45F3146F8934A355 CRC64;

Query March 94.0%; Score 94; DB 1; Length 427;
 Best local similarity 100.0%; Pred. No. 6.2e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LDDPTKICEQIEYFGD 17
 |||||
 Db 10 LDDPTKICEQIEYFGD 26

RESULT 2
 ID LAA_XENLA STANDARD; PRT; 428 AA.
 AC P28048;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Lopus La protein homolog A (La ribonucleoprotein A) (La autoantigen homolog A).
 GN LAA1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Oocyte;
 RX MEDLINE=93287095; PubMed=8510143;
 RA Scherly D., Stutz F., Lin-Marg N., Clarkson S.G.;
 RT "La proteins from Xenopus laevis. cDNA cloning and developmental expression.";
 RT J. Mol. Biol. 231:196-204(1993).
 RU J. Mol. Biol. 231:196-204(1993).
 CC -1- FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' terminus of virtually all nascent polymerase III transcripts (by similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- DEVELOPMENTAL STAGE: Barely detectable in stage I/II oocytes, accumulate in stage III/IV oocytes, then exhibit a roughly constant steady state level in mature oocytes, eggs, and early embryos.
 CC -1- PTM: Phosphorylated (Probable).
 CC -1- MISCELLANEOUS: There are two forms of La, Laa and Lab, in xenopus.
 CC -1- SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN.
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
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 CC -----
 CC EMBL, X68817; CAA48715.1; -.
 DR PIR, S33818; S33818.
 DR InterPro, IPR002344; Lopus_La.
 DR InterPro, IPR006630; Lopus_La.
 DR InterPro, IPR000504; RNA_rec_mot.
 DR Pfam, PF05383; La; 1.
 DR Pfam, PF00076; rtm; 1.
 DR PRINTS, PR00302; LUPUSLA.
 DR SMART, SM00715; LA; 1.
 DR SMART, SM00360; RRM; 1.
 DR PROSITE, PS50102; RRM; 1.
 DR PROSITE, PS00030; RRM_RNP_1; 1.
 KW RNA-binding; Nuclear protein; Phosphorylation.

FT DOMAIN 111 203 RNA-BINDING (RRM).
 FT DOMAIN 196 212 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 316 332 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 SQ SEQUENCE 428 AA; 48864 MW; AEB3A38B7D2E3EC3 CRC64;

Query March 88.0%; Score 88; DB 1; Length 428;
 Best local similarity 94.1%; Pred. No. 6.1e-07;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDDPTKICEQIEYFGD 17
 |||||
 Db 11 LDDPTKICEQIEYFGD 27

RESULT 3
 ID LA_BOVIN STANDARD; PRT; 404 AA.
 AC P10881;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lopus La protein homolog (La ribonucleoprotein) (La autoantigen homolog).
 GN SSB.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pituitary;
 RX MEDLINE=89202037; PubMed=2468131;
 RA Chan E.K.L., Sullivan K.F., Tan E.M.;
 RT "Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences for RNA-binding.";
 RT Nucleic Acids Res. 17:2233-2244(1989).
 RU Nucleic Acids Res. 17:2233-2244(1989).
 CC -1- FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' terminus of virtually all nascent polymerase III transcripts. It is associated with precursor forms of RNA polymerase III transcripts including crRNA and 4.5S, 5S, 7S, and 7-2 RNAs.
 CC -1- SUBUNIT: Interacts with DDX15 (by similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- PTM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES ARE AT THE C-TERMINAL PART OF THE PROTEIN.
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
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 CC -----
 CC EMBL, X13698; CAA31986.1; -.
 DR PIR, S03849; S03849.
 DR InterPro, IPR002344; Lopus_La.
 DR InterPro, IPR006630; Lopus_La.
 DR InterPro, IPR000504; RNA_rec_mot.
 DR Pfam, PF05383; La; 1.
 DR Pfam, PF00076; rtm; 1.
 DR PRINTS, PR00302; LUPUSLA.
 DR SMART, SM00715; LA; 1.
 DR SMART, SM00360; RRM; 1.
 DR PROSITE, PS50102; RRM; 1.
 DR PROSITE, PS00030; RRM_RNP_1; 1.
 KW RNA-binding; Nuclear protein; Phosphorylation.
 FT DOMAIN 111 187 RNA-BINDING (RRM).
 SQ SEQUENCE 404 AA; 46534 MW; 4EB30B5C62AD6A1 CRC64;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:01:41; Search time 7.24022 Seconds
(without alignments)
129.452 Million cell updates/sec

Title: US-09-836-073-15

Perfect score: 100

Sequence: 1 LDLDTKICEQIEFYRGDF 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	94	94.0	427	1	LAB_XENLA
2	88	88.0	428	1	LAB_XENLA
3	76	76.0	404	1	LA_BOVIN
4	76	76.0	408	1	LA_HUMAN
5	76	76.0	415	1	LA_MOUSE
6	76	76.0	415	1	LA_RAT
7	53	53.0	1164	1	RPO2_COMPLEX
8	53	53.0	1164	1	RPO2_VACCV
9	53	53.0	1164	1	RPO2_VARV
10	51	51.0	1221	1	V143_NPVAC
11	50	50.0	183	1	IPYR_MTCPU
12	48	48.0	383	1	LA_AEDAL
13	48	48.0	390	1	LA_DROME
14	46	46.0	495	1	THIC_LBEPIN
15	45	45.0	506	1	TCMO_PETCR
16	44	44.0	490	1	IFET4_HUMAN
17	44	44.0	1069	1	PCHT_HUMAN
18	43	43.0	366	1	DHPH_THRIN
19	43	43.0	711	1	ETP2_MXYVL
20	43	43.0	711	1	ETP2_SFYKA
21	43	43.0	2184	1	POLG_ECOLI
22	42	42.0	270	1	YC87_METUA
23	41	41.0	298	1	LAH1_SCHPO
24	41	41.0	438	1	2277_HUMAN
25	41	41.0	1104	1	2406_HUMAN
26	40	40.0	176	1	IPYR_HAERIN
27	40	40.0	247	1	ADCI_RHILLO
28	40	40.0	236	1	ADCS_RHILLO
29	40	40.0	261	1	ADCC_RHILLO
30	40	40.0	466	1	SRO9_YEAST
31	40	40.0	474	1	SYE_VIBPA
32	40	40.0	552	1	FET4_YEAST
33	40	40.0	608	1	ALB1_SALSA

34	40	40.0	608	1	ALB2_SALSA
35	40	40.0	755	1	SEC6_RAT
36	40	40.0	756	1	SEC6_HUMAN
37	40	40.0	2911	1	FBN2_HUMAN
38	39.5	39.5	297	1	YX01_CAEL
39	39.5	39.5	859	1	ST7_HUMAN
40	39.5	39.5	967	1	SYL_PYRHO
41	39	39.0	175	1	IPYR_PSEPK
42	39	39.0	191	1	Y948_METUA
43	39	39.0	245	1	YCEL_BACST
44	39	39.0	264	1	GRAX_HUMAN
45	39	39.0	305	1	HEM6_VIBCH

ALIGNMENTS

RESULT 1
LAB_XENLA STANDARD; PRT; 427 AA.
AC P28049;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Lupus La protein homolog B (La ribonucleoprotein B) (La autoantigen homolog B).
GN LAB1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8335;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocyte;
RX MEDLINE=93287095; PubMed=8510143;
RA Scherly D., Stultz F., Lin-Mary N., Clarkson S.G.;
RT "La proteins from Xenopus laevis. cDNA cloning and developmental expression.";
RT J. Mol. Biol. 231:196-204(1993).
RL
CC -|- FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' terminus of virtually all nascent polymerase III transcripts (By similarity).
CC -|- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -|- DEVELOPMENTAL STAGE: Barely detectable in stage I/II oocytes, accumulate in stage III/IV oocytes, then exhibit a roughly constant steady state level in mature oocytes, eggs, and early embryos.
CC -|- PTM: Phosphorylated (Probable).
CC -|- MISCELLANEOUS: There are two forms of La, LaA and LaB, in xenopus.
CC -|- SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN.
CC -|- SIMILARITY: Contains 1 RNA recognition motif (RNM) domain.
CC
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CC
CC EMBL: X68818; CAA48716.1; -
CC PIR: S33817; S33817.
CC InterPro: IPR002344; Lupus_La.
CC InterPro: IPR006630; Lupus_La_dom.
CC InterPro: IPR00504; RNA_rec_mot.
CC 3fam: PFO5383; La; 1.
CC 3fam: PFO0076; rrm; 1.
CC PRINTS: PR00302; LUPUSLA.
CC SMART: SM00715; LA; 1.
CC SMART: SM00360; RRM; 1.
CC PROSITE: PSS0102; RRM; 1.

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A:Reference number: A72850; MUID:94303173; PMID:8030224

A:Accession: H72861

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-125, 'F', 127-1148, 'F', 1150-1221 <AYR>

A:Cross-references: GB:L22858; NID:G510708; PIDN:AAA66725.1; PID:G559164

C:Genetics:

A:Gene: Ac-helicase

C:Superfamily: AcMNPV helicase

C:Keywords: ATP; DNA binding; DNA repair; DNA replication; hydrolase; nucleotide binding

F:917-924/Region: nucleotide-binding motif A (P-loop)

Query Match 51.0%; Score 51; DB 1; Length 1221;

Best Local Similarity 61.5%; Pred. No. 6.9;

Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 DTRICEQIEYFPG 16

Db 440 DTRLCVSLGYFPG 452

RESULT 15

F90570

hypothetical protein MYPV 4700 [Imported] - Mycoplasma pulmonis (strain UAB CTIP)

C:Species: Mycoplasma pulmonis

C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001

C:Accession: F90570

R:Chabaud, I.; Hellig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;

Nucleic Acids Res. 29, 2145-2153, 2001

A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm

A:Reference number: A99512; MUID:21267165; PMID:11353084

A:Accession: F90570

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-183 <KUR>

A:Cross-references: GB:AL445566; PID:G14089884; PIDN:CAC13643.1; GSPDB:GN00153

A:Experimental source: strain UAB CTIP

C:Genetics:

A:Gene: MYPV 4700

A:Genetic code: SGC3

C:Superfamily: inorganic pyrophosphatase

Query Match 50.0%; Score 50; DB 2; Length 183;

Best Local Similarity 47.1%; Pred. No. 1.4;

Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 DLDTRICEQIEYFPG 18

Db 111 DLDKXWLEIKYFFSNY 127

Search completed: September 10, 2004, 18:02:33
Job time : 16.0782 secs

A:Title: The complete DNA sequence of vaccinia virus.
 A:Reference number: A42531; MUID:91021027; PMID:2219722
 A:Contents: annotation; possible protein-coding frames
 A>Note: neither amino acid nor nucleotide sequence is given
 C:Superfamily: DNA-directed RNA polymerase 132K polypeptide
 C:Keywords: leucine zipper; nucleotidyltransferase; transcription; zinc finger
 F:484-505/Region: leucine zipper motif
 F:1087-1106/Region: zinc finger CCCC motif

Query Match 53.0%; Score 53; DB 1; Length 1164;
 Best Local Similarity 58.8%; Pred. No. 3.1;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 LDLDTRICEQIEYFGD 17
 |||:|||||:|:
 DB 503 LDLEKKICEYIRSYKD 519

RESULT 10

RNVZCP
 DNA-directed RNA polymerase (EC 2.7.7.6) 132K chain - cowpox virus (strain Brighton Red)
 C:Species: cowpox virus
 C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 11-Jun-1999
 C:Accession: A31879
 R:Patel, D.D.; Pickup, D.J.
 J:Virol. 63, 1076-1086, 1989

A:Title: The second-largest subunit of the poxvirus RNA polymerase is similar to the cor
 A:Reference number: A31879; MUID:89125698; PMID:2915377
 A:Accession: A31879
 A:Molecule type: DNA
 A:Residues: 1-1164 <PART>
 A:Cross-references: GB:M26173; NID:G323393; PIDN:AAA42919.1; PID:G323394
 C:Comment: This enzyme consists of at least seven subunits whose molecular weights are 1

A:Gene: rpo132
 C:Superfamily: DNA-directed RNA polymerase 132K polypeptide
 C:Keywords: nucleotidyltransferase; transcription; zinc finger

Query Match 53.0%; Score 53; DB 1; Length 1164;
 Best Local Similarity 58.8%; Pred. No. 3.1;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 LDLDTRICEQIEYFGD 17
 |||:|||||:|:
 DB 503 LDLEKKICEYIRSYKD 519

RESULT 11

T28566
 DNA-directed RNA polymerase (EC 2.7.7.6) 133K chain - variola major virus
 C:Species: variola major virus
 C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
 C:Accession: T28566
 R:Maesung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Uteerback, T.R.; Knight, J.C.; Aubin

Nature 366, 748-751, 1993
 A:Title: Potential virulence determinants in terminal regions of variola smallpox virus
 A:Reference number: Z20488; MUID:94088747; PMID:8264798
 A:Accession: T28566
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1164 <MS>
 A:Cross-references: EMBL:L22579; NID:G623595; PIDN:AAA60876.1; PID:G439046
 A:Experimental source: strain Bangladesh-1975
 C:Superfamily: DNA-directed RNA polymerase 132K polypeptide
 C:Keywords: nucleotidyltransferase; transcription

Query Match 53.0%; Score 53; DB 2; Length 1164;
 Best Local Similarity 58.8%; Pred. No. 3.1;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 LDLDTRICEQIEYFGD 17
 |||:|||||:|:
 DB 503 LDLEKKICEYIRSYKD 519

RESULT 12

A25R protein - variola minor virus (strain Garcia-1966)
 F72166
 C:Species: variola minor virus
 C:Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
 C:Accession: F72166
 R:Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Saifonov, P.F.; Maesung, R.F.; Lopez

A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
 A:Reference number: A72150
 A:Accession: F72166
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1164 <SHC>
 A:Cross-references: GB:Y16780; NID:G5830555; PIDN:CAB54728.1; PID:G5830689
 A:Experimental source: strain Garcia-1966
 C:Genetics:

A:Gene: A25R
 C:Superfamily: DNA-directed RNA polymerase 132K polypeptide

Query Match 53.0%; Score 53; DB 2; Length 1164;
 Best Local Similarity 58.8%; Pred. No. 3.1;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 LDLDTRICEQIEYFGD 17
 |||:|||||:|:
 DB 503 LDLEKKICEYIRSYKD 519

RESULT 13

G36850
 A24R protein - variola virus (strain India-1967)
 C:Species: variola virus
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2001
 C:Accession: G36850
 R:Binov, V.M.

submitted to GenBank, November 1992
 A:Reference number: A36859
 A:Accession: G36850
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1164 <BLI>
 A:Cross-references: GB:X69198; NID:G456758; PIDN:CAA49069.1; PID:G297307
 C:Superfamily: DNA-directed RNA polymerase 132K polypeptide

Query Match 53.0%; Score 53; DB 2; Length 1164;
 Best Local Similarity 58.8%; Pred. No. 3.1;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 LDLDTRICEQIEYFGD 17
 |||:|||||:|:
 DB 503 LDLEKKICEYIRSYKD 519

RESULT 14

H0NNAV
 helicase (EC 3.6.1.-) - Autographa californica nuclear polyhedrosis virus
 C:Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 19-Jan-2001
 C:Accession: A38499; H72861
 R:Liu, A.; Garstens, E.B.

Virol. 181, 336-347, 1991
 A:Title: Nucleotide sequence of a gene essential for viral DNA replication in the baculo
 A:Reference number: A38499; MUID:91134998; PMID:1994581
 A:Accession: A38499
 A:Molecule type: DNA
 A:Residues: 1-1221 <LUA>
 A:Cross-references: EMBL:M57687
 R:Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.

Virol. 202, 586-605, 1994
 A:Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.

Gene 126, 265-268, 1993
 A>Title: Isolation of rat cDNA clones coding for the autoantigen SS-B/La: Detection of
 A:Reference number: JCI494; MUID:93246255; PMID:7916708
 A:Accession: JCI494
 A:Molecule type: mRNA
 A:Residues: 1-415 <SEM>
 A:Cross-references: GB:X67859; NID:G55778; PIDN:CAA48043.1; PID:G55779
 A:Experimental source: liver
 C:Comment: This protein associates with a variety of small RNA molecules, most of which
 act as a transcription termination factor.
 C:Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
 C:Keywords: phosphoprotein; RNA binding
 F:112-178/Domain: ribonucleoprotein repeat homology <RRM>
 F:113-118/Region: RNA-binding RNP2 motif
 F:151-158/Region: RNA-binding RNP1 motif
 F:127-415/Domain: phosphorylated #status predicted <PHY>

Query Match 76.0%; Score 76; DB 1; Length 415;
 Best Local Similarity 81.2%; Pred. No. 0.00021;
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LDTKICEQIEYFGDF 18
 | : |||||
 Db 13 LEAKICHQIEYFGDF 28

RESULT 6
 T30953
 hypothetical protein C44E4.4 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #ext_change 31-Jan-2000
 C:Accession: T30953
 R:Sammons, L.; Wohldmann, P.; Gillam, B.
 submitted to the EMBL Data Library, August 1999
 A:Description: The sequence of C. elegans cosmid C44E4.
 A:Reference number: Z20945
 A:Accession: T30953
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-396 <SAM>
 A:Cross-references: EMBL:AF003140; PIDN:AB54169.1
 A:Experimental source: strain Bristol N2; clone C44E4
 C:Genetics:
 A:Map position: 1
 A:Introns: 45/1; 114/3
 A>Note: C44E4.4
 C:Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology

Query Match 58.0%; Score 58; DB 2; Length 396;
 Best Local Similarity 62.5%; Pred. No. 0.16;
 Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 DLDTKICEQIEYFGD 17
 | : |||||
 Db 11 DADQKIKOLEYFFGN 26

RESULT 7
 H89777
 capsular polysaccharide synthesis enzyme Cap5P [imported] - Staphylococcus aureus (strain
 C:Species: Staphylococcus aureus
 C>Date: 10-May-2001 #sequence_revision 10-May-2001 #ext_change 22-Oct-2001
 C:Accession: H89777
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
 C.; Shibata, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A>Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: H89777
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-391 <KTR>

A:Cross-references: GB:BA000018; PID:G13700080; PIDN:BAE41379.1; GSPDB:GN00149
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: capP
 C:Superfamily: lipopolysaccharide biosynthesis protein bplD

Query Match 54.0%; Score 54; DB 2; Length 391;
 Best Local Similarity 81.8%; Pred. No. 0.68;
 Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 KICEQIEYFG 16
 : |||||
 Db 366 RICEAIEYFG 376

RESULT 8
 T37411
 RNA polymerase subunit rpol32 - vaccinia virus (strain Ankara)
 C:Species: vaccinia virus
 A:Variety: strain Ankara
 C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #ext_change 18-Feb-2000
 C:Accession: T37411
 R:Antoine, G.; Schellinger, F.; Falkner, F.G.; Dörner, F.
 submitted to the EMBL Data Library, March 1997
 A:Description: The complete genomic sequence of the Modified Vaccinia Ankara (MVA) strain
 A:Reference number: Z20877
 A:Accession: T37411
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-1156 <ANT>
 A:Cross-references: EMBL:U94848; PIDN:AB96526.1
 A:Experimental source: strain Ankara
 C:Genetics:
 A>Note: MVA135R
 C:Superfamily: DNA-directed RNA polymerase 132K polypeptide

Query Match 53.0%; Score 53; DB 2; Length 1156;
 Best Local Similarity 58.8%; Pred. No. 3.1;
 Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 LDDTKICEQIEYFGD 17
 |||||
 Db 495 LDLEKKICEYRSYMD 511

RESULT 9
 RNV28T
 DNA-directed RNA polymerase (EC 2.7.7.6) 132K chain - vaccinia virus
 N:Alternate names: A24R protein
 C:Species: vaccinia virus
 A>Note: host Homo sapiens (man)
 C>Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #ext_change 11-Jun-1999
 C:Accession: H42519; A38517
 R:Goebel, S.J.; Johnson, G.P.; Perkins, M.E.; Davis, S.W.; Winslow, J.P.; Paolletti, E.
 Virology 179, 517-563, 1990
 A>Title: Appendix to "The complete DNA sequence of vaccinia virus".
 A:Reference number: A42501
 A:Accession: H42519
 A:Molecule type: DNA
 A:Residues: 1-1164 <GOB>
 A:Cross-references: GB:M35027; NID:G335317; PIDN:AAA48148.1; PID:G335496
 A:Experimental source: strain Copenhagen
 R:Amegdzle, B.Y.; Holmes, M.H.; Cole, N.B.; Jones, E.V.; Earl, P.L.; Moss, B.
 Virology 180, 88-98, 1991
 A>Title: Identification, sequence, and expression of the gene encoding the second-large
 A:Reference number: A38517; MUID:91082452; PMID:1824607
 A:Accession: A38517
 A:Molecule type: DNA
 A:Residues: 1-1164 <AME>
 A:Cross-references: EMBL:M37415; NID:G335800; PIDN:AAA72882.1; PID:G335801
 A:Experimental source: strain WR
 R:Goebel, S.J.; Johnson, G.P.; Perkins, M.E.; Davis, S.W.; Winslow, J.P.; Paolletti, E.
 Virology 179, 247-266, 1990

F.112-178/Domain: ribonucleoprotein repeat homology <RNM>
 F.113-118/Region: RNA-binding RNP2 motif
 F.151-158/Region: RNA-binding RNP1 motif
 F.128-428/Domain: phosphorylated #status predicted <PHY>

Query Match 88.0%; Score 88; DB 1; Length 428;
 Best Local Similarity 94.1%; Pred. No. 2.5e-06;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LDDTKICEQIEYFGDF 17
 |||||
 Db 11 LDDTKICEQIEYFGDF 27

RESULT 3

S03849
 ribonucleoprotein la - bovine
 N:Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 31-Dec-1990 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
 C:Accession: S03849

R:Chan, E.K.L.; Sullivan, K.F.; Tan, E.M.
 Nucleic Acids Res. 17, 2233-2244, 1989
 A:Title: Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences
 A:Reference number: S03848; MUID:89202037; PMID:2468131

A:Accession: S03849

A:Molecule type: mRNA

A:Residues: 1-404 <CHA>

A:Cross-references: EMBL:X13698; NID:g755; PIDN:CAA31986.1; PID:g756

A:Note: Part of this sequence was confirmed by protein sequencing

C:Comment: This protein associates with a variety of small RNA molecules, most of which
 act as a transcription termination factor.

C:Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology

C:Keywords: blocked amino end; phosphoprotein; RNA binding

F.112-178/Domain: ribonucleoprotein repeat homology <RNM>

F.113-118/Region: RNA-binding RNP2 motif

F.151-158/Region: RNA-binding RNP1 motif

F.128-404/Domain: phosphorylated #status predicted <PHY>

Query Match 76.0%; Score 76; DB 1; Length 404;
 Best Local Similarity 81.2%; Pred. No. 0.0002;
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 LDTKICEQIEYFGDF 18
 |||||
 Db 13 LEAKICHOIEYFGDF 28

RESULT 4

A31888
 ribonucleoprotein la - human
 N:Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B; Sjogren syndrome antigen
 C:Species: Homo sapiens (man)
 C:Date: 21-May-1990 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
 C:Accession: A31888; S03848; J22956; A61051; S11013; I5553; I70205; I70206; A31273

R:Chambers, J.C.; Kennan, D.; Martin, B.J.; Keene, J.D.

U. Biol. Chem. 263, 18043-18051, 1988

A:Title: Genomic structure and amino acid sequence domains of the human la autoantigen.

A:Reference number: A31888; MUID:89053970; PMID:3192525

A:Accession: A31888

A:Molecule type: mRNA

A:Residues: 1-408 <CHA>

A:Cross-references: GB:J04205; NID:g178686; PIDN:AAA51885.1; PID:g178687

R:Chan, E.K.L.; Sullivan, K.F.; Tan, E.M.

Nucleic Acids Res. 17, 2233-2244, 1989

A:Title: Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences

A:Reference number: S03848; MUID:89202037; PMID:2468131

A:Accession: S03848

A:Molecule type: mRNA

A:Residues: 1-408 <CHA>

A:Cross-references: EMBL:X13697; NID:g36414; PIDN:CAA31985.1; PID:g36415

R:Chambers, J.C.; Keene, J.D.
 Proc. Natl. Acad. Sci. U.S.A. 82, 2115-2119, 1985

A:Title: Isolation and analysis of cDNA clones expressing human lupus la antigen.

A:Reference number: A22956; MUID:85166283; PMID:3856888

A:Accession: A22956

A:Molecule type: mRNA

A:Residues: 45-97, 'LK' <CH3>

A:Cross-references: GB:J04205

A:Note: this sequence has been revised in reference A31888

R:Nyman, U.; Ringertz, N.R.; Petersson, I.

Immunol. Lett. 22, 65-72, 1989

A:Title: Demonstration of an amino terminal la epitope recognized by human anti-la sera.

A:Reference number: A61051; MUID:89379261; PMID:2476379

A:Accession: A61051

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-19, 'E', 21-47 <NYM>

R:Sturges, A.D.; Peterson, M.G.; McNeilage, L.J.; Whittingham, S.; Coppel, R.L.

J. Immunol. 140, 3212-3218, 1988

A:Title: Characteristics and epitope mapping of a cloned human autoantigen la.

A:Reference number: S11013; MUID:88199081; PMID:2452201

A:Accession: S11013

A:Molecule type: mRNA

A:Residues: 'E', 55-287, 'V', 289-408 <STU>

A:Cross-references: EMBL:M20328; NID:g337456; PIDN:AAA6577.1; PID:g337457

R:Kohsaka, H.; Yamamoto, K.; Fujii, H.; Mura, H.; Miyasaka, N.; Nishioaka, K.; Miyamoto, J.

Clin. Invest. 85, 1566-1574, 1990

A:Title: Fine epitope mapping the human SS-B/La protein: Identification of a distinct au

A:Reference number: I5553; MUID:90237237; PMID:1692037

A:Accession: I5553

A:Molecule type: mRNA

A:Status: translated from GB/EMBL/DBJ

A:Residues: 81-107 <RES>

A:Cross-references: GB:M5261; NID:g338491; PIDN:AAA36652.1; PID:g338495

A:Accession: I70205

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 174-224 <RE2>

A:Cross-references: GB:M5263; NID:g338492; PIDN:AAA36653.1; PID:g338496

A:Accession: I70206

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 279-342 <RE3>

A:Cross-references: GB:M5262; NID:g338493; PIDN:AAA36654.1; PID:g338497

C:Comment: This protein associates with a variety of small RNA molecules, most of which
 act as a transcription termination factor.

C:Genetics:

A:Gene: GDB:SSB

A:Cross-references: GDB:125359; OMIM:109090

A:Map position: 2

A:Introns: 22/3; 57/2; 115/3; 151/3; 185/2; 209/2; 223/3; 264/3; 380/2

C:Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology

C:Keywords: phosphoprotein; RNA binding

F.112-178/Domain: ribonucleoprotein repeat homology <RNM>

F.113-118/Region: RNA-binding RNP2 motif

F.151-158/Region: RNA-binding RNP1 motif

F.128-408/Domain: phosphorylated #status experimental <PHY>

Query Match 76.0%; Score 76; DB 1; Length 408;
 Best Local Similarity 81.2%; Pred. No. 0.0002;
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 LDTKICEQIEYFGDF 18
 |||||
 Db 13 LEAKICHOIEYFGDF 28

RESULT 5

J01494
 ribonucleoprotein la - rat
 N:Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 24-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
 C:Accession: J01494; S25145
 R:Semsei, I.; Troester, H.; Bartsch, H.; Schwemmler, M.; Igloi, G.L.; Bachmann, M.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:33:11; Search time 14.0782 Seconds
(without alignments)
122.988 Million cell updates/sec

Title: US-09-836-073-15

Perfect score: 100

Sequence: 1.LDLDTKICEQIEHYFGDF 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	94.0	427	1	S33817	ribonucleoprotein
2	88.0	428	1	S33818	ribonucleoprotein
3	76.0	404	1	S03849	ribonucleoprotein
4	76.0	408	1	A31888	ribonucleoprotein
5	76.0	415	1	UC1494	ribonucleoprotein
6	58.0	396	2	T30953	hypothetical prote
7	54.0	391	2	H89777	capsular polysacch
8	53.0	1156	2	T37411	RNA polymerase sub
9	53.0	1164	1	RNVZBT	DNA-directed RNA p
10	53.0	1164	1	RNVZCP	DNA-directed RNA p
11	53.0	1164	2	T28566	A25R protein - var
12	53.0	1164	2	F72166	A24R protein - var
13	53.0	1164	2	G36850	helicase (EC 3.6.1
14	51.0	1221	1	HUNNAV	hypothetical prote
15	50.0	183	2	F90570	p143 DNA helicase
16	48.0	190	2	A47569	la/SS-B homolog D-
17	48.0	390	2	A53773	ribonucleoprotein
18	48.0	390	2	A53781	DNA helicase P143
19	48.0	1222	2	T41835	hypothetical prote
20	47.0	166	2	T32701	hypothetical prote
21	47.0	529	2	T00677	hypothetical prote
22	45.0	399	2	T01035	trans-cinnamate 4-
23	45.0	308	2	T14907	hypothetical prote
24	44.0	165	2	T29244	BH-protocadherin-a
25	44.0	1069	2	T00043	BH-protocadherin p
26	44.0	1072	2	T00041	BH-protocadherin p
27	44.0	1200	2	T00042	hypothetical prote
28	44.0	1743	2	T26859	hypothetical prote
29	43.0	292	2	T02349	hypothetical prote

30	43.0	366	2	JQ0513	phenylalanine dehy
31	43.0	505	2	B90181	Na+/H+ antiporter
32	43.0	658	2	D96566	hypothetical prote
33	43.0	759	2	AC0368	probable autotrans
34	43.0	788	2	A71076	hypothetical prote
35	42.0	199	2	A11512	weakly methyltrans
36	42.0	270	2	F64460	hypothetical prote
37	42.0	277	2	AD0121	probable exported
38	42.0	421	2	AE2473	hypothetical prote
39	42.0	1055	2	AD2499	hypothetical prote
40	41.5	140	2	C96957	hypothetical prote
41	41.0	63	2	C96942	probable Zn-depend
42	41.0	199	2	B97180	probable type II r
43	41.0	260	2	H71979	RNA binding protei
44	41.0	298	2	T38937	RNA-binding protei
45	41.0	298	2	T43542	

ALIGNMENTS

RESULT 1
S33817
ribonucleoprotein la.B - African clawed frog
N:Alternate names: autoantigen SS-B/la; ribonucleoprotein SS-B
C:Species: Xenopus laevis (African clawed frog)
C>Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C:Accession: S33817; S28544
R:Schery, D.; Stutz, F.; Lin-Marg, N.; Clarkson, S.G.
J. Mol. Biol. 231, 196-204, 1993
A>Title: la proteins from Xenopus laevis. cDNA cloning and developmental expression.
A:Reference number: S33817; MUID:93287095; PMID:8510143
A:Accession: S33817
A:Molecule type: mRNA
A:Residues: 1-427 <SCH>
A:Cross-references: EMBL:X68818; NID:G64875; PIDD:CAA48716.1; PIDD:G64876
C:Comment: This protein associates with a variety of small RNA molecules, most of which
ay act as a transcription termination factor.
C:Keywords: ribonucleoprotein la; ribonucleoprotein repeat homology
C:Superfamily: phosphoprotein; RNA binding
F:150-157/Region: RNA-binding RNP1 motif
F:227-427/Domain: phosphorylated #status predicted <PHY>

Query Match 94.0%; Score 94; DB 1; Length 427;
Best Local Similarity 100.0%; Pred. No. 2.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LDLDTKICEQIEHYFGD 17
DB 10 LDLDTKICEQIEHYFGD 26

RESULT 2
S33818
ribonucleoprotein la.A - African clawed frog
N:Alternate names: autoantigen SS-B/la; ribonucleoprotein SS-B
C:Species: Xenopus laevis (African clawed frog)
C>Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
R:Schery, D.; Stutz, F.; Lin-Marg, N.; Clarkson, S.G.
J. Mol. Biol. 231, 196-204, 1993
A>Title: la proteins from Xenopus laevis. cDNA cloning and developmental expression.
A:Reference number: S33817; MUID:93287095; PMID:8510143
A:Accession: S33818
A:Molecule type: mRNA
A:Residues: 1-428 <SCH>
A:Cross-references: EMBL:X68817; NID:G64873; PIDD:CAA48715.1; PIDD:G64874
C:Comment: This protein associates with a variety of small RNA molecules, most of which
ay act as a transcription termination factor.
C:Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology
C:Keywords: phosphoprotein; RNA binding

```

DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, last annotation update)
DE Similar to KIA00731 protein.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 1, PAC
RT clone: p0439C11."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP01080; BAA90356.1; -.
DR Gramene; Q9LJ02; -.
DR InterPro; IPR006607; DUF DM15.
DR InterPro; IPR006630; Lupus_La_dom.
DR Pfam; PF05383; La; 1.
DR SMART; SM00684; DM15; 3.
DR SMART; SM00715; La; 1.
SQ SEQUENCE 928 AA; 103745 MW; 53FC46E24A446E84 CRC64;

Query Match 49.0%; Score 48.5; DB 10; Length 928;
Best Local Similarity 68.8%; Pred. No. 25;
Matches 11; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

OY 3 LEAKICHOIEYF-GD 17
DB 278 LRAKILTOVEYFSGD 293

RESULT 15
O4678 PRELIMINARY; PRT; 91 AA.
AC O44678;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein Cl4C6.12.
GN Cl4C6.12.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Wilson R.;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA David M., Wohlmann P., Bauer C., Antoniou B.;
RT "The sequence of C. elegans cosmid Cl4C6.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF039051; AAB94258.2; -.
KW Hypothetical protein.
SQ SEQUENCE 91 AA; 10407 MW; D16D2BD4011F8762 CRC64;

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Query Match 48.5%; Score 48; DB 5; Length 91;
Best Local Similarity 69.2%; Pred. No. 3;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 6 KICHOIEYFSGD 18
DB 6 KICNIEYMTGDF 18

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Search completed: September 10, 2004, 18:00:07
Job time : 42.229 secs

DE	CapsP.
GN	Staphylococcus aureus.
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX	NCBI_TaxID=1280;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Reynolds and Newman;
RX	MEDLINE=97388587; PubMed=9245821;
RA	Sau S., Bhasin N., Wann E.R., Lee J.C., Foster T.J., Lee C.Y.;
RT	"the Staphylococcus aureus allelic genetic loci for serotype 5 and 8 capsule expression contain the type-specific genes flanked by common genes";
RL	J. Microbiol. 143:0-0(0).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Reynolds and Newman;
RX	MEDLINE=98101481; PubMed=9440531;
RA	Kaiser K.B., Lee J.C.;
RT	"Staphylococcus aureus caps5 and capsP genes functionally complement mutations affecting enterobacterial common antigen biosynthesis in Escherichia coli.";
RL	J. Bacteriol. 180:403-406(1998).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Reynolds and Newman;
RX	MEDLINE=98125727; PubMed=9466251;
RA	Bhaain N., Albus A., Michon F., Livolsi P.J., Park J.-S., Lee J.C.;
RT	"Identification of a gene essential for O-acetylation of the Staphylococcus aureus type 5 capsular polysaccharide.";
RL	Mol. Microbiol. 27:9-21(1998).
RN	[4]
RP	SEQUENCE FROM N.A.
RC	STRAIN=Reynolds and Newman;
RA	Bagga N., Wann E.R., Foster T.J., Lee J.C.;
RL	Submitted (DEC-1996) to the EMBL/genbank/DBJ databases.
DR	HMBI: U81973; AAC64099.1; -.
DR	HMBP: P27828; IACD.
DR	GO; GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity; IEA.
DR	GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
DR	GO; GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.
DR	InterPro: IPR003331; Epimerase_2.
DR	Pfam: PF02350; Epimerase_2; 1.
DR	TIGFAMS; TIGR00236; wecB; 1.
SQ	SEQUENCE 391 AA; 44328 MW; B0105F690DB7CF1D CRC64;
Query Match	
Best Local Similarity 72.7%; Pred. No. 8.7;	
Matches	8; Conservative 1; Mismatches 2; Indels 0; Gaps 0.
OY	6 KICHOIEYFG 16 : :
DB	366 RICEAIEYFG 376
RESULT 12	
G99X57	PRELIMINARY; PRT; 391 AA.
ID	Q99X57
AC	Q99X57;
DT	01-JUN-2001 (TREMBLrel. 17, Created)
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE	Capsular polysaccharide synthesis enzyme CapsP.
GN	CAP OR SAVO164 OR SA0159.
OS	staphylococcus aureus (strain Mu50 / ATCC 700699), and
OC	Staphylococcus aureus (strain N315).
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX	NCBI_TaxID=158878; 158879;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX	MEDLINE=21311952; PubMed=1418146;
RA	Kuroda W., Ohta T., Uchiyama T., Baba T., Yuzawa H., Kobayashi I.,

```

RT      "Whole genome sequencing of methicillin-resistant Staphylococcus aureus." ;
RL      Lancel 357:1225-1240 (2001) .
DR      EMBL; AP003358; BAB56326.1; -.
DR      EMBL; AF003129; BAB41379.1; -.
DR      PIR; H89777; H89777.
DR      HSSP; P27828; 1F6D.
DR      GO; GO:0008761; F:UDP-N-acetylglucosamine-2-epimerase activity; IEA.
DR      GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
DR      GO; GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.
DR      InterPro; IPR003331; Epimerase_2.
DR      Pfam; PF02350; Epimerase_2; 1.
DR      TIGRFAMs; TIGR00236; webC; 1.
KW      Complete proteome.
SQ      SEQUENCE   391 AA;  44372 MW;  DDDFFFA715BCECC CRC64;

Query Match          49.5%; Score 49; DB 16; Length 391;
Best Local Similarity 72.7%; Pred. No. 8.7;
Matches      8; Conservative    1; Mismatches     2; Indels      0; Gaps      0;

OY      6 KICHOIEYYFG 16
       :||| |||||
DB      366 RICEALIEYFG 376

RESULT 13
Q8LMF9      PRELIMINARY;      PRT;      481 AA.
ID      Q8LMF9
AC      Q8LMF9;
DT      01-OCT-2002 (TREMBLrel. 22, Created)
DI      01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT      01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE      Hypothetical protein.
GN      OSUNBA01114.12.
OS      Oryza sativa (Japonica cultivar-group).
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC      Ehrhartoideae; Oryzaceae; Oryza.
OX      NCBI_TaxID=39947;
RN      [1]
RP      WING R.A., YU Y., Soderlund C., Chen M., Kim H.-R., Rambo T.,
RA      Saeki C., Henry D., Oates R., Simmons J.;
RT      "Rice Genomic Sequence.";
RL      Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AC105730; AAM51838.1; -.
DR      Gramene; Q8LMF9; -.
DR      InterPro; IPR006630; Lupus_La_dom.
DR      Pfam; PF05183; La; 1.
DR      SMART; SM00715; LA; 1.
KW      Hypothetical protein.
SQ      SEQUENCE   481 AA;  49959 MW;  6EA2BED311191362 CRC64;

Query Match          49.5%; Score 49; DB 10; Length 481;
Best Local Similarity 60.0%; Pred. No. 11;
Matches      9; Conservative     2; Mismatches     4; Indels      0; Gaps      0;

OY      3 LEAKICHIEYFGD 17
       :||: ||||| |
DB      307 LRAELKCHIEYFSD 321

RESULT 14
Q9LJO2      PRELIMINARY;      PRT;      928 AA.
ID      Q9LJO2
AC      Q9LJO2;
DT      01-OCT-2000 (TREMBLrel. 15, Created)
```


OC SpERMATOPHYTES: Magnoliophyta; eudicotyledons: core eudicots; rosids;
 OC eucotsids II; Brassicales; Brassicaceae; Arabidopsids.
 OK NCBI_TaxID=3702;
 [1]
 RP SEQUENCE FROM N.A.
 RA Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
 RA Bahr J., Bowser L., Carinici P., Dale J.M., Goldsmith A.D.,
 RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
 RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
 RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
 RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M.,
 RA Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RA "Arabidopsis cDNA clones."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carinici P.,
 RA Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,
 RA Hsuan V.W., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
 RA Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,
 RA Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
 RA Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RA "Arabidopsis ORF clones."
 RT Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY050403; AAK91419.1; -
 DR EMBL; BT000588; AAN18157.1; -
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR InterPro; IPR002344; Lupus_La.
 DR InterPro; IPR006630; Lupus_La.dom.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF05383; La; 1.
 DR Pfam; PF00076; rrm; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PS50102; RRM; 1.
 SQ SEQUENCE 422 AA; 46842 MW; 4EC4BBBF1E068F0E CRC64;
 Query Match 50.5%; Score 50; DB 10; Length 422;
 Best Local Similarity 60.0%; Pred. No. 6.4;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 Oy 3 LEAKICHOIEYFGD 17
 Db 103 LNKITROVEYFSD 117
 RESULT 9
 OBNYN8 PRELIMINARY; PRT; 381 AA.
 AC OBNYN8;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Capsular polysaccharide synthesis enzyme Cap8P.
 CN CAP8P OR MW0139.
 OS Staphylococcus aureus (strain MW2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=196620;
 RX MEDLINE=22040717; PubMed=12044378;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwano K., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA."
 RL Lancet 359:1819-1827(2002).
 DR EMBL; AP004822; BAB94004.1; -.

DR GO; GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity; IEA.
 DR GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
 DR GO; GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.
 DR InterPro; IPR003331; Epimerase_2.
 DR Pfam; PF02350; Epimerase_2; 1.
 DR TIGRFAMs; TIGR00236; wecB; 1.
 KW Complete proteome.
 SQ SEQUENCE 381 AA; 43106 MW; 125E4D5D1904779C CRC64;
 Query Match 49.5%; Score 49; DB 16; Length 381;
 Best Local Similarity 72.7%; Pred. No. 8.5;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Oy 6 KICHOIEYFG 16
 Db 366 RICEAIEYFG 366
 RESULT 10
 P72382 PRELIMINARY; PRT; 391 AA.
 ID P72382
 AC P72382;
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Cap8P.
 DN CAP8P.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Becker;
 RA MEDLINE=96178981; PubMed=8606192;
 RA Sau S., Lee C.Y.;
 RT "Cloning of type 8 capsule genes and analysis of gene clusters for the
 RT production of different capsular polysaccharides in Staphylococcus
 RT aureus."
 RL J. Bacteriol. 178:2118-2126(1996).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Becker;
 RA MEDLINE=97197525;
 RA Sau S., Sun J., Lee C.Y.;
 RT "Molecular characterization and transcriptional analysis of type 8
 RT capsule genes in Staphylococcus aureus."
 RL J. Bacteriol. 179:1614-1621(1997).
 DR EMBL; U73374; AAB49445.1; -
 DR HSPB; P27828; IFED.
 DR GO; GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity; IEA.
 DR GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
 DR GO; GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.
 DR InterPro; IPR003331; Epimerase_2.
 DR Pfam; PF02350; Epimerase_2; 1.
 DR TIGRFAMs; TIGR00236; wecB; 1.
 SQ SEQUENCE 391 AA; 42427 MW; 1E8D9FA93BC76F0D CRC64;
 Query Match 49.5%; Score 49; DB 2; Length 391;
 Best Local Similarity 72.7%; Pred. No. 8.7;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Oy 6 KICHOIEYFG 16
 Db 366 RICEAIEYFG 376
 RESULT 11
 P95709 PRELIMINARY; PRT; 391 AA.
 ID P95709
 AC P95709;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

RESULT 5
QZTT0 ID 072T10 PRELIMINARY; PRT; 401 AA.
AC Q72T10; 01-JUN-2003 (TEMBLrel. 24, Created)
DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Similar to sjogren syndrome antigen B (Autoantigen La).
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC045392; AAH45392.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002344; Lups_La.
DR InterPro; IPR006630; Lups_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 401 AA; 46138 MW; 2EF032FDD3916291 CRC64;

Query Match 62.6%; Score 62; DB 13; Length 401;
Best Local Similarity 73.3%; Pred. No. 0.064;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 LEAKICHOIEYFGD 17
DB 10 LERKVAQIEYFGD 24

RESULT 6
Q8T8V5 ID 08T8V5 PRELIMINARY; PRT; 390 AA.
AC Q8T8V5; 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE AT2034P.
GN LA OR CG10922.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephyrididae; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Flise E.,
RA George R., Gonzalez W., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celinker S.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY075257; AA68124.1; -.
DR FLYbase; FBGN001638; La.
DR GO; GO:0008098; F:5S rRNA primary transcript binding; IDA.
DR GO; GO:0003723; F:RNA binding; NAS.
DR InterPro; IPR002344; Lups_La.
DR InterPro; IPR006630; Lups_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.

DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 390 AA; 44869 MW; 797FDE26B903C909 CRC64;

Query Match 51.5%; Score 51; DB 5; Length 390;
Best Local Similarity 64.3%; Pred. No. 4.1;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 EAKICHOIEYFGD 17
DB 51 ERAITROVEYFGD 64

RESULT 7
Q9FL36 ID 09FL36 PRELIMINARY; PRT; 411 AA.
AC Q9FL36; 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Similarity to RNA-binding protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroside II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=98344145; PubMed=9679202;
RA Kaneo T., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence
RT features of the regions of 1,381,565 bp covered by twenty one
RT physically assigned pl and TAC clones.";
RL DNA Rep. 5:131-145 (1998).
DR EMBL; AB010698; BAB11080.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002344; Lups_La.
DR InterPro; IPR006630; Lups_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 411 AA; 45655 MW; A2EF62EB5B98099 CRC64;

Query Match 50.5%; Score 50; DB 10; Length 411;
Best Local Similarity 60.0%; Pred. No. 6.3;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 LEAKICHOIEYFGD 17
DB 92 LMQKIRQVEYFGD 106

RESULT 8
Q94A38 ID 094A38 PRELIMINARY; PRT; 422 AA.
AC Q94A38; 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE AT5G46250/MP12.3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

DR GO:0005634; C:nucleus; IDA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
SQ SEQUENCE 381 AA; 4391 MW; 2E2DEF1452C0F0E9 CRC64;

Query Match
Best Local Similarity 96.0%; Score 95; DB 11; Length 381;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ALEAKICHOIEYFGDF 18
Db 12 ALEAKICHOIEYFGDF 28

RESULT 2
Q8BTU4 PRELIMINARY; PRT; 415 AA.
ID Q8BTU4;
AC Q8BTU4;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Sjogren syndrome antigen B.
GN SSB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NO; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK088677; BAC40498.1; -.
DR MGD; MGI:98423; Seb.
DR GO:0005634; C:nucleus; IDA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR EMBL; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 415 AA; 47657 MW; A7545C7686AC6363 CRC64;

Query Match
Best Local Similarity 96.0%; Score 95; DB 11; Length 415;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ALEAKICHOIEYFGDF 18
Db 12 ALEAKICHOIEYFGDF 28

RESULT 3
Q7ZTK2 PRELIMINARY; PRT; 427 AA.
ID Q7ZTK2;
AC Q7ZTK2;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Similar to lupus LA protein homolog B.

```

```

OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenoipodinae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Struhsberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC046654; AA446654.1; -.
DR GO:0005634; C:nucleus; IEA.
DR GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 2.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 427 AA; 48996 MW; 1E7CD82D8AB9C69A CRC64;

Query Match
Best Local Similarity 70.7%; Score 70; DB 13; Length 427;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 LEAKICHOIEYFGD 17
Db 12 LDTKICHOIEYFGD 26

RESULT 4
Q8OH15 PRELIMINARY; PRT; 206 AA.
ID Q8OH15;
AC Q8OH15;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Untranslated region binding-protein.
GN UBP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA L'Ecuylar T.J., Fang H.-L.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF467897; AAL76269.1; -.
DR GO:0005634; C:nucleus; IEA.
DR GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 206 AA; 23992 MW; 965B637DFDFB90B9 CRC64;

Query Match
Best Local Similarity 69.7%; Score 69; DB 13; Length 206;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LEAKICHOIEYFGD 17
Db 13 LESKICHOIEYFGN 27

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:29:01; Search time 41.229 Seconds
(without alignments)
137.751 Million cell updates/sec

Title: US-09-836-073-14

Perfect score: 99

Sequence: 1 AALEAKICHQIEHYRGDF 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL.25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp Vertebrate.*
14: sp Unclassified.*
15: sp_rv1rus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	95	96.0	381	11	Q9CYB9 mus musculus
2	95	96.0	415	11	Q8BTU4 Q8BTU4 mus musculus
3	70	70.7	427	13	Q7ZTK2 Q7ZTK2 xenopus lae
4	69	69.7	206	13	Q8QHS2 gallus gallus
5	62	62.6	401	13	Q7ZTIO Q7ZTIO brachydanio
6	51	51.5	390	5	Q8T8V5 Q8T8V5 drosophila
7	50	50.5	411	10	Q9FL36 Q9FL36 arabidopsis
8	50	50.5	422	10	Q9A3B8 Q9A3B8 arabidopsis
9	49	49.5	381	16	Q8NWN8 Q8NWN8 staphylococ
10	49	49.5	381	2	P72382 P72382 staphylococ
11	49	49.5	391	2	P95709 P95709 staphylococ
12	49	49.5	391	16	Q9X577 Q9X577 staphylococ
13	49	49.5	481	10	Q8LMP9 Q8LMP9 oryza sativ
14	48.5	48.5	928	10	Q9LJ02 Q9LJ02 oryza sativ
15	48	48.5	91	5	O44678 O44678 caenorhabdi
16	48	48.5	545	10	O80567 O80567 arabidopsis

17	47	47.5	119	10	Q9ZP89 Q9ZP89 neurotheca
18	47	47.5	396	5	O01806 O01806 caenorhabdi
19	47	47.5	547	10	Q7XVC6 Q7XVC6 oryza sativ
20	46	46.5	568	16	Q9KJL7 Q9KJL7 vibrio chol
21	45	45.5	478	16	Q87G58 Q87G58 vibrio para
22	44.5	44.9	839	5	Q18841 Q18841 caenorhabdi
23	44	44.4	826	10	Q940X9 Q940X9 arabidopsis
24	44	44.4	2349	5	O81455 O81455 plasmodium
25	43.5	43.9	788	17	O58603 O58603 pyrococcus
26	43	43.4	134	16	Q825D7 Q825D7 streptomyce
27	43	43.4	150	10	Q80788 Q80788 arabidopsis
28	43	43.4	239	10	Q9SMD8 Q9SMD8 laminaria d
29	43	43.4	381	16	Q8Z632 Q8Z632 salmoneilla
30	43	43.4	386	16	Q83BP5 Q83BP5 coxiella bu
31	43	43.4	389	10	Q850T8 Q850T8 oryza sativ
32	43	43.4	523	10	Q94K80 Q94K80 arabidopsis
33	43	43.4	596	5	O8T6A8 O8T6A8 caenorhabdi
34	43	43.4	654	4	Q96NNA Q96NNA homo sapien
35	43	43.4	654	6	O95KA5 O95KA5 macaca fasc
36	43	43.4	658	5	O18215 O18215 caenorhabdi
37	43	43.4	863	10	Q7XO50 Q7XO50 oryza sativ
38	43	43.4	1126	5	O86EP0 O86EP0 cryptospori
39	43	43.4	1126	5	Q7YX10 Q7YX10 homo sapien
40	43	43.4	1136	4	Q7Z6L5 Q7Z6L5 clostridium
41	42.5	42.9	577	16	Q97DB6 Q97DB6 bacteroides
42	42.5	42.9	748	16	Q8AAX3 Q8AAX3 brassica ol
43	42	42.4	96	10	Q9AUG1 Q9AUG1 helicobacte
44	42	42.4	200	16	Q7VIA1 Q7VIA1 lactobacilli
45	42	42.4	244	16	Q88YAS Q88YAS lactobacilli

ALIGNMENTS

RESULT 1	PRELIMINARY;	PRT;	381 AA.
ID Q9CYB9	Q9CYB9		
AC Q9CYB9	01-JUN-2001 (TRMBLrel. 17, Created)		
DT 01-JUN-2001	(TRMBLrel. 17, Last sequence update)		
DT 01-OCT-2003	(TRMBLrel. 25, Last annotation update)		
DE Sjogren syndrome antigen B.			
GN SSB.			
OS Mus musculus (Mouse).			
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX NCBI_TaxId=10090;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=C57BL/6J; TISSUE=Embryo;			
RX MEDLINE=21085660; PubMed=11217551;			
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA Arakawa T., Hara A., Fukunishi Y., Komoto H., Adachi J., Fukuda S.,			
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,			
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,			
RA Kadota K., Matsumura H.A., Ashburner M., Batalov S., Casavant T.,			
RA Fleischmann W., Gaasterland T., Glasi C., King B., Kochi H.,			
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,			
RA Schriml L.M., Stabli F., Suzuki R., Tomita M., Wagner L., Mashio T.,			
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,			
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,			
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,			
RA Lyons P., Marchionni L., Mashima U., Mazzarelli J., Mombauts P.,			
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,			
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,			
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,			
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,			
RA Hayashizaki Y.,			
RT "Functional annotation of a full-length mouse cDNA collection."			
RL Nature 409:685-690(2001).			
DR EMBL; AK017822; BAB30957.1; -			
DR MGD; MGI:98423; Ssb.			

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C:Species: *Vibrio cholerae*

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 28-Apr-2003

C:Accession: C82379

R:Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.; Chardon, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, R. L. R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A:Reference number: AB2035; M0ID:20406833; PMID:10952301

A:Accession: C82379

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-568 <HEI>

A:Cross-references: GB:AE004434; GB:AE003853; NID:g9658531; PIDN:AAF96979.1; GSPDB:GN001

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VCA1086

A:Map position: 2

C:Superfamily: response regulator, hnr type; response regulator homology

Query Match 46.5%; Score 46; DB 2; Length 568;

Best Local Similarity 50.0%; Pred. No. 10;

Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 LEAKICHOIEYFG 16

DB 156 LMEEMCHQVEHIFG 169

RESULT 15

T20230

hypothetical protein CS4G10.2 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T20230

R:Matthews, L.

Submitted to the EMBL Data Library, June 1996

A:Reference number: Z19240

A:Accession: T20230

A:Status: preliminary; translated from GB/EMBL/DDAT

A:Molecule type: DNA

A:Residues: 1-839 <MTL>

A:Cross-references: EMBL:Z75532; PIDN:CAA99812.1; GSPDB:GN00023; CESP:CS4G10.2

A:Experimental source: clone CS4G10

C:Genetics:

A:Gene: CESP:CS4G10.2

A:Map position: 5

A:introns: 12/1; 34/3; 69/3; 326/1; 432/3; 535/3; 668/2

Query Match 44.9%; Score 44.5; DB 2; Length 839;

Best Local Similarity 57.9%; Pred. No. 27;

Matches 11; Conservative 1; Mismatches 2; Indels 5; Gaps 1;

QY 3 LEAKI-----CHOIEYFG 16

DB 382 LEAKIGELSGSHOIEPFG 400

Search completed: September 10, 2004, 18:02:31
Job time: 15.0782 secs

RESULT 10

T00677 hypochemical protein At2g43970 [imported] - Arabidopsis thaliana

N:Alternate names: hypochemical protein F613.10

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001

C:Accession: T00677; G84872

R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, June 1998

A:Description: Arabidopsis thaliana chromosome II BAC F613 genomic sequence.

A:Reference number: Z14180

A:Accession: T00677

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-529 <R0>

A:Cross-references: EMBL:AC004005; NID:G3212846; PID:G3212854

A:Experimental source: cultivar Columbia

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Wolfat, K.S.; Cronan, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, L.; euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: G84872

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-529 <STO>

A:Cross-references: GB:AE002093; NID:G3212854; PIDN:AAC23405.1; GSPDB:GNO0139

C:Genetics:

A:Gene: F613.10; At2g43970

A:Map position: 2

A:Introns: 200/3; 228/1; 259/3; 283/3; 310/2; 344/3; 367/3; 421/3

Query Match

Best Local Similarity	48.5%	Score 48;	DB 2;	Length 529;
Matches	8;	Conservative	2;	Mismatches 2;
			Indels	0;
			Gaps	0;

OY 6 KICHOIEYFGD 17

DB 196 KIVNQVEYFSD 207

RESULT 11

T30953 hypochemical protein C44E4.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000

C:Accession: T30953

R:Sammons, L.; Wohlmann, P.; Gilling, B.

submitted to the EMBL Data Library, August 1999

A:Description: The sequence of C. elegans cosmid C44E4.

A:Reference number: Z20945

A:Accession: T30953

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-396 <SAM>

A:Cross-references: EMBL:AF003140; PIDN:AAB54169.1

A:Experimental source: strain Bristol N2; clone C44E4

C:Genetics:

A:Map position: 1

A:Introns: 45/1; 114/3

A:Note: C44E4.4

C:Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology

Query Match

Best Local Similarity	47.5%	Score 47;	DB 2;	Length 396;
Matches	8;	Conservative	3;	Mismatches 3;
			Indels	0;
			Gaps	0;

OY 4 EAKICHOIEYFGD 17

DB 13 DOKIKOLEYFSGN 26

RESULT 12

T38937 rna binding protein - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T38937

R:Baccock, K.; Churruar, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, April 1997

A:Reference number: Z21818

A:Accession: T38937

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-298 <BAD>

A:Cross-references: EMBL:Z94864; PIDN:CAB08173.1; GSPDB:GNO0066; SPDB:SPAC57A10.10C

A:Experimental source: strain 972h-; cosmid c57A10

C:Genetics:

A:Gene: SPDB:SPAC57A10.10C

A:Map position: 1

A:Introns: 72/1

Query Match	46.5%	Score 46;	DB 2;	Length 298;
Best Local Similarity	50.0%	Score 50;	DB 2;	Length 298;
Matches	7;	Conservative	4;	Mismatches 3;
			Indels	0;
			Gaps	0;

OY 4 EAKICHOIEYFGD 17

DB 64 EAEVLKQVEYFSD 77

RESULT 13

T3542 RNA-binding protein Lal homolog - fission yeast (Schizosaccharomyces pombe)

N:Alternate names: La autoantigen; ribonucleoprotein La homolog

C:Species: Schizosaccharomyces pombe

C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000

C:Accession: T43542; T43325

R:Van Horn, D.O.; Yoo, C.O.; Xue, D.; Shi, H.; Wolin, S.L.

RNA 3, 1434-1443, 1997

A:Title: The La protein in Schizosaccharomyces pombe: a conserved yet dispensable phosph

A:Reference number: Z22560; MUID:98067398; PMID:9404894

A:Accession: T43542

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-298 <VAN>

A:Cross-references: EMBL:AF022949; PIDN:AAB82145.1

R:Utsumi, R.

submitted to the EMBL Data Library, February 1998

A:Description: Screening of S. pombe cDNA library using E. coli defective in signal tran

A:Reference number: Z22428

A:Accession: T43325

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-298 <UTS>

A:Cross-references: EMBL:AB011371; PIDN:BAA24981.1

C:Genetics:

A:Gene: slal

A:Function: the binding of the La protein to RNA precursors is required for the endo

C:Keywords: phosphoprotein; RNA binding

Query Match	46.5%	Score 46;	DB 2;	Length 298;
Best Local Similarity	50.0%	Score 50;	DB 2;	Length 298;
Matches	7;	Conservative	4;	Mismatches 3;
			Indels	0;
			Gaps	0;

OY 4 EAKICHOIEYFGD 17

DB 64 EAEVLKQVEYFSD 77

RESULT 14

G82379 response regulator VCA1086 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

R.Scherly, D.; Stutz, F.; Lin-Marq, N.; Clarkeon, S.G.
 J. Mol. Biol. 231, 196-204, 1993
 A>Title: La proteins from *Xenopus laevis*. cDNA cloning and developmental expression.
 A/Reference number: S33817; MUID:93287095; PMID:8510143
 A/Accession: S33818
 A/Molecule type: mRNA
 A/Residues: 1-428 <SCH>
 A/Cross-references: EMBL:X68817; NID:g64873; PID:CAA48715.1; PID:g64874
 C/Comment: This protein associates with a variety of small RNA molecules, most of which
 act as a transcription termination factor.
 C/Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology
 C/Keywords: phosphoprotein; RNA binding
 F.112-178/Domain: ribonucleoprotein repeat homology <RRM>
 F.113-118/Region: RNA-binding RNP motif
 F.151-158/Region: RNA-binding RNP motif
 F.128-428/Domain: phosphorylated #status predicted <PHY>

Query Match 66.7%; Score 66; DB 1; Length 428;
 Best Local Similarity 78.6%; Pred. No. 0.0035;
 Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 EAKICHOIEYFGD 17
 : ||| |||||
 Db 14 DTKICQIEYFGD 27

RESULT 6
 A/Accession: A53773
 La/SS-B homolog D-1a - fruit fly (*Drosophila melanogaster*)
 C/Species: *Drosophila melanogaster*
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
 C/Accession: A53773
 R/Bal, C.; Li, Z.; Tolias, P.P.
 Mol. Cell. Biol. 14, 5123-5129, 1994
 A>Title: Developmental characterization of a *Drosophila* RNA-binding protein homologous to
 A/Reference number: A53773; MUID:94309632; PMID:8035794
 A/Accession: A53773
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-390 <BAI>
 A/Cross-references: GB:U07652; NID:g464019; PID:AAA20518.1; PID:g464020
 C/Genetics:
 A/Gene: FlyBase:la
 A/Cross-references: FlyBase:Fgn0011638
 C/Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology
 C/Keywords: leucine zipper; RNA binding

Query Match 51.5%; Score 51; DB 2; Length 390;
 Best Local Similarity 64.3%; Pred. No. 1;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 EAKICHOIEYFGD 17
 : ||| |||||
 Db 51 ERAIRQVEYFGD 64

RESULT 7
 A/Accession: A53781
 ribonucleoprotein la - fruit fly (*Drosophila melanogaster*)
 C/Species: *Drosophila melanogaster*
 C/Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 20-Sep-1999
 C/Accession: A53781
 R/Yoo, C.J.; Wolin, S.L.
 Mol. Cell. Biol. 14, 5412-5424, 1994
 A>Title: La proteins from *Drosophila melanogaster* and *Saccharomyces cerevisiae*: a yeast
 A/Reference number: A53781; MUID:94309661; PMID:8035818
 A/Accession: A53781
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-390 <YOO>
 A/Cross-references: GB:L3298; NID:g488469; PID:g488470
 C/Genetics:
 A/Gene: FlyBase:la

A/Cross-references: FlyBase:Fgn0011638
 C/Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology
 C/Keywords: RNA binding

Query Match 51.5%; Score 51; DB 2; Length 390;
 Best Local Similarity 64.3%; Pred. No. 1;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 EAKICHOIEYFGD 17
 : ||| |||||
 Db 51 ERAIRQVEYFGD 64

RESULT 8
 A/Accession: H89777
 capsular polysaccharide synthase enzyme Caps [imported] - *Staphylococcus aureus* (strain
 H89777)
 C/Species: *Staphylococcus aureus*
 C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C/Accession: H89777
 R./Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
 ma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A>Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
 A/Reference number: A89758; MUID:21311952; PMID:11418146
 A/Accession: H89777
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-391 <KUR>
 A/Cross-references: GB:BA000018; PID:g1370080; PID:BA841379.1; GSPDB:GN00149
 A/Experimental source: strain N315
 C/Genetics:
 A/Gene: cap
 C/Superfamily: lipopolysaccharide biosynthesis protein bplD

Query Match 49.5%; Score 49; DB 2; Length 391;
 Best Local Similarity 72.7%; Pred. No. 2.2;
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 KICHOIEYFG 16
 : ||| |||||
 Db 366 RICEALEYFG 376

RESULT 9
 T32701
 hypothetical protein C14C6.12 - *Caenorhabditis elegans*
 C/Species: *Caenorhabditis elegans*
 C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C/Accession: T32701
 R./David, M.; Wohldmann, P.; Bauer, C.; Antoniou, B.
 submitted to the EMBL Data Library, December 1997
 A/Description: The sequence of *C. elegans* cosmid C14C6.
 A/Reference number: Z21210
 A/Accession: T32701
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-166 <DAV>
 A/Cross-references: EMBL:AF030051; PID:BA894258.1; GSPDB:GN00023; CESP:C14C6.12
 A/Experimental source: strain Bristol N2; clone C14C6
 C/Genetics:
 A/Gene: CESP:C14C6.12
 A/Map position: 5
 A/Intons: 42/1, 156/3

Query Match 48.5%; Score 48; DB 2; Length 166;
 Best Local Similarity 69.2%; Pred. No. 1.4;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 KICHOIEYFGDF 18
 : ||| |||||
 Db 81 KICNVIEYMTGDF 93

A:Reference number: S03848; MUID:89202037; PMID:2468131
 A:Accession: S03848
 A:Molecule type: mRNA
 A:Residues: 1-408 <CH>
 A:Cross-references: EMBL:X13697; NID:G36414; PIDN:CAA31985.1; PID:G36415
 R:Chambers, J.C.; Keene, J.D.
 Proc. Natl. Acad. Sci. U.S.A. 82, 2115-2119, 1985
 A>Title: Isolation and analysis of cDNA clones expressing human lupus La antigen.
 A:Reference number: A22956; MUID:85166283; PMID:3856888
 A:Accession: A22956
 A:Molecule type: mRNA
 A:Residues: 45-97, 'LK' <CH>
 A:Cross-references: GB:J04205
 A:Note: this sequence has been revised in reference A31888
 R:Nyman, U.; Ringertz, N.R.; Petersson, I.
 Immunol. Lett. 22, 65-72, 1989
 A>Title: Demonstration of an amino terminal La epitope recognized by human anti-La sera.
 A:Reference number: A61051; MUID:89379261; PMID:2476379
 A:Accession: A61051
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-19, 'E', '21-47' <NYM>
 R:Sturges, A.D.; Peterson, M.G.; McNeillage, L.J.; Whittingham, S.; Coppel, R.L.
 J. Immunol. 140, 3212-3218, 1988
 A>Title: Characteristics and epitope mapping of a cloned human autoantigen La.
 A:Reference number: S11013; MUID:86199081; PMID:2452201
 A:Accession: S11013
 A:Molecule type: mRNA
 A:Residues: 'E', '55-287', 'V', '289-408' <STU>
 A:Cross-references: EMBL:M20328; NID:G337456; PIDN:AAA36577.1; PID:G337457
 R:Kohsaka, H.; Yamamoto, K.; Fujii, H.; Mura, H.; Miyasaka, N.; Nishiohara, K.; Miyamoto, J.
 Clin. Invest. 85, 1566-1574, 1990
 A>Title: Fine epitope mapping the human SS-B/La protein: Identification of a distinct autoantigen.
 A:Reference number: 15553; MUID:90237237; PMID:1692037
 A:Accession: 15553
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 81-107 <RES>
 A:Cross-references: GB:M35261; NID:G338491; PIDN:AAA36652.1; PID:G338495
 A:Accession: 170205
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 174-224 <RE2>
 A:Cross-references: GB:M35263; NID:G338492; PIDN:AAA36653.1; PID:G338496
 A:Accession: 170206
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 279-342 <RE3>
 A:Cross-references: GB:M35262; NID:G338493; PIDN:AAA36654.1; PID:G338497
 C:Comment: This protein associates with a variety of small RNA molecules, most of which act as a transcription termination factor.
 C:Genetic: GDB:SSB
 A:Gene: GDB:SSB
 A:Cross-references: GDB:125359; OMIM:109090
 A:Map position: 2
 A:Introns: 22/3; 57/2; 115/3; 151/3; 185/2; 209/2; 223/3; 264/3; 380/2
 C:Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
 C:Keywords: phosphoprotein; RNA binding
 F:112-118/Domain: ribonucleoprotein repeat homology <RMM>
 F:113-118/Region: RNA-binding RNP2 motif
 F:151-158/Region: RNA-binding RNP1 motif
 F:228-408/Domain: phosphorylated #status experimental <PHY>

Query Match 100.0%; Score 99; DB 1; Length 408;
 Best Local Similarity 100.0%; Pred. No. 9.8e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AALEKICHOIEYFGDF 18
 |||||
 Db 11 AALEKICHOIEYFGDF 28

J:1494
 ribonucleoprotein La - rat
 N:Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 24-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
 C:Accession: J:1494; S25145
 R:Semsel, I.; Troester, H.; Bartsch, H.; Schwemmler, M.; Igloi, G.L.; Bachmann, M.
 Gene 126, 265-268, 1993
 A>Title: Isolation of rat cDNA clones coding for the autoantigen SS-B/La: Detection of SS-B/La antigen in human sera.
 A:Reference number: J:1494; MUID:93246255; PMID:7916708
 A:Accession: J:1494
 A:Molecule type: mRNA
 A:Residues: 1-415 <SEM>
 A:Cross-references: GB:X67859; NID:G55778; PIDN:CAA48043.1; PID:G55779
 A:Experimental source: liver
 C:Comment: This protein associates with a variety of small RNA molecules, most of which act as a transcription termination factor.
 C:Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
 C:Keywords: phosphoprotein; RNA binding
 F:113-178/Domain: ribonucleoprotein repeat homology <RMM>
 F:113-118/Region: RNA-binding RNP2 motif
 F:151-158/Region: RNA-binding RNP1 motif
 F:227-415/Domain: phosphorylated #status predicted <PHY>

Query Match 100.0%; Score 99; DB 1; Length 415;
 Best Local Similarity 100.0%; Pred. No. 1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AALEKICHOIEYFGDF 18
 |||||
 Db 11 AALEKICHOIEYFGDF 28

RESULT 4

S33817
 ribonucleoprotein La.B - African clawed frog
 N:Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
 C:Accession: S33817; S28544
 R:Scherer, D.; Stutz, F.; Lan-Marg, N.; Clarkson, S.G.
 J. Mol. Biol. 231, 196-204, 1993
 A>Title: La protein from Xenopus laevis. cDNA cloning and developmental expression.
 A:Reference number: S33817; MUID:93287095; PMID:8510143
 A:Accession: S33817
 A:Molecule type: mRNA
 A:Residues: 1-427 <SCH>
 A:Cross-references: EMBL:X68818; NID:G64875; PIDN:CAA48716.1; PID:G64876
 C:Comment: This protein associates with a variety of small RNA molecules, most of which act as a transcription termination factor.
 C:Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
 C:Keywords: phosphoprotein; RNA binding
 F:112-117/Domain: ribonucleoprotein repeat homology <RMM>
 F:113-117/Region: RNA-binding RNP2 motif
 F:150-157/Region: RNA-binding RNP1 motif
 F:227-427/Domain: phosphorylated #status predicted <PHY>

Query Match 70.7%; Score 70; DB 1; Length 427;
 Best Local Similarity 80.0%; Pred. No. 0.00074;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 LEAKICHOIEYFGD 17
 |||||
 Db 12 LDRICHOIEYFGD 26

RESULT 5

S33818
 ribonucleoprotein La.A - African clawed frog
 N:Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
 C:Accession: S33818; S28545

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:33:11; Search time 14.0782 Seconds
(without alignments)
122.988 Million cell updates/sec

Title: US-09-836-073-14

Perfect score: 99

Sequence: 1 AALEAKICHQIEYFGDF 18

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR 78:*

1: pirl:*

2: pirl:*

3: pirl:*

4: pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	99	100.0	404	1	S03849
2	99	100.0	408	1	A31888
3	99	100.0	415	1	JC1494
4	70	70.7	427	1	S33817
5	66	66.7	428	1	S33818
6	51	51.5	380	2	A53773
7	51	51.5	390	2	A53781
8	49	49.5	391	2	H89777
9	48	48.5	166	2	T32701
10	48	48.5	529	2	T00677
11	47	47.5	396	2	T30953
12	46	46.5	298	2	T38937
13	46	46.5	298	2	T43542
14	46	46.5	568	2	C82379
15	44.5	44.9	839	2	T20230
16	43.5	43.9	788	2	A71076
17	43	43.4	150	2	A64488
18	43	43.4	381	2	AB0734
19	43	43.4	506	2	T14907
20	43	43.4	658	2	T19487
21	42.5	42.9	577	2	D97337
22	42	42.4	542	2	A42478
23	42	42.4	432	2	D72313
24	42	42.4	424	2	T46197
25	42	42.4	482	2	B35843
26	42	42.4	505	2	B90181
27	42	42.4	541	2	H71887
28	42	42.4	542	2	G64657
29	42	42.4	658	2	D96656

30	42	42.4	1131	2	T15617	hypothetical prote
31	41	41.4	87	2	C84494	hypothetical prote
32	41	41.4	251	2	B40969	folate-binding pro
33	41	41.4	419	2	AH0417	integrinase [impor
34	41	41.4	469	2	C70357	hypothetical prote
35	41	41.4	506	2	F85016	probable RING zinc
36	41	41.4	573	1	CSBT	catalase (EC 1.11.
37	41	41.4	1156	2	T37411	RNA polymerase sub
38	41	41.4	1164	1	RNVZ8T	DNA-directed RNA p
39	41	41.4	1164	1	RNVZCP	DNA-directed RNA p
40	41	41.4	1164	2	T28566	DNA-directed RNA p
41	41	41.4	1164	2	F72166	A258 protein - var
42	41	41.4	1164	2	G36850	DNA-directed DNA p
43	41	41.4	1220	1	DJBECS	DNA-directed DNA p
44	41	41.4	1220	2	T42573	helicase (EC 3.6.1
45	41	41.4	1221	1	HJWVAV	

ALIGNMENTS

RESULT 1
S03849
ribonucleoprotein la - bovine
N/Alternate names: autoantigen SS-B/la; ribonucleoprotein SS-B
C/Species: Bos primigenius taurus (cattle)
C/Date: 31-Dec-1990 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C/Accession: S03849
R/Chan, E.K.L.; Sullivan, K.F.; Tan, E.M.
Nucleic Acids Res. 17, 2233-2244, 1989
A/Title: Ribonucleoprotein SS-B/la belongs to a protein family with consensus sequences
A/Reference number: S03848; MUID:89202037; PMID:2468131
A/Accession: S03849
A/Molecule type: mRNA
A/Residues: 1-404 <CHA>
A/Cross-References: EMBL:X13698; NID:g755; PIDN:CAJ1986.1; PID:g756
A/Note: Part of this sequence was confirmed by protein sequencing
C/Comment: This protein associates with a variety of small RNA molecules, most of which
act as a transcription termination factor.
C/Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology
C/Keywords: blocked amino end, phosphoprotein; RNA binding
F/117-178/Domain: ribonucleoprotein repeat homology <RRM>
F/113-118/Region: RNA-binding RNP2 motif
F/151-158/Region: RNA-binding RNP1 motif
F/228-404/Domain: phosphorylated #status predicted <PHY>

Query Match 100.0%; Score 99; DB 1; Length 404;
Best Local Similarity 100.0%; Pred. No. 9.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AALEAKICHQIEYFGDF 18
DB 11 AALEAKICHQIEYFGDF 28

RESULT 2
A31888
ribonucleoprotein la - human
N/Alternate names: autoantigen SS-B/la; ribonucleoprotein SS-B; Sjogren syndrome antigen
C/Species: Homo sapiens (man)
C/Date: 21-May-1990 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C/Accession: A31888; S03848; A22956; A61051; S11013; I55553; I70205; I70206; A31273
R/Chambers, J.C.; Kenan, D.; Martin, B.J.; Keene, J.D.
J. Biol. Chem. 263, 18043-18051, 1988
A/Title: Genomic structure and amino acid sequence domains of the human la autoantigen.
A/Reference number: A31888; MUID:89053970; PMID:3192525
A/Accession: A31888
A/Molecule type: mRNA
A/Residues: 1-408 <CHA>
A/Cross-References: GB:04205; NID:g178686; PIDN:AAA51885.1; PID:g178687
R/Chan, E.K.L.; Sullivan, K.F.; Tan, E.M.
Nucleic Acids Res. 17, 2233-2244, 1989
A/Title: Ribonucleoprotein SS-B/la belongs to a protein family with consensus sequences

DR InterPro; IPR002344; Lupus_La.
 DR InterPro; IPR006630; Lupus_La.dom.
 DR InterPro; IPR00504; RNA_rec_mot.
 DR Pfam; PF05383; La; 1.
 DR Pfam; PF00076; rrm; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PS50102; RRM; 1.
 SQ SEQUENCE 367 AA; 40389 MW; 129BF02581DD1148 CRC64;

Query Match 46.4%; Score 45; DB 10; Length 367;
 Best Local Similarity 60.0%; Pred. No. 23;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 3 LEAKICHOIEYQFGD 17
 DB 147 LRLKIVKQVEYQFTD 161

RESULT 15

O9LHL3 PRELIMINARY; PRT; 455 AA.
 AC O9LHL3;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE RNA-binding protein-like.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia;
 RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
 RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia;
 RX MEDLINE=20363099; PubMed=10907853;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
 RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,
 RT TAC and BAC clones."
 RL DNA Res. 7:217-221(2000).
 DR EMBL; AP002041; BAB02607.1; -;
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR InterPro; IPR002344; Lupus_La.
 DR InterPro; IPR006630; Lupus_La.dom.
 DR InterPro; IPR00504; RNA_rec_mot.
 DR Pfam; PF05383; La; 1.
 DR Pfam; PF00076; rrm; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PS50102; RRM; 1.
 SQ SEQUENCE 455 AA; 48958 MW; E88117B2C3BBA9 CRC64;

Query Match 46.4%; Score 45; DB 10; Length 455;
 Best Local Similarity 60.0%; Pred. No. 28;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 3 LEAKICHOIEYQFGD 17
 DB 144 LRLKIVKQVEYQFTD 158

DR SMART: SM00360; RM: 1.
DR PROSITE: PSS0102; RM: 1
SQ SEQUENCE 343 AA; 37628 MW; 655FCE0879FB8D7B CRC64;

Query Match
Best Local Similarity 47.4%; Score 46; DB 10; Length 343;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 AALEAKICHOIEYQFD 17
DB 111 ADIAQKIKQVEYQFSD 127

RESULT 12

ID Q8U3P2 PRELIMINARY; PRT; 395 AA.
AC Q8U3P2;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Dehydrogenase.
GN PF0415.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_Taxid=2261;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome."
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF010164; AAL80539.1; -
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR002372; Bac_PQQ_repeat.
DR SMART; SM00564; PQQ; 5.
KW Complete proteome.
SQ SEQUENCE 395 AA; 43482 MW; 946EC9C97EB327D4 CRC64;

Query Match
Best Local Similarity 47.4%; Score 46; DB 17; Length 395;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 ALEAKICHOIEYQ 14
DB 19 AWEGKICENIEYQ 31

RESULT 13

ID Q9VU19 PRELIMINARY; PRT; 519 AA.
AC Q9VU19;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG10006 protein.
GN CG10006.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RC MEDLINE=20196006; Pubmed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananthakrishnan P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Anil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhattacharya D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck P., Brocktein P., Brothier P.,
RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Dwyer A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegyan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison A.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Martel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Switzkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003532; AAF49687.1; -
DR FlyBase; FBgn0036461; CG10006.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0046873; F:metal ion transporter activity; IEA.
DR GO; GO:0030001; P:metal ion transport; IEA.
DR InterPro; IPR003689; Zn_transp_zfp.
DR Pfam; PF02535; Zfp; 1.
SQ SEQUENCE 519 AA; 56866 MW; 670677CC0E125DAC CRC64;

Query Match
Best Local Similarity 47.4%; Score 46; DB 5; Length 519;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 5 AKICHOIEYQFDF 18
DB 395 AVLCHEPHELGDF 408

RESULT 14

ID Q9SEU9 PRELIMINARY; PRT; 367 AA.
AC Q9SEU9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNA-binding protein homolog.
GN RBP1.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_Taxid=3708;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Topas; TISSUE=Late-uninucleate microspores;
RA Smekal P., Janotov I., Pechan P.M.;
RT "A novel Brassica napus L. pollen-specific gene belongs to a nucleic-acid-binding protein family."
RL Sex. Plant Reprod. 13:127-134(2000).
DR EMBL; AF094825; AAF00075.2; -
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.

DE pyrophosphokinase, 8-dihydro-6-hydroxymethylpterin-pyrophosphokinase
DE protein (EC 2.7.6.3).
GN FOLK OR RSC2628 OR RS00932.
OC Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Guzy J., Mangenot S.,
RA Ariat M., Billault A., Broctier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunac S., Demange N.,
RA Gaspin C., Levie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Siquier P., Thebault P., Whalen M., Winkler P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.",
RL Nature 415:497-502(2002).
RN EMBL; AL646071; CAD16335.1; -
DR GO; GO:0003848; F:2-amino-4-hydroxy-6-hydroxymethylidihydrope. . .; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0009365; P:folic acid and derivative biosynthesis; IEA.
DR InterPro; IPR000550; HPPK.
DR Pfam; PF01288; HPPK; 1.
DR TIGRFAMs; TIGR01498; FOLK; 1.
DR PROSITE; PS00794; HPPK; 1.
KW Transferase; Complete proteome.
SQ SEQUENCE 169 AA; 18179 MW; 829CD87425C21F36 CRC64;

Query Match 47.4%; Score 46; DB 16; Length 169;
Best local Similarity 72.7%; Pred. No. 6.8;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy 6 KICHQIEYQRC 16
Db 71 RICHIEDQFG 81

RESULT 11
Q94LDO
ID Q94LDO PRELIMINARY; PRT; 343 AA.
AC Q94LDO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative RNA-binding protein.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Euharidiales; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=cnv. Nipponbare;
RA Bueli C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Ganeberger K.,
RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Tselirin T.,
RA Riggs F., Heiao U., Ziemann V., Blunt S., Pai G., VanAken S.E.,
RA Uteerback T.R., Feldblum T.V., Quackenbush J., Salzberg S.L.,
RA White O., Fraser C.M.;
RT "Oryza sativa chromosome 3 BAC OSUNBA0026A15 genomic sequence.",
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN EMBL; AC084404; AAK50577.1; -
DR Gramene; Q94LDO; -
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002344; LupaLa.
DR InterPro; IPR006630; LupaLa.dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; Trm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SMO0715; LA; 1.

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RESULT 5
ID Q7ZT10 PRELIMINARY; PRT; 401 AA.
AC Q7ZT10;
DT 01-JUN-2003 (TEMBLrel. 24, Created)
DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Similar to sjogren syndrome antigen B (Autoantigen La).
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC045392; AAH45392.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002344; Iupus_La.
DR InterPro; IPR006630; Iupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 401 AA; 46138 MW; 2EF032FDD3916291 CRC64;

Query Match
Best Local Similarity 55.7%; Score 54; DB 13; Length 401;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 LEAKICHOIEYQFGD 17
Db 10 LEKVAEQIEYVFGD 24

RESULT 6
ID Q44678 PRELIMINARY; PRT; 91 AA.
AC Q44678;
DT 01-JUN-1998 (TEMBLrel. 06, Created)
DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Hypothetical protein C14C6.12.
GN C14C6.12.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodicerinae; Caenorhabditis.
NCBI_TaxID=6239;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Wilson R.;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018 (1998).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA David W., Wohlmann P., Bauer C., Antoniou B.;
RT "The sequence of C. elegans cosmid C14C6.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN (3)
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;

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RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
RN (4)
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Wilson R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF039051; AAB94258.2; -.
KW Hypothetical protein.
SQ SEQUENCE 91 AA; 10407 MW; D16D2BD4011F8762 CRC64;

Query Match
Best Local Similarity 50.5%; Score 49; DB 5; Length 91;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 KICHOIEYQFGDF 18
Db 6 KICNVIEYVTDGF 18

RESULT 7
ID Q7XT99 PRELIMINARY; PRT; 1560 AA.
AC Q7XT99;
DT 01-OCT-2003 (TEMBLrel. 25, Created)
DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE OSJNB0008A08.11 protein.
GN OSJNB0008A08.11.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
NCBI_TaxID=4530;
RN (1)
RP SEQUENCE FROM N.A.
RA Fu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F.,
RA Jia J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y.,
RA Zhao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W.,
RA Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Han B., Feng Q.,
RA Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu Z.,
RA Chen L., Fan D.L., Wang Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu X.H.,
RA Lu T.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y., Hu H., Jia P.X.,
RA Qian Y.M., Ying K., Zhou B., Chen Z.H., Hao P., Zhang L., Wu M.,
RA Zhang R.Q., Guan J.P., Hong G.F.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL606589; CAB01603.1; -.
SQ SEQUENCE 1560 AA; 177753 MW; 172320FF3797C6F0 CRC64;

Query Match
Best Local Similarity 49.5%; Score 48; DB 10; Length 1560;
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 ALEAKICHOIEYQFG 16
Db 1136 AVEFQWCHRYMWFQFG 1150

RESULT 8
ID Q96NN4 PRELIMINARY; PRT; 654 AA.
AC Q96NN4;
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE Hypothetical protein FLJ30499.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Nishi T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H.,

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DR GO:0005634; C:nucleus; IDA.
 DR InterPro; IPR002344; Lupus_La.
 DR InterPro; IPR006630; Lupus_La_dom.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF05383; La; 1.
 DR Pfam; PF00076; rrm; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 SQ SEQUENCE 381 AA; 43891 MW; 2E2DEF1452C0F0E9 CRC64;

Query Match 89.7%; Score 87; DB 11; Length 381;
 Best Local Similarity 94.1%; Pred. No. 1.4e-06;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 ALEAKICHOIEYQFDF 18
 |||||
 Db 12 ALEAKICHOIEYFGDF 28

RESULT 2

O8BTU4 PRELIMINARY; PRT; 415 AA.
 ID O8BTU4;
 AC O8BTU4;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Sjogren syndrome antigen B.
 GN SSB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=NO; TISSUE=Thymus;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK088677; BAC40498.1; -.
 DR MGD; MGI:98423; Ssb.
 DR GO; GO:0005634; C:nucleus; IDA.
 DR InterPro; IPR002344; Lupus_La.
 DR InterPro; IPR006630; Lupus_La_dom.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF05383; La; 1.
 DR Pfam; PF00076; rrm; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PS50102; RRM; 1.
 DR PROSITE; PS00030; RRM_RNP_1; 1.
 SQ SEQUENCE 415 AA; 47657 MW; A7545C7686A6363 CRC64;

Query Match 89.7%; Score 87; DB 11; Length 415;
 Best Local Similarity 94.1%; Pred. No. 1.6e-06;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 ALEAKICHOIEYQFDF 18
 |||||
 Db 12 ALEAKICHOIEYFGDF 28

RESULT 3

O7ZTK2 PRELIMINARY; PRT; 427 AA.
 ID O7ZTK2;
 AC O7ZTK2;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Similar to lupus LA protein homolog B.

OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC046654; AAH46654.1; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR InterPro; IPR002344; Lupus_La.
 DR InterPro; IPR006630; Lupus_La_dom.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF00076; rrm; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 2.
 DR PROSITE; PS50102; RRM; 1.
 DR PROSITE; PS00030; RRM_RNP_1; 1.
 SQ SEQUENCE 427 AA; 48996 MW; 1E7CD82D8AB9C69A CRC64;

Query Match 63.9%; Score 62; DB 13; Length 427;
 Best Local Similarity 73.3%; Pred. No. 0.032;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 3 LEAKICHOIEYQFDF 17
 |||||
 Db 12 LDTKICHOIEYFGDF 26

RESULT 4

O8OHI5 PRELIMINARY; PRT; 206 AA.
 ID O8OHI5
 AC O8OHI5;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Untranslated region binding-protein.
 GN UBP.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA L'Ecuylar T.J., Fang H.-L.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF467897; AAL76269.1; -.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR InterPro; IPR002344; Lupus_La.
 DR InterPro; IPR006630; Lupus_La_dom.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF05383; La; 1.
 DR Pfam; PF00076; rrm; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PS50102; RRM; 1.
 DR PROSITE; PS00030; RRM_RNP_1; 1.
 SQ SEQUENCE 206 AA; 23992 MW; 965B62F7DFPB90E9 CRC64;

Query Match 62.9%; Score 61; DB 13; Length 206;
 Best Local Similarity 73.3%; Pred. No. 0.022;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 3 LEAKICHOIEYQFDF 17
 |||||
 Db 13 LESKICHOIEYFGDF 27

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:29:01; Search time 41.229 Seconds
(without alignments)
137.751 Million cell updates/sec

Title: US-09-836-073-12

Perfect score: 97

Sequence: 1 AALEAKICHQIEYQFGDF 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL.25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	89.7	381	11	Q9CYB9 mus musculus
2	87	89.7	415	11	Q8BTU4 Q8btu4 mus musculus
3	62	63.9	427	13	Q7ZTK2 xenopus lae
4	61	62.9	206	13	Q8QH15 Q8qh15 gallus gall
5	54	55.7	401	13	Q7ZT10 Q7zt10 brachydanio
6	49	50.5	91	5	Q44678 Q44678 caenorhabdi
7	48	49.5	1560	10	Q7X199 Q7x199 oryza sativ
8	47	48.5	654	4	Q96NN4 Q96nn4 homo sapien
9	47	48.5	654	6	Q95KX5 Q95kx5 macaca fasc
10	46	47.4	169	16	Q8XK47 Q8xk47 ralestonia s
11	46	47.4	343	10	Q94ID0 Q94id0 oryza sativ
12	46	47.4	335	17	Q8UJ32 Q8uj32 pyrococcus
13	46	47.4	519	5	Q9VU19 Q9vu19 dirosophila
14	45	46.4	367	10	Q9SEU9 Q9seu9 brassica na
15	45	46.4	455	10	Q91HL3 Q91hl3 arabidopsis
16	45	46.4	1456	10	Q9FNM9 Q9fnm9 oryza sativ

17	45	46.4	1456	10	Q7X975 Q7x975 oryza sativ
18	44	45.4	96	10	Q9AUG1 Q9aug1 brassica ol
19	44	45.4	129	4	Q96M13 Q96m13 homo sapien
20	44	45.4	149	4	Q9NX22 Q9nx22 homo sapien
21	44	45.4	160	4	Q8NC35 Q8nc35 homo sapien
22	44	45.4	228	11	Q8C0L2 Q8c0l2 mus musculus
23	44	45.4	230	11	Q8CHL4 Q8chl4 mus musculus
24	44	45.4	381	11	Q8BX42 Q8bx42 mus musculus
25	44	45.4	382	4	Q96HP5 Q96hp5 homo sapien
26	44	45.4	433	4	Q81XR3 Q81xr3 homo sapien
27	44	45.4	505	11	Q8R518 Q8r518 mus musculus
28	44	45.4	535	11	Q9D856 Q9d856 mus musculus
29	44	45.4	535	11	Q9D909 Q9d909 mus musculus
30	44	45.4	539	4	Q8N6Y3 Q8n6y3 homo sapien
31	44	45.4	567	10	Q7X6F9 Q7x6f9 oryza sativ
32	44	45.4	568	16	Q9KX17 Q9kx17 vibrio chol
33	44	45.4	571	5	Q7Z1R8 Q7z1r8 plasmodium
34	44	45.4	582	11	Q7T0E0 Q7t0e0 mus musculus
35	44	45.4	626	4	Q9NXC4 Q9nxc4 homo sapien
36	44	45.4	647	4	Q9H6T8 Q9h6t8 homo sapien
37	44	45.4	660	11	Q9DAT9 Q9dat9 mus musculus
38	44	45.4	661	11	Q80TG2 Q80tg2 mus musculus
39	44	45.4	701	5	Q9VSL7 Q9vsl7 dirosophila
40	44	45.4	749	4	Q13433 Q13433 homo sapien
41	44	45.4	765	11	Q8C145 Q8c145 mus musculus
42	44	45.4	765	11	Q7TTP9 Q7tpp9 mus musculus
43	44	45.4	835	4	Q9ULF5 Q9ulf5 homo sapien
44	44	45.4	1230	10	Q9LD66 Q9ld66 oryza sativ
45	44	45.4	1381	10	Q84J29 Q84j29 oryza sativ

ALIGNMENTS

RESULT 1
ID Q9CYB9 PRELIMINARY; PRT; 381 AA.
AC Q9CYB9;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Sjogren syndrome antigen B.
GN SSB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arai K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamahata S.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Jostincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni U., Mashima U., Mazzarelli U., Mombauts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohzuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK017822; BAB30957.1; -;
DR MGD; MGI:98423; Ssb.

RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
LT2." ;

RU Nature 413:852-856(2001).

CC -1- FUNCTION: Mediates magnesium influx to the cytosol.

CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + Mg(2+) (Out) = ADP + phosphate +

Mg(2+) (In).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: Belongs to the cation transport ATPases family (P-type

ATPases). Subfamily IIB.

CC -----

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CC -----

CC EMBL; U07843; AAA68988.1; -.

DR EMBL; AE008909; AAL23275.1; -.

DR PIR; B57147; B57147.

DR StyGene; SG10230; mgCA.

DR InterPro; IPR006415; ATPase-IIB_Mg.

DR InterPro; IPR001757; ATPase_E1-E2.

DR InterPro; IPR004014; Cation_ATPase_N.

DR InterPro; IPR008250; E1-E2_ATPase_Reg.

DR InterPro; IPR000695; H_ATPase.

DR Pfam; PF00690; Cation_ATPase_N; 1.

DR Pfam; PF00122; E1-E2_ATPase; 1.

DR Pfam; PF00702; Hydrolyase; 1.

DR PRINTS; PR00119; CATTPASE.

DR PRINTS; PR00120; HATPASE.

DR TIGRFAMs; TIGR01524; ATPase-IIB_Mg; 1.

DR TIGRFAMs; TIGR01494; ATPase_P-type; 5.

DR PROSITE; PS00154; ATPase_E1_E2; 1.

KW Hydrolyase; Magnesium; Transmembrane; Phosphorylation; ATP-binding;

Complete proteome.

KW DOMAIN . 98

FT TRANSSEM . 1

FT DOMAIN . 98

FT TRANSSEM . 98

FT DOMAIN . 119

FT TRANSSEM . 120

FT DOMAIN . 121

FT TRANSSEM . 141

FT DOMAIN . 142

FT TRANSSEM . 291

FT DOMAIN . 312

FT TRANSSEM . 321

FT DOMAIN . 321

FT TRANSSEM . 339

FT DOMAIN . 340

FT TRANSSEM . 699

FT DOMAIN . 700

FT TRANSSEM . 719

FT DOMAIN . 720

FT TRANSSEM . 728

FT DOMAIN . 729

FT TRANSSEM . 748

FT DOMAIN . 749

FT TRANSSEM . 770

FT DOMAIN . 771

FT TRANSSEM . 794

FT DOMAIN . 795

FT TRANSSEM . 803

FT DOMAIN . 804

FT TRANSSEM . 822

FT DOMAIN . 823

FT TRANSSEM . 835

FT DOMAIN . 836

FT TRANSSEM . 855

FT DOMAIN . 856

FT TRANSSEM . 870

FT DOMAIN . 871

FT TRANSSEM . 890

FT DOMAIN . 891

FT TRANSSEM . 902

FT MOD_RES . 379

FT METAL . 335

FT METAL . 335

FT METAL . 645

FT METAL . 645

FT METAL . 649

FT METAL . 713

FT METAL . 713

FT METAL . 738

FT METAL . 742

FT METAL . 742

SEQUENCE 902 AA; 99782 MM; 3D2712E9A074C957 CRC64;

Query Match 42.3%; Score 41; DB 1; Length 902;

Best Local Similarity 46.2%; Pred. No. 37;

Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 AKVCHQIEYQFD 17

DB 581 AKVCHQIEYQFD 593

Search completed: September 10, 2004, 17:53:05
Job time : 8.24022 secs

RA Satou M., Tamse R., Vayenberg M., Wallender E.K., Wong C., Yamamura Y.,
 RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RT "Empirical analysis of transcriptional activity in the Arabidopsis
 genome.";
 RL Science 302:842-846(2003).
 CC -1- FUNCTION: Essential for proper development of leaves and floral
 CC organs, and formation of axillary meristems.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=1;
 CC Comment=number of isoforms are produced. According to EST
 CC sequences;
 CC Name=1;
 CC isoId=O04379-1; Sequence=Displayed;
 CC -1- TISSUE SPECIFICITY: Widely expressed at low levels.
 CC -1- DEVELOPMENTAL STAGE: Expressed throughout all developmental
 CC stages.
 CC -1- SIMILARITY: Belongs to the argonaute family.
 CC -1- SIMILARITY: Contains 1 PAZ domain.
 CC -1- SIMILARITY: Contains 1 Piwi domain.
 CC -1- CAUTION: Ref.2 (AA079718) sequence differs from that shown due to
 CC erroneous gene model prediction.
 CC -----
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 CC -----
 CC DR EMBL; U91995; AAC18440.1; -;
 CC DR EMBL; AC007932; AAD4975.1; -;
 CC DR EMBL; AC020889; AAF79718.1; ALT_SEQ.
 CC DR EMBL; E000941; AAN41341.1; -;
 CC DR InterPro; IPR003100; PAZ.
 CC DR InterPro; IPR003165; Piwi.
 CC DR Pfam; PF02170; PAZ; 1.
 CC DR Pfam; PF02171; Piwi; 1.
 CC DR PROSITE; PS50821; PAZ; 1.
 CC DR PROSITE; PS50822; Piwi; 1.
 CC KM Developmental protein; Alternative splicing.
 CC FT DOMAIN 391 501 PAZ.
 CC FT DOMAIN 676 997 Piwi.
 CC FT DOMAIN 13 104 GLY-RICH.
 CC SQ SEQUENCE 1048 AA; 116190 MW; 3E51463A09C541 CRC64;
 CC -----
 CC Query Match 43.3%; Score 42; DB 1; Length 1048;
 CC Best Local Similarity 46.2%; Pred. No. 29;
 CC Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 CC -----
 CC QY 3 LEAKICHOIEYQF 15
 CC Db 915 VDSKICHPTEFDF 927
 CC -----
 CC RESULT 14
 CC TCNO PETCR STANDARD; PRT; 506 AA.
 CC AC 043033;
 CC DT 15-DEC-1998 (Rel. 37, Created)
 CC DT 15-DEC-1998 (Rel. 37, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DE Trans-cinnamate 4-monoxygenase (EC 1.14.13.11) (Cinnamic acid
 CC 4-hydroxylase) (CA4H) (CAH) (P450CA4) (Cytochrome P450 73).
 CC GN CYP7A10 OR CYP73.
 CC OS Petroselinum crispum (Parsley) (Petroselinum hortense).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; asterids;
 CC Campanulids; Apiales; Apiaceae; Apioidae; apioid superclade;
 CC OC Apium clade; Petroselinum.
 CC OX NCBI_TaxID=4043;
 CC RA [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=95320184; PubMed=7597051;
 RA Logemann E., Paristke M., Hahlbrock K.;
 RT "Modes of expression and common structural features of the complete
 RT phenylalanine ammonia-lyase gene family in parsley.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:5905-5909(1995).
 CC -1- FUNCTION: Controls carbon flux to pigments essential for
 CC pollination or UV protection, to numerous phytoalexins synthesized
 CC by plants when challenged by pathogens, and to lignins.
 CC -1- CATALYTIC ACTIVITY: Trans-cinnamate + NADPH + O(2) = 4-
 CC hydroxycinnamate + NADP(+) + H(2)O.
 CC -1- PATHWAY: Lignin biosynthesis.
 CC -1- PATHWAY: Phenylpropanoid metabolism; second step.
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
 CC -----
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 CC -----
 CC DR EMBL; L38898; AAC1660.1; -;
 CC DR PIR; T14907; T14907.
 CC DR InterPro; IPR001128; Cytochrome_P450.
 CC DR Pfam; PF00067; P450; 1.
 CC DR PRINTS; PR00385; P450.
 CC DR PROSITE; PS00086; CYTOCHROME_P450; 1.
 CC KM Oxidoreductase; Monooxygenase; Heme; NADP.
 CC FT METAL 448 448 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 CC SQ SEQUENCE 506 AA; 58047 MW; 32F0EB959D69CF CRC64;
 CC -----
 CC Query Match 42.3%; Score 41; DB 1; Length 506;
 CC Best Local Similarity 42.9%; Pred. No. 20;
 CC Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 CC -----
 CC QY 5 AKICHOIEYQFDF 18
 CC Db 215 SRLAQSEYHFGDF 228
 CC -----
 CC RESULT 15
 CC ATMA_SALTY STANDARD; PRT; 902 AA.
 CC AC P36640;
 CC DT 01-JUN-1994 (Rel. 29, Created)
 CC DT 01-JUN-1994 (Rel. 29, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DE Mg(2+) transport ATPase, P-type 1 (EC 3.6.3.2).
 CC GN MGT4 OR STM4456.
 CC OS Salmonella typhimurium.
 CC OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC OC Enterobacteriaceae; Salmonella.
 CC OX NCBI_TaxID=602;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=LT2; / SGSC1412 / ATCC 700720;
 CC MEDLINE=21534948; PubMed=11677609;
 CC RX McCelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 CC Courtney L., Portwillik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 CC Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 CC Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
 CC Waterston R., Wilson R.K.;
 CC RA [2]
 CC RT "Magnesium transport in Salmonella typhimurium: mgtA encodes a P-type
 CC ATPase and is regulated by Mgt2+ in a manner similar to that of the
 CC mgtB P-type ATPase.";
 CC RL J. Bacteriol. 177:2654-2662(1995).
 CC RN [2]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
 CC MEDLINE=21534948; PubMed=11677609;
 CC RX McCelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 CC Courtney L., Portwillik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 CC Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 CC Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,
 CC Waterston R., Wilson R.K.;
 CC RA [1]

OS Saccharomyces cerevisiae (Baker's Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetidae; Saccharomycetaceae; Saccharomyces.
 OK NCBI_TaxID=4932;
 RN [1]
 RN SEQUENCE OF 12-573 FROM N.A.
 RX MEDLINE=87053966; PubMed=3536508;
 RA Hartig A., Ruis H.;
 RT "Nucleotide sequence of the Saccharomyces cerevisiae CTT1 gene and
 RL deduced amino-acid sequence of yeast catalase T.";
 RL Eur. J. Biochem. 160:487-490 (1986).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP Wedler H., Scharfe M., Wedler E., Manbut R.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE FROM N.A.
 RA Hernandez K., Weber N., Widfli P., Schmidheini T.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE OF 1-74 FROM N.A.
 RX MEDLINE=86230135; PubMed=2423850;
 RA Spevak W., Hartig A., Weindl P., Ruis H.;
 RT "Home control region of the catalase T gene of the yeast
 RL Saccharomyces cerevisiae.";
 RL Mol. Gen. Genet. 203:73-78 (1986).
 RN [5]
 RN SEQUENCE OF 405-409.
 RC STRAIN=ATCC 44827 / SKQ2N;
 RX MEDLINE=97190279; PubMed=9038161;
 RA Norbeck J., Blomberg A.;
 RT "Metabolic and regulatory changes associated with growth of
 RL Saccharomyces cerevisiae in 1.4 M NaCl. Evidence for osmotic
 RT induction of glycerol dissimilation via the dihydroxyacetone
 RT pathway.";
 RL J. Biol. Chem. 272:5544-5554 (1997).
 CC -1- FUNCTION: Occurs in almost all aerobically respiring organisms and
 CC serves to protect cells from the toxic effects of hydrogen
 CC peroxide.
 CC -1- CATALYTIC ACTIVITY: 2 H(2)O(2) = O(2) + 2 H(2)O.
 CC -1- COFACTOR: Heme group.
 CC -1- SUBUNIT: Homotetramer.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- MISCELLANEOUS: This is one of two catalases in S.cerevisiae; the
 CC other is catalase A, which is the peroxisomal form.
 CC -1- SIMILARITY: Belongs to the catalase family.
 CC -----
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 CC -----
 DR EMBL: X04625; CAA28298.1; -;
 DR EMBL: Z72873; CAA97090.1; -;
 DR EMBL: M30256; AAA34540.1; -;
 DR PIR: S64383; CSBYT.
 DR HSSP: P04040; 1PAJ.
 DR GenBank: 141400; -;
 DR SGD: S0003320; CTT1.
 DR GO: GO:0006950; P:response to stress; IDA.
 DR InterPro: IPR002226; Catalase.
 DR Pfam: PF00199; catalase; 1.
 DR PRINTS: PR00067; CATALASE.
 DR ProDom: PD000510; Catalase; 1.
 DR PROSITE: PS00437; CATALASE_1; 1.
 DR PROSITE: PS00438; CATALASE_2; 1.
 DR Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide;
 KW Multigene family.
 FT ACT_SITE 75 75 BY SIMILARITY.
 FT ACT_SITE 148 148 BY SIMILARITY.

FT METAL 362 362 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 FT CONFLICT 440 440 D -> V (IN REF. 1).
 FT CONFLICT 550 550 C -> G (IN REF. 1).
 SQ SEQUENCE 573 AA; 65741 MW; E03380543767377B CMC64;
 Query Match 43.3%; Score 42; DB 1; Length 573;
 Best Local Similarity 53.3%; Pred. No. 16;
 Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
 QY 3 LEAKICHOIEQFGD 17
 DB 191 IMPESIHQITFMFGD 205
 RESULT 13
 AGOI_ARATH STANDARD; PRT; 1048 AA.
 ID AGOI_ARATH
 AC 004379; Q9LPE3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Argonaute protein.
 GN AGOI OR A1G48410 OR F1A17.3 OR T1N15.2.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OK NCBI_TaxID=3702;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia; TISSUE=leaf;
 RX MEDLINE=98090460; PubMed=9427751;
 RA Bohmert K., Camus I., Bellini C., Bouchet D., Caboche M., Benning C.;
 RT "AGO1 defines a novel locus of Arabidopsis controlling leaf
 RT development.";
 RL EMBL J. 17:170-180 (1998).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
 RA Dunn P., Egu P., Feldhym T.V., Feng J.-D., Pong B., Fujii C.Y.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Malti R., Marziani A.,
 RA Miltschker J., Miranda M., Nguyen M., Nierman W.C., Osborne B.T.,
 RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 408:816-820 (2000).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=22954850; PubMed=14593172;
 RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
 RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
 RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
 RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
 RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
 RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
 RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gujral M., Hansen N.F.,
 RA Hayashizaki Y., Johnson-Hopson C., Huan V.W., Iida K., Karnes M.,
 RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
 RA Kamuya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,

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RPSD_MYCGE          STANDARD;          PRT;          497 AA.
ID   P47491; Q49487;
AC   P47491-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DR   01-FEB-1996 (Rel. 33, Last annotation update)
DE   16-OCT-2001 (Rel. 40, Last annotation update)
GN   RNA polymerase sigma factor rpoD (Sigma-A).
OS   Mycoplasma genitalium.
OC   Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX   NCBI_TaxID=2097;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 33530 / G-37;
RA   Frazer C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA   Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA   Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhmann J.L.,
RA   Nguyen D.T., Uterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA   Tomb J.F., Dougherty B.A., Bott K.F., Hu P.-C., Luetter T.S.,
RA   Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT   "The minimal gene complement of Mycoplasma genitalium.";
RL   Science 270:397-403 (1995).
RN   [2]
RP   SEQUENCE OF 223-323 FROM N.A.
RC   STRAIN=ATCC 33530 / G-37;
RA   MEDLINE=92051396; PubMed=1945886;
RA   Peterson S.N., Schramm N., Hu P.-C., Bott K.F., Hutchison C.A. III;
RT   "A random sequencing approach for placing markers on the physical map
RT   of Mycoplasma genitalium.";
RL   Nucleic Acids Res. 19:6027-6031 (1991).
CC   -1- FUNCTION: The sigma factor is an initiation factor that promotes
CC   attachment of the RNA polymerase to specific initiation sites and
CC   then is released. This is the primary sigma-factor of this
CC   bacteria (by similarity).
CC   -1- SIMILARITY: Belongs to the sigma-70 factor family.
CC   -----
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CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL; U39703; AAC71469.1; -
DR   EMBL; X61535; CAB98133.1; -
DR   PIR; E64227; E64227.
DR   HSSP; P00579; 1SIG.
DR   TIGR; MG249; -.
DR   InterPro; IPR009043; RNA_pol_sigma.
DR   InterPro; IPR007627; Sigma70_r2.
DR   InterPro; IPR007624; Sigma70_r3.
DR   InterPro; IPR009943; Sigma70.
DR   Pfam; PF04542; sigma70_r2_1.
DR   Pfam; PF04539; sigma70_r3_1.
DR   PRINTS; PR00046; SIGMA70FCT.
DR   PROSITE; PS00715; SIGMA70_1; 1.
DR   PROSITE; PS00716; SIGMA70_2; 1.
DR   Transcription regulation; Sigma factor; DNA-directed RNA polymerase;
KW   DNA-binding; Complete proteome.
FT   DOMAIN 274 287 POLYMERASE CORE BINDING (POTENTIAL).
FT   DNA BIND 451 470 H-T-H MOTIF (BY SIMILARITY).
FT   CONFLICT 224 232 DFE80RIA -> NINGLP (IN REF. 2).
SQ   SEQUENCE 497 AA; 57661 MW; ADE06CA68F59A5 CRC64;

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RESULT 11
RPSD_MYCPN          STANDARD;          PRT;          499 AA.
ID   P78022;
AC   P78022;
DT   01-NOV-1997 (Rel. 35, Created)
DR   01-NOV-1997 (Rel. 35, Last sequence update)
DE   16-OCT-2001 (Rel. 40, Last annotation update)
GN   RNA polymerase sigma factor rpoD (Sigma-A).
OS   Mycoplasma pneumoniae.
OC   Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX   NCBI_TaxID=2104;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 29342 / M129;
RA   MEDLINE=97105885; PubMed=8948633;
RA   Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
RA   Herrmann R.;
RT   "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT   pneumoniae.";
RL   Nucleic Acids Res. 24:4420-4449 (1996).
CC   -1- FUNCTION: The sigma factor is an initiation factor that promotes
CC   attachment of the RNA polymerase to specific initiation sites and
CC   then is released. This is the primary sigma-factor of this
CC   bacteria (by similarity).
CC   -1- SIMILARITY: Belongs to the sigma-70 factor family.
CC   -----
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CC   -----
DR   EMBL; AE000047; AAB96132.1; -
DR   PIR; S73810; S73810.
DR   HSSP; P00579; 1SIG.
DR   InterPro; IPR009043; RNA_pol_sigma.
DR   InterPro; IPR007627; Sigma70_r2.
DR   InterPro; IPR007624; Sigma70_r3.
DR   InterPro; IPR009943; Sigma70.
DR   Pfam; PF04542; sigma70_r2_1.
DR   Pfam; PF04539; sigma70_r3_1.
DR   PRINTS; PR00046; SIGMA70FCT.
DR   PROSITE; PS00715; SIGMA70_1; 1.
DR   PROSITE; PS00716; SIGMA70_2; 1.
DR   Transcription regulation; Sigma factor; DNA-directed RNA polymerase;
KW   DNA-binding; Complete proteome.
FT   DOMAIN 276 289 POLYMERASE CORE BINDING (POTENTIAL).
FT   DNA BIND 453 472 H-T-H MOTIF (BY SIMILARITY).
SQ   SEQUENCE 499 AA; 57796 MW; 7981C3BDE7C1E1 CRC64;

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Query Match      43.3%; Score 42; DB 1; Length 497;
Best Local Similarity 47.1%; Pred. No. 13;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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Query Match      43.3%; Score 42; DB 1; Length 499;
Best Local Similarity 47.1%; Pred. No. 14;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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CC -----
 DR EMBL; X68817; CAA48715.1; -
 DR PIR; S33818; S33818.
 DR InterPro; IPR002344; Lupus_La.
 DR InterPro; IPR006630; Lupus_La_dom.
 DR InterPro; IPR00504; RNA_rec_mot.
 DR Pfam; PF05383; La; 1.
 DR Pfam; PF00076; xrm; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PS0102; RRM; 1.
 DR PROSITE; PS0030; RRM_RNP_1; 1.
 DR RNA-binding; Nuclear protein; Phosphorylation.
 DR RNA-binding; Nuclear protein; RNA-BINDING (RRM).
 FT DOMAIN 111 203 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 196 212 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 FT DOMAIN 316 332 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
 SQ SEQUENCE 428 AA; 48864 MW; AEB3A38B7D2E3EC3 CRC64;

Query Match 59.8%; Score 58; DB 1; Length 428;
 Best Local Similarity 71.4%; Pred. No. 0.019;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 EAKICHQIEYFGD 17
 Db 14 DTKICEQIEYFGD 27

RESULT 7
 LA AEDAL STANDARD; PRT; 383 AA.
 ID LA AEDAL
 AC 026457;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE La protein homolog (La ribonucleoprotein) (La autoantigen homolog).
 OS Aedes albopictus (Forest day mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes.
 NC NCB1_TaxID=1160;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=96135233; PubMed=8551578;
 RA Pardigon N., Straus J.H.;
 RT "Mosquito homolog of the La autoantigen binds to Sindbis virus RNA.";
 RL J. Virol. 70:1173-1181(1996).
 CC -1- FUNCTION: May be involved in transcription termination by RNA
 polymerase III. Binds RNA and DNA. Binds to the 3' end of the
 CC minus strand of Sindbis virus RNA. This may be significant for
 CC Sindbis virus RNA replication.
 CC -1- SUBCELLULAR LOCATION: Nuclear. Primarily nuclear, but significant
 CC amounts are present in the cytoplasm.
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
 CC -1- SIMILARITY: TO VERTEBRATE PROTEIN LA.
 CC -----
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CC -----
 DR EMBL; S80954; AAB35931.1; -
 DR InterPro; IPR002344; Lupus_La.
 DR InterPro; IPR006630; Lupus_La_dom.
 DR InterPro; IPR00504; RNA_rec_mot.
 DR Pfam; PF05383; La; 1.
 DR Pfam; PF00076; xrm; 1.
 DR PRINTS; PR00302; LUPUSLA.

DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PS50102; RRM; 1.
 DR PROSITE; PS0030; RRM_RNP_1; FALSE NEG.
 DR RNA-binding; Nuclear protein; DNA-BINDING.
 DR RNA-binding; Nuclear protein; RNA-BINDING (RRM).
 FT DOMAIN 141 228
 FT DOMAIN 196 212
 SQ SEQUENCE 383 AA; 44430 MW; 4E5C8F21C40F452 CRC64;

Query Match 48.5%; Score 47; DB 1; Length 383;
 Best Local Similarity 60.0%; Pred. No. 1.4;
 Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 LEASTIRQIEYFGD 17
 Db 43 LEASTIRQIEYFGD 57

RESULT 8
 LA DROME STANDARD; PRT; 390 AA.
 ID LA DROME
 AC P40796; Q24375; Q9VIN2;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE La protein homolog (La ribonucleoprotein) (La autoantigen homolog).
 GN LA OR CG10922.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NC NCB1_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Cancon-S; TISSUE=Ovary;
 RX MEDLINE=94309632; PubMed=8035794;
 RA Bai C., Li Z., Tollas P.P.;
 RT "Developmental characterization of a Drosophila RNA-binding protein
 RT homologous to the human systemic lupus erythematosus-associated
 RT La/SS-B autoantigen.";
 RL Mol. Cell. Biol. 14:5123-5129(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94309661; PubMed=8035818;
 RA Yoo C.J., Molin S.L.;
 RT "La proteins from Drosophila melanogaster and Saccharomyces
 RT cerevisiae: a yeast homolog of the La autoantigen is dispensable for
 RT growth.";
 RL Mol. Cell. Biol. 14:5412-5424(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amandes P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang O., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chame M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballou R.M., Basu A., Bakendole J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Bortch M.A., Bouck J., Brooks P., Brotler P.,
 RA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira J., Fleischmann W.,
 RA Folsler A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D.A., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

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DR EMBL, L00993; AAA39415.1; -
 DR EMBL, BC003820; AAH03820.1; -
 DR EMBL, Y07951; CAA69249.1; -
 DR MGI, MGI:38423; Sab.
 DR GO, GO:0005634; C:nucleus; IDA.
 DR InterPro; IPR002344; Lupus_La.
 DR InterPro; IPR006630; Lupus_La.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF05383; La; 1.
 DR Pfam; PF00076; xrm; 1.
 DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PS50102; RRM; 1.
 DR PROSITE; PS00030; RRM_RNP_1; 1.
 DR RNA-binding; Nuclear protein; Phosphorylation.
 DR RNA-binding; Nuclear protein; Phosphorylation.
 FT DOMAIN 111 187
 SQ SEQUENCE 415 AA; 47756 MW; 2D75197692FDC933 CRC64;

Query Match 89.7%; Score 87; DB 1; Length 415;
 Best Local Similarity 94.1%; Pred. No. 1.8e-07;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ALEAKICHOIEYFGDF 18
 Db 12 ALEAKICHOIEYFGDF 28

RESULT 5
 LAB_XENLA STANDARD; PRT; 427 AA.
 AC P28049;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Lupus La protein homolog B (La ribonucleoprotein B) (La autoantigen
 DE homolog B).
 GN LAB1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Oocyte;
 RX MEDLINE=93287095; PubMed=8510143;
 RA Scherly D., Stutz F., Lin-Marg N., Clarkson S.G.;
 RT "La proteins from Xenopus laevis. cDNA cloning and developmental
 RT expression.";
 RL J. Mol. Biol. 231:196-204(1993).
 CC -1- FUNCTION: La protein plays a role in the transcription of RNA
 CC polymerase III. It is most probably a transcription termination
 CC factor. Binds to the 3' terminus of virtually all nascent
 CC polymerase III transcripts (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- DEVELOPMENTAL STAGE: Barely detectable in stage I/II oocytes,
 CC accumulate in stage III/IV oocytes, then exhibit a roughly
 CC constant steady state level in mature oocytes, eggs, and early
 CC embryos.
 CC -1- PTM: Phosphorylated (Probable).
 CC -1- MISCELLANEOUS: There are two forms of La, LaA and LaB, in xenopus.
 CC -1- SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN.
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
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DR EMBL, X68818; CAA48716.1; -
 DR PIR, S33817; S33817.
 DR InterPro; IPR002344; Lupus_La.
 DR InterPro; IPR006630; Lupus_La.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF05383; La; 1.
 DR Pfam; PF00076; xrm; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PS50102; RRM; 1.
 DR PROSITE; PS00030; RRM_RNP_1; FALSE NEG.
 DR RNA-binding; Nuclear protein; Phosphorylation.
 DR RNA-binding; Nuclear protein; Phosphorylation.
 FT DOMAIN 110 202
 FT DOMAIN 315 331
 SQ SEQUENCE 427 AA; 48995 MW; 45F3146F8934A355 CRC64;

Query Match 63.9%; Score 62; DB 1; Length 427;
 Best Local Similarity 73.3%; Pred. No. 0.0039;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 LEAKICHOIEYFGDF 17
 Db 12 LDTKICEQIEYFGDF 26

RESULT 6
 LAA_XENLA STANDARD; PRT; 428 AA.
 AC P28048;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Lupus La protein homolog A (La ribonucleoprotein A) (La autoantigen
 DE homolog A).
 GN LAA1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Oocyte;
 RX MEDLINE=93287095; PubMed=8510143;
 RA Scherly D., Stutz F., Lin-Marg N., Clarkson S.G.;
 RT "La proteins from Xenopus laevis. cDNA cloning and developmental
 RT expression.";
 RL J. Mol. Biol. 231:196-204(1993).
 CC -1- FUNCTION: La protein plays a role in the transcription of RNA
 CC polymerase III. It is most probably a transcription termination
 CC factor. Binds to the 3' terminus of virtually all nascent
 CC polymerase III transcripts (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- DEVELOPMENTAL STAGE: Barely detectable in stage I/II oocytes,
 CC accumulate in stage III/IV oocytes, then exhibit a roughly
 CC constant steady state level in mature oocytes, eggs, and early
 CC embryos.
 CC -1- PTM: Phosphorylated (Probable).
 CC -1- MISCELLANEOUS: There are two forms of La, LaA and LaB, in xenopus.
 CC -1- SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN.
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
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DR PROSITE; PS00030; RRM_RNP_1; 1.
 KM Systemic lupus erythematosus; RNA-binding; Phosphorylation;
 NM Nuclear protein.
 FT DOMAIN 111 187 RNA-BINDING (RRM).
 FT MOD_RES 366 366 PHOSPHORYLATION (BY CK2).
 SQ SEQUENCE 408 AA; 46837 MW; EC153C15F9187PC4 CRC64;
 Query Match 93.8%; Score 91; DB 1; Length 408;
 Best Local Similarity 94.4%; Pred. No. 3.5e-08;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AALEAKICHQIEYFGDF 18
 |||||
 DB 11 AALEAKICHQIEYFGDF 28

RESULT 3
 ID LA RAT STANDARD; PRT; 415 AA.
 AC P38656;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lupus La protein homolog (La ribonucleoprotein) (La autoantigen
 DE homolog).
 GN SSB OR SS-B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93246255; PubMed=7916708;
 RA Semsei I., Troester H., Bartsch H., Schwemmler M., Igloi G.L.,
 RA Bachmann M.;
 RT "Isolation of rat cDNA clones coding for the autoantigen SS-B/La:
 RT detection of species-specific variations.";
 RL Gene 126:265-268(1993).
 CC -1- FUNCTION: La protein plays a role in the transcription of RNA
 CC polymerase III. It is most probably a transcription termination
 CC factor. Binds to the 3' terminus of virtually all nascent
 CC polymerase III transcripts. It is associated with precursor forms
 CC of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S,
 CC and 7-2 RNAs.
 CC -1- SUBUNIT: Interacts with DDX15 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- PTM: Phosphorylated (By similarity).
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
 CC
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 CC
 CC EMBL; X67859; CAA48043.1; -.
 CC PIR; JCI494; JCI494.
 CC InterPro; IPR002344; Lupus_La.
 CC InterPro; IPR006630; Lupus_La_dom.
 CC InterPro; IPR000504; RNA_rec_mot.
 CC Pfam; PF00383; La; 1.
 CC Pfam; PF00076; rrm; 1.
 CC PRINTS; PR00302; LUPUSLA.
 CC SMART; SM00715; La; 1.
 CC SMART; SM00360; RRM; 1.
 CC PROSITE; PS0102; RRM; 1.
 CC PROSITE; PS00030; RRM_RNP_1; 1.
 CC KW RNA-binding; Nuclear protein; Phosphorylation.
 CC FT DOMAIN 111 187 RNA-BINDING (RRM).
 CC SEQUENCE 415 AA; 47777 MW; 033FD9CC18475F98 CRC64;

Query Match 93.8%; Score 91; DB 1; Length 415;
 Best Local Similarity 94.4%; Pred. No. 3.5e-08;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AALEAKICHQIEYFGDF 18
 |||||
 DB 11 AALEAKICHQIEYFGDF 28

RESULT 4
 ID LA MOUSE STANDARD; PRT; 415 AA.
 AC P32067;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Lupus La protein homolog (La ribonucleoprotein) (La autoantigen
 DE homolog).
 GN SSB OR SS-B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93203630; PubMed=8454877;
 RA Topfner F., Gordon T., McCluskey J.;
 RT "Characterization of the mouse autoantigen La (SS-B). Identification
 RT of conserved RNA-binding motifs, a putative ATP binding site and
 RT reactivity of recombinant protein with poly(U) and human
 RT autoantibodies.";
 RL J. Immunol. 150:3091-3100(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Umed T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mallya S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE OF 1-11 FROM N.A.
 RA Groelz D., Bachmann M.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: La protein plays a role in the transcription of RNA
 CC polymerase III. It is most probably a transcription termination
 CC factor. Binds to the 3' terminus of virtually all nascent
 CC polymerase III transcripts. It is associated with precursor forms
 CC of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S,
 CC and 7-2 RNAs.
 CC -1- SUBUNIT: Interacts with DDX15 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- PTM: Phosphorylated (By similarity).
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

FT DOMAIN 111 187 RNA-BINDING (RRM).
 SQ SEQUENCE. 404 AA; 46534 MW; 4EE30B5C262A06A1 CRC64;
 Query Match 93.8%; Score 91; DB 1; Length 404;
 Best Local Similarity 94.4%; Pred. No. 3.4e-08;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AALEAKICHQIRYRGDF 18
 |||||
 DB 11 AALEAKICHQIRYRGDF 28

RESULT 2
 ID LA_HUMAN STANDARD; PRT; 408 AA.
 AC P05455;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Lupus La protein (Sjogren syndrome type B antigen) (SS-B) (La ribonucleoprotein) (La autoantigen).
 GN SSB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_taxid:9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=89202037; PubMed=2468131;
 RA Chan E.K.L., Sullivan K.F., Tan E.M.;
 RT "Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences for RNA-binding.";
 RL Nucleic Acids Res. 17:2233-2244 (1989).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=89053970; PubMed=3192525;
 RA Chambers J.C., Kenan D., Martin B.J., Keene J.D.;
 RT "Genomic structure and amino acid sequence domains of the human La autoantigen.";
 RL J. Biol. Chem. 263:18043-18051 (1988).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Placenta, and Skeletal muscle;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Abramson R.D., Mullen B.A.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stachenko M., Soares W.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield J.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [4]
 RN SEQUENCE OF 54-97 FROM N.A.
 RX MEDLINE=88199081; PubMed=2452201;
 RA Sturgees A.D., Peterson M.G., McNeilage L.J., Whittingham S.,
 RA Coppel R.S.;
 RT "Characteristics and epitope mapping of a cloned human autoantigen La.";
 RL J. Immunol. 140:3212-3218 (1988).
 RN [5]

RP SEQUENCE OF 54-97 FROM N.A.
 RX MEDLINE=8516283; PubMed=3856888;
 RA Chambers J.C., Keene J.D.;
 RT "Isolation and analysis of cDNA clones expressing human lupus La antigen.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:2115-2119 (1985).
 RN [6]
 RN FUNCTION.
 RP MEDLINE=89251617; PubMed=2470590;
 RA Gottlieb E., Steltz J.A.;
 RT "Function of the mammalian La protein: evidence for its action in transcription termination by RNA polymerase III.";
 RL EMBL J. 8:851-861 (1989).
 RN [7]
 RN PHOSPHORYLATION.
 RP MEDLINE=97207017; PubMed=9054510;
 RA Fan H., Sakulich A.L., Goodier J.L., Zhang X., Qin J., Marate R.J.;
 RT "Phosphorylation of the human La antigen on serine 366 can regulate recycling of RNA polymerase III transcription complexes.";
 RL Cell 88:707-715 (1997).
 RN [8]
 RN INTERACTION WITH DDX15.
 RP MEDLINE=22346609; PubMed=12458796;
 RA Fouraux M.A., Kolkman M.J.M., Van der Heijden A., De Jong A.S.,
 RA Van Venrooij W.J., Pruijn G.J.M.;
 RT "The human La (SS-B) autoantigen interacts with DDX15/hp43, a putative DEAD-box RNA helicase.";
 RL RNA 8:1428-1443 (2002).
 CC -1- FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor forms of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S, and 7-2 RNAs.
 CC -1- SUBUNIT: Interacts with DDX15.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- PTM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES ARE AT THE C-TERMINAL PART OF THE PROTEIN.
 CC -1- PTM: The N-terminus is blocked.
 CC -1- DISEASE: Sera from patients with systemic lupus erythematosus often contain antibodies that react with the normal cellular La protein as if this antigen was foreign.
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
 CC -----
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 CC -----
 CC EMBL: X13697; CAA31985.1; -;
 DR EMBL: J04205; AAB51885.1; -;
 DR EMBL: BC001289; AAB01289.1; -;
 DR EMBL: BC020818; AAB20818.1; -;
 DR PIR: A31888; A31888.
 DR Genew: HGNC:11316; SSB.
 DR MIM: 109090; -;
 DR GO: GO:0030529; C:ribonucleoprotein complex; TAS.
 DR GO: GO:0003729; F:mRNA binding; TAS.
 DR GO: GO:0000049; F:tRNA binding; TAS.
 DR GO: GO:0008334; P:histone mRNA metabolism; TAS.
 DR GO: GO:0006400; P:tRNA modification; TAS.
 DR InterPro: IPR002344; Lupus La.
 DR InterPro: IPR006630; Lupus La dom.
 DR InterPro: IPR000504; RNA_rec_mot.
 DR Pfam: PF05383; La; 1.
 DR Pfam: PF00076; trm; 1.
 DR PRINTS: PR00302; LUPUSLA.
 DR SMART: SM00715; LA; 1.
 DR SMART: SM00360; RRM; 1.
 DR PROSITE: PS0102; RRM; 1.

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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:01:41; Search time 7.24022 Seconds
(without alignments)
129.452 Million cell updates/sec

Title: US-09-836-073-12

Perfect score: 97

Sequence: 1 AALEKICHQIEYFGDF 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	91	93.8	404	1 LA_BOVIN	P10881 bos taurus
2	91	93.8	408	1 LA_HUMAN	P05455 homo sapien
3	91	93.8	415	1 LA_RAT	P38656 rattus norv
4	87	89.7	415	1 LA_MOUSE	P32067 mus musculu
5	62	63.9	427	1 LAB_XENLA	P28049 xenopus lae
6	58	59.8	428	1 LAB_XENLA	P28048 xenopus lae
7	47	48.5	383	1 LA_AEDAL	Q26457 aedes albop
8	43	44.3	390	1 LA_DROME	P40796 drosophila
9	42	43.3	482	1 LBP_RABIT	P17454 oryctolagus
10	42	43.3	487	1 RPSD_MYCGE	P47491 mycoplasma
11	42	43.3	499	1 RPSD_MYCPN	P78022 mycoplasma
12	42	43.3	573	1 CATT_YEAST	P06115 saccharomyc
13	42	43.3	1048	1 AGOI_ARATH	Q04379 arabidopsis
14	42	43.3	506	1 TCMO_PPCRC	Q43033 petroselinu
15	41	42.3	902	1 ATMA_SALTY	P36640 salmoneilla
16	41	42.3	988	1 PINN_ARATH	O9XG1 arabidopsis
17	40	41.2	357	1 CARA_BUCBP	P59376 buchnera ap
18	40	41.2	490	1 IFT4_HUMAN	O14879 homo sapien
19	40	41.2	591	1 Y875_CHLTR	O84883 chlamydia t
20	40	41.2	1107	1 MYIB_MOUSE	P46755 mus musculu
21	40	41.2	1136	1 MYIB_RAT	O05096 rattus norv
22	40	41.2	2556	1 NTCL_HUMAN	P46531 homo sapien
23	39	40.2	158	1 YV02_HUMAN	O99765 homo sapien
24	39	40.2	231	1 MTNA_BACSU	O32028 bacillus su
25	39	40.2	310	1 PP12_TOBAC	O04857 nicotiana t
26	39	40.2	461	1 FUMC_RICPR	O9ZCQ4 rickettsia
27	39	40.2	501	1 XYLB_LACPE	P19399 lactobacill
28	39	40.2	532	1 VP33_ARATH	O94K17 arabidopsis
29	39	40.2	812	1 PLMN_MOUSE	P20918 mus musculu
30	39	40.2	997	1 AGOL_ARATH	O96J33 arabidopsi
31	39	40.2	1174	1 KPCI_COCHR	O42632 cochlidolu
32	39	40.2	1433	1 VGLM_BUNYW	P45055 bunyamwera
33	39	40.2	2483	1 COA2_HUMAN	O00763 homo sapien

34	38.5	39.7	1036	1 OG11_HUMAN	O15294 homo sapien
35	38.5	39.7	1036	1 OG11_RAT	P56558 rattus norv
36	38	39.2	298	1 LAH1_SCHPO	P87058 schizosach
37	38	39.2	479	1 PRL2_ARATH	O39190 arabidopsis
38	38	39.2	487	1 GARB_CHICV	O823w6 chlamydomo
39	38	39.2	505	1 TCNO_ARATH	P92294 arabidopsis
40	38	39.2	505	1 TCNO_CICAR	O81928 cicer aric
41	38	39.2	505	1 TCNO_GLYEC	O96423 glycyrrhiza
42	38	39.2	505	1 TCNO_HELTV	O04468 helianthus
43	38	39.2	505	1 TCNO_PEA	O43067 pieum sativ
44	38	39.2	505	1 TCNO_PHAU	P37115 phaseolus a
45	38	39.2	505	1 TCNO_ZINEL	Q43240 zinnia eleg

ALIGNMENTS

RESULT 1
LA_BOVIN STANDARD; PRT; 404 AA.
ID LA_BOVIN
AC P10881;
DT 01-UTL-1989 (Rel. 11, Created)
DT 01-UTL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lupus La protein homolog (La ribonucleoprotein) (La autoantigen
DE homolog).
GN SSB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Plutitary; PubMed=2468131;
RX MEDLINE=89202037; Pubmed=2468131;
RA Chan E.K.L., Sullivan K.F., Tan E.M.;
RT "Ribonucleoprotein SS-B/La belongs to a protein family with consensus
sequences for RNA-binding".
RT Nucleic Acids Res. 17:2233-2244(1989).
RL
CC -1- FUNCTION: La protein plays a role in the transcription of RNA
CC polymerase III. It is most probably a transcription termination
CC factor. Binds to the 3' termin of virtually all nascent
CC polymerase III transcripts. It is associated with precursor forms
CC of RNA polymerase III transcripts including crna and 4.5S, 5S, 7S,
CC and 7-2 RNAs.
CC -1- SUBUNIT: Interacts with DDX15 (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- PTM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES ARE AT THE
CC C-TERMINAL PART OF THE PROTEIN.
CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
CC
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CC
CC EMBL; X13698; CAA31986.1; -
DR JIR; S03849; S03849.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR Pfam; PIR000504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
KM RNA-binding; Nuclear protein; Phosphorylation.

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Best Local Similarity 47.1%; Pred. No. 39;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 ALEAKICHQIEYQFGDF 18

Db 382 SLDKTVGHDEESQFGDF 398

RESULT 15

transcription factor sigma A - *Mycoplasma pneumoniae* (strain ATCC 29342)

N;Alternate names: hypothetical protein H91_orf499

C;Species: Mycoplasma pneumoniae

A; Variety: ATCC 29342
C: Date: 27-Feb-1997 #

C;Accession: S73810
C;Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 0/-Dec-1995

C;ACCESSION: S/3610
R:Himmelreich, R.;

Nucleic Acids Res. 24, 4420-4449, 1996

A;Title: Complete sequence analysis of

A;Reference number: S73327; MUID:97105885; PMID:8948633

A;Accession: S73810

A;Status: preliminary

A;Molecule type: LNA
A;Residues: 1-499 <HTM>

A;RESIDUES: 1-499 <HIM>

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996

C;Genetics:

A;Gene: sigl

A; Genetic co

C; Superfamily:

Keywords: DNA binding; sigma factor; transcription initiation
E-254-487/Domain: transcription factor sigma katE homoj

F/254-48//Description: CLAIMS INFLATION FACTOR STUDY

Query Match 43.3%; Score 42; DB 2; Length 499;

Best Local Similarity 47.18; Pred. No. 39;

Matches	8	Conservative	3	Mismatches	6	Indels	0	Gaps	0
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1. **Introduction**

QY 2 ALEAKICHQIEYQFGDF 18

Db 384 SLDKTVGHDEESQFGDF 400

Search completed: September 10, 2004, 18:02:30
Job time : 16.0782 secs

ribonucleoprotein La - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 20-Sep-1999
C:Accession: A53781
R:Yoo, C.J.; Molin, S.L.
Mol. Cell. Biol. 14, 5412-5424, 1994
A>Title: La proteins from Drosophila melanogaster and Saccharomyces cerevisiae: a yeast
A:Reference number: A53781; MUID:94309661; PMID:8035818
A:Accession: A53781
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-390 <YOO>
A:Cross-references: GB:L32988; NID:G488469; PID:G488470
C:Genetics:
A:Gene: FlyBase:La
A:Cross-references: FlyBase:FBgn0011638
C:Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
C:Keywords: RNA binding

Query Match 44.3%; Score 43; DB 2; Length 390;
Best Local Similarity 57.1%; Pred. No. 21;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Oy 4 EAKICHOIEYQFGD 17
Db 51 ERAIRQVEYFYFGD 64

RESULT 11
T15617
hypothetical protein C25F6.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15617
R:Bentley, D.
A:Description: The sequence of C. elegans cosmid C25F6.
A:Reference number: Z18377
A:Accession: T15617
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1131 <BEN>
A:Cross-references: EMBL:U93742; NID:G1049455; PID:G1049459; PIDN:AAA0434.1; CESP:C25F6
C:Genetics:
A:Gene: CESP:C25F6.2
A:Introns: 105/1; 210/3; 283/3; 316/1; 346/2; 463/3; 566/1; 722/2; 897/1; 991/2; 1032/1;

Query Match 44.3%; Score 43; DB 2; Length 1131;
Best Local Similarity 70.0%; Pred. No. 60;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 8 CHQIEYQFGD 17
Db 1019 CHRIQTFQGD 1028

RESULT 12
T19585
hypothetical protein C30H6.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Sep-2000
C:Accession: T19585
R:Morimoto, B.
A:Submitted to the EMBL Data Library, October 1996
A:Reference number: Z19148
A:Accession: T19585
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-360 <WIL>
A:Cross-references: EMBL:Z81044; PIDN:CAB02806.1; GSPDB:GN00022; CESP:C30H6.2
C:Genetics:
A:Gene: CESP:C30H6.2

A:Map position: 4
A:Introns: 43/2; 67/3; 111/3; 149/3; 231/3
C:Superfamily: Caenorhabditis elegans hypothetical protein C30H6.2

Query Match 43.3%; Score 42; DB 2; Length 360;
Best Local Similarity 46.2%; Pred. No. 28;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 5 AKICHOIEYQFGD 17
Db 269 AVICHELPHREIGD 281

RESULT 13
B35843
lipopolysaccharide-binding protein - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 20-Aug-1999
C:Accession: B35843; A46553
R:Schumann, R.R.; Leong, S.R.; Flagg, G.W.; Gray, P.W.; Wright, S.D.; Mathison, J.C.; Tr
Science 249, 1429-1431, 1990
A>Title: Structure and function of lipopolysaccharide binding protein.
A:Reference number: A35843; MUID:90385281; PMID:2402637
A:Accession: B35843
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-482 <SCH>
A:Cross-references: GB:M5534; NID:G165467; PIDN:AAA99235.1; PID:G165468
R:Tobias, P.S.; Soldau, K.; Ulevitch, R.J.
J. Exp. Med. 164, 777-793, 1986
A>Title: Isolation of a lipopolysaccharide-binding acute phase reactant from rabbit seru
A:Reference number: A46553; MUID:86306528; PMID:2427635
A:Accession: A46553
A:Molecule type: protein
A:Residues: 27-55, 'XG', 58-62, 'P', 64-65 <TOB>
C:Superfamily: lipopolysaccharide-binding protein
C:Keywords: acute phase

Query Match 43.3%; Score 42; DB 2; Length 482;
Best Local Similarity 80.0%; Pred. No. 38;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 3 LEAKICHOIE 12
Db 194 LESKICHOIE 203

RESULT 14
B64227
transcription initiation factor sigma A - Mycoplasma genitalium
N:Alternate names: RNA polymerase sigma-A factor
C:Species: Mycoplasma genitalium
C>Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 21-Jul-2000
C:Accession: B64227
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Uterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.;
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A>Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200; MUID:96026346; PMID:7569993
A:Accession: B64227
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-497 <TIG>
A:Cross-references: GB:U9703; GB:L43967; NID:G3844835; PIDN:AACT1469.1; PID:G1045940; T
A:Experimental source: strain G-37
C:Genetics:
A:Genetic code: SGC3
C:Superfamily: transcription initiation factor sigma katf homology
C:Keywords: DNA binding; sigma factor; transcription initiation
F:252-485/Domain: transcription initiation factor sigma katf homology <KTF>

Query Match 43.3%; Score 42; DB 2; Length 497;

A:Reference number: S03848; MUID:89202037; PMID:2468131
 A:Accession: S03848
 A:Molecule type: mRNA
 A:Residues: 1-408 <CH2>
 A:Cross-references: EMBL:X13697; NID:G36414; PIDN:CAA31985.1; PID:G36415
 R:Chambers, J.C.; Keene, J.D.
 Proc. Natl. Acad. Sci. U.S.A. 82, 2115-2119, 1985
 A:Title: Isolation and analysis of cDNA clones expressing human lupus La antigen.
 A:Reference number: A22956; MUID:85166283; PMID:3856888
 A:Accession: A22956
 A:Molecule type: mRNA
 A:Residues: 45-97, 'LK', <CH3>
 A:Cross-references: GB:J04205
 A:Note: this sequence has been revised in reference A31888
 R:Nyman, U.; Ringertz, N.R.; Petersson, I.
 Immunol. Lett. 22, 65-72, 1989
 A:Title: Demonstration of an amino terminal La epitope recognized by human anti-La sera.
 A:Reference number: A61051; MUID:89379261; PMID:2476379
 A:Accession: A61051
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-19, 'E', '21-47' <NYM>
 R:Sturges, A.D.; Peterson, M.G.; McNeillage, L.D.; Whittingham, S.; Coppel, R.L.
 J. Immunol. 140, 3212-3218, 1988
 A:Title: Characteristics and epitope mapping of a cloned human autoantigen La.
 A:Reference number: S11013; MUID:88199081; PMID:2452201
 A:Accession: S11013
 A:Molecule type: mRNA
 A:Residues: 'E', '55-287', 'V', '289-408' <STU>
 A:Cross-references: EMBL:M20328; NID:G337456; PIDN:AAA36577.1; PID:G337457
 R:Kobayashi, H.; Yamamoto, K.; Fujii, H.; Mura, H.; Miyasaka, N.; Miyamoto, J.
 Clin. Invest. 85, 1566-1574, 1990
 A:Title: Fine epitope mapping the human SS-B/La protein: Identification of a distinct an
 A:Reference number: 155553; MUID:90237237; PMID:1692037
 A:Accession: 155553
 A:Molecule type: translated from GB/EMBL/DBJ
 A:Residues: 81-107 <RES>
 A:Cross-references: GB:M35261; NID:G338491; PIDN:AAA36652.1; PID:G338495
 A:Accession: 170205
 A:Molecule type: translated from GB/EMBL/DBJ
 A:Residues: 174-224 <RE2>
 A:Cross-references: GB:M35263; NID:G338492; PIDN:AAA36653.1; PID:G338496
 A:Accession: 170206
 A:Molecule type: translated from GB/EMBL/DBJ
 A:Residues: 279-342 <RE3>
 A:Cross-references: GB:M35262; NID:G338493; PIDN:AAA36654.1; PID:G338497
 C:Comment: This protein associates with a variety of small RNA molecules, most of which
 act as a transcription termination factor.
 C:Genetics:
 A:Gene: GDB:SSB
 A:Cross-references: GDB:125359; OMIM:109090
 A:Map position: 2
 A:Introns: 22/3; 57/2; 115/3; 151/3; 185/2; 209/2; 223/3; 264/3; 380/2
 C:Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
 C:Keywords: phosphoprotein; RNA binding
 F:112-178/Domain: ribonucleoprotein repeat homology <RRM>
 F:113-118/Region: RNA-binding RNP2 motif
 F:151-158/Region: RNA-binding RNP1 motif
 F:228-408/Domain: phosphorylated #status experimental <PHY>

Query Match 93.8%; Score 91; DB 1; Length 408;
 Best Local Similarity 94.4%; Pred. No. 2e-07;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 AALEAKICHQIEYFGDF 18
 |||||
 Db 11 AALEAKICHQIEYFGDF 28

JC1494
 ribonucleoprotein La - rat
 N:Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 24-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
 C:Accession: JC1494; S25145
 R:Semsei, I.; Troester, H.; Bartsch, H.; Schwemmler, M.; Igloi, G.L.; Bachmann, M.
 Gene 126, 265-268, 1993
 A:Title: Isolation of rat cDNA clones coding for the autoantigen SS-B/La: Detection of B
 A:Reference number: JC1494; MUID:93246255; PMID:7916708
 A:Accession: JC1494
 A:Molecule type: mRNA
 A:Residues: 1-415 <SEM>
 A:Cross-references: GB:X67859; NID:G55778; PIDN:CAA48043.1; PID:G55779
 A:Experimental source: liver
 C:Comment: This protein associates with a variety of small RNA molecules, most of which
 act as a transcription termination factor.
 C:Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
 C:Keywords: phosphoprotein; RNA binding
 F:112-178/Domain: ribonucleoprotein repeat homology <RRM>
 F:113-118/Region: RNA-binding RNP2 motif
 F:151-158/Region: RNA-binding RNP1 motif
 F:227-415/Domain: phosphorylated #status predicted <PHY>

Query Match 93.8%; Score 91; DB 1; Length 415;
 Best Local Similarity 94.4%; Pred. No. 2e-07;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 AALEAKICHQIEYFGDF 18
 |||||
 Db 11 AALEAKICHQIEYFGDF 28

RESULT 4
 S33817
 ribonucleoprotein La.B - African clawed frog
 N:Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
 C:Accession: S33817; S28544
 R:Schery, D.; Stutz, F.; Lin-Marg, N.; Clarkson, S.G.
 J. Mol. Biol. 231, 196-204, 1993
 A:Title: La proteins from Xenopus laevis. cDNA cloning and developmental expression.
 A:Reference number: S33817; MUID:93287095; PMID:8510143
 A:Accession: S33817
 A:Molecule type: mRNA
 A:Residues: 1-427 <SCH>
 A:Cross-references: EMBL:X68818; NID:964875; PIDN:CAA48716.1; PID:964876
 C:Comment: This protein associates with a variety of small RNA molecules, most of which
 act as a transcription termination factor.
 C:Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
 C:Keywords: phosphoprotein; RNA binding
 F:112-117/Domain: ribonucleoprotein repeat homology <RRM>
 F:113-117/Region: RNA-binding RNP2 motif
 F:150-157/Region: RNA-binding RNP1 motif
 F:227-427/Domain: phosphorylated #status predicted <PHY>

Query Match 63.9%; Score 62; DB 1; Length 427;
 Best Local Similarity 73.3%; Pred. No. 0.015;
 Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 3 LEAKICHQIEYFGDF 17
 |||||
 Db 12 LDRICQIEYFGDF 26

RESULT 5
 S33818
 ribonucleoprotein La.A - African clawed frog
 N:Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
 C:Accession: S33818; S28545

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:33:11; Search time 14.0782 Seconds
(without alignments)
122.988 Million cell updates/sec

Title: US-09-836-073-12

Perfect score: 97

Sequence: 1 AALEAKICHQIEYFGDF 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 78:*
2: D1:1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91	93.8	404	1 S03849	ribonucleoprotein
2	91	93.8	408	1 A31888	ribonucleoprotein
3	91	93.8	415	1 JCI1494	ribonucleoprotein
4	62	63.9	427	1 S33817	ribonucleoprotein
5	58	59.8	428	1 S33818	ribonucleoprotein
6	49	50.5	166	2 T32701	hypothetical prote
7	44	45.4	568	2 C82379	response regulator
8	44	45.4	752	2 G02273	Liv-1 protein - hu
9	43	44.3	390	2 A53773	La/SS-B homolog D-
10	43	44.3	390	2 A53781	ribonucleoprotein
11	43	44.3	1131	2 T15617	hypothetical prote
12	42	43.3	360	2 T15655	hypothetical prote
13	42	43.3	482	2 B35843	lipopolysaccharide
14	42	43.3	497	2 E64227	transcription init
15	42	43.3	499	2 S73810	transcription init
16	42	43.3	541	2 H71887	hypothetical prote
17	42	43.3	542	2 G64627	hypothetical prote
18	42	43.3	573	1 CSBT	catalase (BC 1.11.
19	42	43.3	1250	2 AF1482	hypothetical prote
20	41	42.3	120	2 AF1482	hypothetical prote
21	41	42.3	150	2 A84488	hypothetical prote
22	41	42.3	391	2 H89777	capsular polysacch
23	41	42.3	506	2 T14907	trans-cinnamate 4-
24	41	42.3	540	2 E75633	conserved hypothet
25	41	42.3	902	2 B57147	Mg2+-transporting
26	41	42.3	902	2 AH1058	Mg(2+) transport A
27	41	42.3	988	2 T52134	Zwille protein (im
28	40.5	41.8	386	2 H86870	hypothetical prote
29	40	41.2	157	2 S58067	probable olfactory

30	40	41.2	159	2 C66967	lactylglutacton 1
31	40	41.2	233	2 A81945	probable adenosyl
32	40	41.2	233	2 D81159	5-methylthiadenos
33	40	41.2	529	2 T00677	hypothetical prote
34	40	41.2	591	2 C71460	hypothetical prote
35	40	41.2	658	2 T19487	hypothetical prote
36	40	41.2	674	2 UC5104	transcription init
37	40	41.2	862	2 T01798	hypothetical prote
38	40	41.2	1078	2 B45439	myosin-I, Myr 1c (
39	40	41.2	1079	2 A45438	myosin I alpha cha
40	40	41.2	1094	2 S32404	myosin heavy chain
41	40	41.2	1107	2 C45439	myosin-I, Myr 1b (
42	40	41.2	1136	2 A45439	myosin I heavy cha
43	40	41.2	1217	2 H89863	hypothetical prote
44	40	41.2	2555	2 A40043	notch protein homo
45	39	40.2	147	2 E95015	glycosyl transfera

ALIGNMENTS

RESULT 1
S03849
ribonucleoprotein La - bovine
N/Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
C/Species: Bos primigenius taurus (cattle)
C/Date: 31-Dec-1990 #sequence_revision 26-May-1994 #ext_change 22-Jun-1999
C/Accession: S03849
R/Chan, E.K.V.; Sullivan, K.F.; Tan, E.M.
Nucleic Acids Res. 17, 2233-2244, 1989
A/Title: Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences
A/Reference number: S03848; PMID:89202037; PMID:2468131
A/Accession: S03849
A/Molecule type: mRNA
A/Residues: 1-404 <CHA>
A/Cross-references: EMBL:X13698; NID:g755; PIDN:CAA31986.1; PID:g756
A/Note: Part of this sequence was confirmed by protein sequencing
C/Comment: This protein associates with a variety of small RNA molecules, most of which
act as a transcription termination factor.
C/Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
C/Keywords: blocked amino end; phosphoprotein; RNA binding
F/112-178/Domain: ribonucleoprotein repeat homology <RNM>
F/113-118/Region: RNA-binding RNP2 motif
F/151-158/Region: RNA-binding RNP1 motif
F/228-404/Domain: phosphorylated #status predicted <PHY>

Query Match 93.8%; Score 91; DB 1; Length 404;
Best Local Similarity 94.4%; Pred. No. 2e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AALEAKICHQIEYFGDF 18
DB 11 AALEAKICHQIEYFGDF 28

RESULT 2
A31888
ribonucleoprotein La - human
N/Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B; Sjogren syndrome antigen
C/Species: Homo sapiens (man)
C/Date: 21-May-1990 #sequence_revision 26-May-1994 #ext_change 22-Jun-1999
C/Accession: A31888; S03848; A22956; A61051; S11013; I55553; I70205; I70206; A31273
R/Chan, E.K.V.; Kenan, D.; Martin, B.J.; Keene, J.D.
J. Biol. Chem. 263, 18043-18051, 1988
A/Title: Genomic structure and amino acid sequence domains of the human La autoantigen.
A/Reference number: A31888; PMID:89053970; PMID:3192525
A/Accession: A31888
A/Molecule type: mRNA
A/Residues: 1-408 <CHA>
A/Cross-references: GB:J04205; NID:g178686; PIDN:AAA51885.1; PID:g178687
R/Chan, E.K.V.; Sullivan, K.F.; Tan, E.M.
Nucleic Acids Res. 17, 2233-2244, 1989
A/Title: Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences

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Mon Sep 13 09:36:24 2004

us-09-836-073-4.rpt

Page 7

Search completed: September 10, 2004, 18:00:03
Job time : 42.229 secs

Best Local Similarity 66.7%; Pred. No. 18;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 KICHOIETFFGD 17
DB 136 KIVNOVEYFSD 207

RESULT 13

Q8A8Y5 PRELIMINARY; PRT; 756 AA.
AC Q8A8Y5;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Conserved hypothetical protein.
GN BT1032.
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_Taxid=818;
RN (1)
RP ;SEQUENCE FROM N.A.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=1263928;
RA Xu J., Bjursell M.K., Hamrod J., Deng S., Carmichael L.K.,
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."
RL Science 299:2074-2076 (2003).
DR EMBL; AE016930; AA076139.1; -
DR InterPro; IPR005887; alpha man.
DR TIGRFAMs; TIGR01180; aman2_put; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 756 AA; 86621 MM; 3DBY906689B45D4 CRC64;

Query Match 47.1%; Score 48; DB 16; Length 756;
Best Local Similarity 38.9%; Pred. No. 26;
Matches 7; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 QOOEAKICHOIETFFGD 18
DB 492 EOYDMSVSHALEYIADF 509

RESULT 14

Q81455 PRELIMINARY; PRT; 2349 AA.
AC Q81455;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
GN PFE0230W.
OS Plasmodium falciiparum (Isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_Taxid=36329;
RN (1)
RP SEQUENCE FROM N.A.
RA Devlin K., Baker S., Davies P., Mungal K., Berriman M., Pain A.,
RA Hall N., Bowman S., Churcher C., Quail M., Barrett B.,
RT Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RA MEDLINE=2255708; PubMed=12368867;
RA Hall N., Pain A., Berriman M., Churcher C., Harris B., Harris D.,
RA Mungall K., Bowman S., Atkin R., Baker S., Barron A., Brooks K.,
RA Buckee C.O., Burrows C., Cherevach I., Chillingworth C.,
RA Chillingworth T., Christodoulou Z., Clark L., Clark R., Corton C.,
RA Croft A., Davies R., Davis P., Dear P., Dearden F., Doggett J.,
RA Felwell T., Goble A., Goodhead I., Gilliam R., Hamlin N., Hance Z.,
RA Harper D., Hauser H., Hornsby T., Holroyd S., Horrocks P.,
RA Humphrey S., Jagels K., James K.D., Johnson D., Kerhornou A.,
RA Knights A., Konfortov B., Kyes S., Larke N., Lawson D., Lennard N.,

RA Line A., Maddison M., McLean J., Mooney P., Moule S., Murphy L.,
RA Oliver K., Ormond D., Price C., Quail M.A., Rabinowitsch E.,
RA Rajandream M.A., Rutter S., Rutherford K.M., Sanders M., Simmonds M.,
RA Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens K.,
RA Taylor K., Tivey A., Unwin L., Whitehead S., Woodward J.,
RA Suletan J.E., Craig A., Newbold C., Barrett B.G.
RT "Sequence of Plasmodium falciiparum chromosomes 1, 3-9 and 13."
RL Nature 419:527-531 (2002).
DR EMBL; AL929351; CAD51412.1; -
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0005351; F:sugar porter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0009401; P:phosphoenolpyruvate-dependent sugar phospho. .; IEA.
DR InterPro; IPR000345; C:cyt heme BS.
DR InterPro; IPR002114; Hpr_Serp_S.
DR InterPro; IPR007087; Znf_C2H2.
DR PROSITE; PS00190; CYTOCHROME_C; 4.
DR PROSITE; PS00589; PHS_HPR_SER; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
KW Hypothetical protein.
SQ SEQUENCE 2349 AA; 291035 MM; FC33BFCCE94D563 CRC64;

Query Match 47.1%; Score 48; DB 5; Length 2349;
Best Local Similarity 38.9%; Pred. No. 79;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 QOOEAKICHOIETFFGD 18
DB 853 OEHVREKCHPCERYPTNY 870

RESULT 15

Q87T57 PRELIMINARY; PRT; 329 AA.
AC Q87T57;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Putative lipid A biosynthesis (kdo2-(lauroyl)-lipid IVA
DE acyltransferase.
GN VP0213.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_Taxid=670;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Naito M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.,
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae."
RL Lancet 361:743-749 (2003).
DR EMBL; AP005073; BAC58476.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008415; F:acyltransferase activity; IEA.
DR GO; GO:0009244; F:lipopolysaccharide core region biosynthesis; IEA.
DR InterPro; IPR004960; LipA acyltrans.
DR Pfam; PF03279; Lip_A_acyltrans; 1.
KW Complete proteome.
SQ SEQUENCE 329 AA; 37996 MM; 3F3C6C41D91E5D0C CRC64;

Query Match 46.6%; Score 47.5; DB 16; Length 329;
Best Local Similarity 44.4%; Pred. No. 13;
Matches 8; Conservative 7; Mismatches 2; Indels 1; Gaps 1;

QY 1 QOOEAKICHOIETFFGD 17
DB 275 EOEDARTCNLEAYFVGD 292

AC O44678; 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein C14C6.12.
 GN C14C6.12.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_Taxid=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA Wilson R.;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RL investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA David M., Wohlmann P., Bauer C., Antoniou B.;
 RT "The sequence of C. elegans cosmid C14C6.";
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RT Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.; (AUG-2003) to the EMBL/GenBank/DBJ databases.
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF039051; AAB94258.2; -
 KW Hypothetical protein.
 SQ SEQUENCE 91 AA; 10407 MW; D16D2BD4011F8762 CRC64;
 QY 2 QOEAKTCHOLEYFGDF 18
 DB 2 QDVYKICNVIEYMTGDF 18
 Query Match 49.0%; Score 50; DB 5; Length 91;
 Best Local Similarity 58.8%; Pred. No. 1.5;
 Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

RESULT 12
 080567 PRELIMINARY; PRT; 545 AA.
 ID 080567
 AC 080567; Q9G5X1;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Expressed protein (VIRF-interacting protein FIP1) (Hypothetical
 DE protein) (AC2943970/F6E13.10).
 GN AT2943970 OR F6E13.10/AT2943970.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid2; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Rounsley S.D., Kaul S., Lin X., Ketchum K.A., Crosby M.L.,
 RA Brandon R.C., Sykes S.M., Mason T.M., Kerlavage A.R., Adams M.D.,
 RA Somerville C.R., Venter J.C.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Lin X.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Town C.D., Kaul S.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Mayda E., Tzifira T., Cilevsky V.;
 RT "Arabidopsis thaliana VIRF-interacting protein FIP1.";
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M.,
 RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Yamamura Y., Yu G.,
 RA Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C.,
 RA Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M.,
 RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
 RA Southwick A., Tracy S.E., Shinzaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RT "Full length cDNA of gene F6E13.10/At2943970 (GI:3212854)." ;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Shinn P.,
 RA Banh J., Bowser L., Carninci P., Chung M.K., Goldsmith A.D.,
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
 RA Nguyen M., Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yu G., Shinzaki K., Davis R.W., Theologis A., Ecker J.R.;
 RT "Arabidopsis cDNA clones." ;
 RN [7]
 RP SEQUENCE FROM N.A.
 RA Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
 RA Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,
 RA Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,
 RA Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinzaki K.,
 RA Davis R.W., Theologis A., Ecker J.R.;
 RT "Arabidopsis cDNA clones." ;
 RN [8]
 RP SEQUENCE FROM N.A.
 RA Shinn P., Chen H., Cheuk R., Kim C.J., Banh J., Bowser L.,
 RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
 RA Lee J.M., Lin J., Miranda M., Narusaka M., Narusaka M., Nguyen M.,
 RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
 RA Shinzaki K., Davis R.W., Theologis A., Ecker J.R.;
 RT "Arabidopsis ORF clones." ;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC004005; AAC23405.2; -
 DR EMBL; AF332565; AA06847.1; -
 DR EMBL; AY056238; AL07087.1; -
 DR EMBL; AF375410; AAK52994.1; -
 DR EMBL; AF367277; AAK56266.1; -
 DR EMBL; AY129474; AAM91060.1; -
 DR JIR; T00677; T00677.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR InterPro; IPR002344; Lupa La.
 DR InterPro; IPR006630; Lupa La_dom.
 DR Pfam; PF05383; La; 1.
 DR PRINTS; PR00302; LUPUSLA.
 KW Hypothetical protein.
 SQ SEQUENCE 545 AA; 60589 MW; E1A933261FE1ED80 CRC64;
 Query Match 47.1%; Score 48; DB 10; Length 545;

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RA. Baggia N Mann E.R., Foster T.J., Lee J.C.;  
RL Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; U81973; AAC4609.1; -.  
DR HSSP; P27828; 1F6D.  
DR GO; GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity; IEA.  
DR GO; GO:0009103; P:lipo polysaccharide biosynthesis; IEA.  
DR GO; GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.  
DR InterPro; IPR003331; Epimerase_2.  
DR Pfam; PF02350; Epimerase_2; 1.  
DR TIGRFAMs; TIGR00236; wecB; 1.  
SQ SEQUENCE 391 AA; 44328 MW; B0105FE690DB7CFID CRC64;  
  
Query Match 51.0%; Score 52; DB 2; Length 391;  
Best Local Similarity 60.0%; Pred. No. 2.9;  
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0  
  
QY 2 QOEAKEICHOLEYRYFG 16  
Db | : ||| |||||  
362 QASRRICEALEYYRG 376  
  
RESULT 10  
ID X 099XK57 PRELIMINARY; PRT; 391 AA.  
AC O99XK57;  
DT 01-JUN-2001 (TrEMBLrel.17, Created)  
DT 01-JUN-2001 (TrEMBLrel.17, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel.24, Last annotation update)  
DE Capsular polysaccharide synthesis enzyme CapSP.  
GN CAP OR SAV0164 OR SA0159.  
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and  
OS Staphylococcus aureus (strain N315).  
OC Bacacteria; Firmicutes; Bacillales; Staphylococcaceae.  
OX NCBI_TaxID=158878, 158879;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECTIS=S.aureus (strain Mu50), and S.aureus (strain N315);  
RX MEDLINE=21311952; PubMed=11418146;  
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,  
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,  
RA Kanemori M., Matsunaru H., Maruyama A., Murakami H., Hosoyama A.,  
RA Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Katco C.,  
RA Sekimizu K., Hirakawa H., Kunihara S., Goto S., Yabuzaki J.,  
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shibata T.,  
RA Hatotani M., Ogasawara N., Hayashi H., Hiratsuku K.;  
RT "Whole genome sequencing of methicillin-resistant Staphylococcus  
RT aureus." ;  
RL Lancet 357:1225-1240 (2001).  
DR EMBL; AP003358; BABS6326.1; -.  
DR EMBL; AP003129; BAB1379.1; -.  
DR PIR; H89777; H89777.  
DR HSSP; P27828; 1F6D.  
DR GO; GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity; IEA.  
DR GO; GO:0009103; P:lipo polysaccharide biosynthesis; IEA.  
DR GO; GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.  
DR InterPro; IPR003331; Epimerase_2.  
DR Pfam; PF02350; Epimerase_2; 1.  
DR TIGRFAMs; TIGR00236; wecB; 1.  
KM Complete proteome.  
SQ SEQUENCE 391 AA; 44372 MW; DDDFFFA715BCCECC CRC64;  
  
Query Match 51.0%; Score 52; DB 16; Length 391;  
Best Local Similarity 60.0%; Pred. No. 2.9;  
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0  
  
QY 2 QOEAKEICHOLEYRYFG 16  
Db | : ||| |||||  
362 QASRRICEALEYYRG 376  
  
RESULT 11  
ID X 044678 PRELIMINARY; PRT; 91 AA.  
AC 044678
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RESULT 5
Q8ZT10 PRELIMINARY; PRT; 401 AA.
ID Q8ZT10
AC Q8ZT10
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to sjogren syndrome antigen B (Autoantigen Ia).
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
NCBI_TaxID=7955;
RX [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Body;
RC Straussberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 401 AA; 46138 MW; 2EF032FDD3916291 CRC64;

Query Match
Best Local Similarity 56.9%; Score 58; DB 13; Length 401;
Pred. No. 0.31;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 EAKICHQIEYYFGD 17
Db 11 EKKAIEQIEYYFGD 24

RESULT 6
Q8T8V5 PRELIMINARY; PRT; 390 AA.
ID Q8T8V5
AC Q8T8V5
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE A122034P.
GN LA OR CG10922.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
RX [1]
RN SEQUENCE FROM N.A.
RP Stapleton M., Brokstein P., Hong L., Aspayani A., Carlson J.,
RA Campe M., Chavez C., Dorett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez W., Guarin H., Krommiller B., Li P., Liso G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Patagas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Ceuliker S.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY052527; A168124.1; -.
DR FlyBase; FBgn011638; la.
DR GO; GO:0008058; F:5S rRNA primary transcript binding; IEA.
DR GO; GO:0003723; F:RNA binding; NAS.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; la; 1.

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DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 390 AA; 44869 MW; 797FDE26B903C909 CRC64;

Query Match
Best Local Similarity 55.9%; Score 57; DB 5; Length 390;
Pred. No. 0.44;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 QQAKICHQIEYYFGD 17
Db 49 KQERAIRQVEYYFGD 64

RESULT 7
Q8NYN8 PRELIMINARY; PRT; 381 AA.
ID Q8NYN8
AC Q8NYN8
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Capsular polysaccharide synthesis enzyme Cap8P.
GN CAP8P OR MW0139.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=196620;
RX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiratsuku K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).
DR EMBL; AP004822; BAB94004.1; -.
DR GO; GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity; IEA.
DR GO; GO:0009103; F:lipopolysaccharide biosynthesis; IEA.
DR GO; GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.
DR InterPro; IPR003331; Epimerase_2.
DR Pfam; PF02350; Epimerase_2; 1.
DR TIGRFAMs; TIGR00236; wecB; 1.
KM Complete proteome.
SQ SEQUENCE 381 AA; 43106 MW; 125E4D5D1904779C CRC64;

Query Match
Best Local Similarity 51.0%; Score 52; DB 16; Length 381;
Pred. No. 2.9;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 QQAKICHQIEYYFG 16
Db 352 QASRRICEAIEYYFG 366

RESULT 8
P72382 PRELIMINARY; PRT; 391 AA.
ID P72382
AC P72382
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CAP8P.
GN CAP8P.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
RX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=Becker;
RC MEDLINE=96178981; PubMed=8606192;

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DR GO:0005634; C:nucleus; IDA.
 DR InterPro; IPR002344; Lupus_La.
 DR InterPro; IPR006630; Lupus_La_dom.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF05383; La; 1.
 DR Pfam; PF00076; rtm; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 DR SEQUENCE 381 AA; 43891 MW; 2E2DEFF1452C0F0E9 CRC64;

Query Match 85.3%; Score 87; DB 11; Length 381;
 Best Local Similarity 100.0%; Pred. No. 5.2e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EAKICHOIEYFGDF 18
 DB 14 EAKICHOIEYFGDF 28

RESULT 2

Q8BTU4 PRELIMINARY; PRT; 415 AA.
 AC Q8BTU4;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Sjogren syndrome antigen B.
 GN SSB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MOD; TISSUE=Thymus;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The PANThOM Consortium;
 RA The RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 DR EMBL; AK088677; BAC04098.1; -
 DR MGD; MGI:98423; Ssb.
 DR GO; GO:0005634; C:nucleus; IDA.
 DR InterPro; IPR002344; Lupus_La.
 DR InterPro; IPR006630; Lupus_La_dom.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF05383; La; 1.
 DR Pfam; PF00076; rtm; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PS50102; RRM; 1.
 DR PROSITE; PS00030; RRM_RNP_1; 1.
 DR SEQUENCE 415 AA; 47657 MW; A7545CT686AC8363 CRC64;

Query Match 85.3%; Score 87; DB 11; Length 415;
 Best Local Similarity 100.0%; Pred. No. 5.7e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EAKICHOIEYFGDF 18
 DB 14 EAKICHOIEYFGDF 28

RESULT 3

Q7ZTK2 PRELIMINARY; PRT; 427 AA.
 AC Q7ZTK2;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Similar to lupus LA protein homolog B.

OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=embryo;
 RC Klein S.; Strassberg R.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC046654; AAH46654.1; -
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003723; P:RNA binding; IEA.
 DR InterPro; IPR002344; Lupus_La.
 DR InterPro; IPR006630; Lupus_La_dom.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF00076; rtm; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 2.
 DR PROSITE; PS50102; RRM; 1.
 DR PROSITE; PS00030; RRM_RNP_1; 1.
 DR SEQUENCE 427 AA; 48996 MW; 1E7CD82D8AB9C69A CRC64;

Query Match 64.7%; Score 66; DB 13; Length 427;
 Best Local Similarity 78.6%; Pred. No. 0.016;
 Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 EAKICHOIEYFGD 17
 DB 13 DTICHOIEYFGD 26

RESULT 4
 Q8QCH15 PRELIMINARY; PRT; 206 AA.
 ID Q8QCH15;
 AC Q8QCH15;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Untranslated region binding-protein.
 GN UBP.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA L'Ecuylar T.J., Fang H.-L.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF467897; AAL76269.1; -
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003723; P:RNA binding; IEA.
 DR InterPro; IPR002344; Lupus_La.
 DR InterPro; IPR006630; Lupus_La_dom.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF05383; La; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR Pfam; PF00076; rtm; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PS50102; RRM; 1.
 DR PROSITE; PS00030; RRM_RNP_1; 1.
 DR SEQUENCE 206 AA; 23992 MW; 965B62F7DFEB90E9 CRC64;

Query Match 63.7%; Score 65; DB 13; Length 206;
 Best Local Similarity 78.6%; Pred. No. 0.011;
 Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 EAKICHOIEYFGD 17
 DB 14 ESKICHOIEYFGN 27

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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:29:01 ; Search time 41.229 Seconds
(without alignments)
137.751 Million cell updates/sec

Title: US-09-836-073-4

Perfect score: 102
Sequence: 1 QOOEAKICHQIEYFGDF 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTRMBL_25:*
1: sp_bacteria:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	85.3	381	11	Q9CYB9
2	87	85.3	415	11	Q8BRT4
3	66	64.7	427	13	Q7ZTK2
4	65	63.7	206	13	Q8OH15
5	58	56.9	401	13	Q7ZPT0
6	57	55.9	390	5	Q8T8V5
7	52	51.0	381	16	Q8NYN8
8	52	51.0	391	2	P72382
9	52	51.0	391	16	Q9X57
10	52	51.0	391	16	Q9X57
11	50	49.0	391	5	Q4678
12	48	47.1	545	10	Q80567
13	48	47.1	756	16	Q8ABY5
14	48	47.1	2349	5	Q81455
15	47.5	46.6	329	16	Q87R57
16	47	46.1	396	5	Q01806

ALIGNMENTS

17	47	46.1	411	10	Q9FL36	Q9FL36 arabidopsis
18	47	46.1	422	10	Q94A38	Q94A38 arabidopsis
19	47	46.1	472	16	Q8D9F3	Q8D9F3 vibrio vuln
20	47	46.1	547	10	Q7XVC6	Q7XVC6 oryza sativ
21	46	45.1	478	16	Q8TGS8	Q8TGS8 vibrio para
22	46	45.1	642	16	Q9KEU7	Q9KEU7 bacillus ha
23	45	44.1	352	16	Q8YMW5	Q8YMW5 anabaena sp
24	45	44.1	481	10	Q8LMP9	Q8LMP9 oryza sativ
25	45	44.1	568	16	Q9KXL7	Q9KXL7 vibrio chol
26	45	44.1	749	2	Q84ID5	Q84ID5 bacteroides
27	45	44.1	1330	5	Q9G0A3	Q9G0A3 droso
28	45	44.1	1858	5	Q8MSU5	Q8MSU5 droso
29	45	44.1	2145	5	Q9W003	Q9W003 droso
30	44.5	43.6	114	16	Q7UT07	Q7UT07 rhodospirill
31	44.5	43.6	928	10	Q9LJ02	Q9LJ02 oryza sativ
32	44	43.1	96	10	Q9AUG1	Q9AUG1 brassica ol
33	44	43.1	329	5	Q8T907	Q8T907 droso
34	44	43.1	329	5	Q9VAX9	Q9VAX9 droso
35	44	43.1	383	10	Q7YIE1	Q7YIE1 oryza sativ
36	44	43.1	472	5	Q95PU7	Q95PU7 chironomus
37	44	43.1	1401	5	Q81SD4	Q81SD4 plasmodium
38	43.5	42.6	788	17	Q58603	Q58603 pyrococcus
39	43.5	42.6	1037	16	Q8XE22	Q8XE22 escherichia
40	43.5	42.6	1037	16	Q8TF84	Q8TF84 escherichia
41	43.5	42.6	1037	16	Q83QMS	Q83QMS shigella fl
42	43	42.2	119	10	Q9ZP89	Q9ZP89 neurotheca
43	43	42.2	240	16	Q8RE78	Q8RE78 fusobacteri
44	43	42.2	255	5	Q9NGG5	Q9NGG5 droso
45	43	42.2	255	5	Q9NEL7	Q9NEL7 droso

RESULTS

Q9CYB9	PRELIMINARY;	PRT;	381 AA.
AC	Q9CYB9;		
DT	01-JUN-2001 (TREMBLrel. 17, Created)		
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)		
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)		
DE	Sjogren syndrome antigen B.		
GN	SSB.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CS7BL/6J; TISSUE=Embryo;		
RX	MEDLINE=21085660; Pubmed=11217851;		
RA	Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
RA	Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,		
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,		
RA	Salto T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Salto R.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,		
RA	Kiehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Ouchibuchi J.,		
RA	Schirml L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA	Sakai K., Okido T., Futuno M., Aono H., Baldarelli R., Barsh G.,		
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,		
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,		
RA	Lyons P., Marchionni L., Maehima J., Mazzarelli J., Monbetsu P.,		
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		
RA	Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,		
RA	Suzuki H., Toyo-oka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,		
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohetsuki S.,		
RA	Hayashizaki Y.,		
RT	"Functional annotation of a full-length mouse cDNA collection."		
RL	Nature 409:885-890(2001).		
DR	EMBL; AK017822; BAB30957.1; -.		
DR	MED; MGI:98423; SSB.		

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NUMB36;
 RX MEDLINE=91310597; PubMed=1856180;
 RA Wu L., Welker N.E.;
 RT "Cloning and characterization of a glutamine transport operon of
 RT Bacillus stearotherophilus NUB36: effect of temperature on
 RT regulation of transcription.";
 RL J. Bacteriol. 173:4877-4888(1991).
 CC -1- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
 CC FOR GLUTAMINE. PROBABLY RESPONSIBLE FOR ENERGY COUPLING TO THE
 CC TRANSPORT SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Membrane-associated (Potential).
 CC -1- INDUCTION: By lack of glutamine.
 CC -1- SIMILARITY: Belongs to the ABC transporter family.
 CC -----
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 CC -----
 CC EMBL; M61017; AAA22483.1; -.
 DR PIR; A42478; A42478.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR003439; ABC_Transporter.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
 DR Amino-acid transporter; Transport; Membrane; ATP-binding.
 FT NP BIND 34 41 ATP (BY SIMILARITY).
 SQ SEQUENCE 242 AA; 27436 MW; 102B1C5B32F31C8 CRC64;
 Query Match 41.2%; Score 42; DB 1; Length 242;
 Best Local Similarity 60.0%; Pred. No. 9.8;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 9 HQLEYVFGDF 18
 DB 5 HQVKKYIGDF 14
 RESULT 14
 FOL2 MOUSE STANDARD; PRT; 251 AA.
 ID FOL2_MOUSE
 AC Q05655;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Folate receptor beta precursor (FR-beta) (Folate receptor 2) (Folate-
 DE binding protein 2).
 GN FOLR2 OR FOLBP2 OR FBP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91373339; PubMed=1894617;
 RA Brigle K.E., Westin E.H., Houghton M.T., Goldman I.D.;
 RT "Characterization of two cDNAs encoding folate-binding proteins from
 RT L1210 murine leukemia cells. Increased expression associated with a
 RT genomic rearrangement.";
 RL J. Biol. Chem. 266:17243-17249(1991).
 CC (2)
 RP SEQUENCE OF 1-49 FROM N.A.
 RX MEDLINE=94140851; PubMed=8307991;
 RA Brigle K.E., Seither R.L., Westin E.H., Goldman I.D.;
 RT "Increased expression and genomic organization of a folate-binding

RT protein homologous to the human placental isoform in L1210 murine
 RT leukemia cell lines with a defective reduced folate carrier.";
 RL J. Biol. Chem. 269:4267-4272(1994).
 CC -1- FUNCTION: Binds to folate and reduced folic acid derivatives and
 CC mediates delivery of 5-methyltetrahydrofolate to the interior of
 CC cells.
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
 CC similarity).
 CC -1- PTM: Eight disulfide bonds are present (Probable).
 CC -1- SIMILARITY: Belongs to the folate receptor family.
 CC -----
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 CC -----
 CC EMBL; M64817; AAA37599.1; -.
 DR PIR; L25338; AAA37594.1; -.
 DR PIR; B40969; B40969.
 DR MGD; MGI:95569; FoltR2.
 DR InterPro; IPR004269; Folt_chemrecept.
 DR Pfam; PF03024; Folate_rec; 1.
 DR Receptor; Glycoprotein; Signal; Placenta; Folate-binding; Membrane;
 KW GPI-anchor; Multigene family; Lipoprotein.
 FT SIGNAL 1 20
 FT CHAIN 21 227
 FT PROPEP 228 251
 FT LIPIID 227 227
 FT CARBOHYD 62 62
 FT CARBOHYD 193 193
 SQ SEQUENCE 251 AA; 28821 MW; 8404EACB1BFECC7 CRC64;
 Query Match 40.2%; Score 41; DB 1; Length 251;
 Best Local Similarity 75.0%; Pred. No. 15;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 8 HQLEYVFGDF 15
 DB 167 CHTPEYFGDF 174
 RESULT 15
 2173 HUMAN STANDARD; PRT; 539 AA.
 ID 2173_HUMAN
 AC Q12899;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Zinc finger protein 173 (Tripartite motif-containing protein 26) (Acid
 DE finger protein) (AFP).
 GN TRIM26 OR ZNF173.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96079113; PubMed=8530076;
 RA Chu T.W., Caposela A., Coleman R., Goel V.L., Nallur G., Gruen J.R.;
 RT "Cloning of a new 'finger' protein gene (ZNF173) within the class I
 RT region of the human MHC.";
 RL Genomics 29:229-239(1995).
 CC (2)
 RP SEQUENCE FROM N.A.
 RX Shima S., Tamiya G., Oka A., Inoko H.;
 RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Skin;

DR PIR; T43542; T43542.
 DR Genedb_Spombe: SPAC57A10.10c; -
 DR InterPro: IPR002344; Lupus_La.
 DR InterPro: IPR006630; Lupus_La_dcm.
 DR InterPro: IPR000504; RNA_rec_mol.
 DR Pfam: PF05383; La; 1.
 DR Pfam: PF00076; rrm; 1.
 DR PRINTS: PR00302; LUPUSLA.
 DR SMART: SM00715; La; 1.
 DR SMART: SM00360; RRM; 1.
 DR PROSITE: PS0102; RRM; 1.
 DR PROSITE: PS00030; RRM_RNP_1; FALSE_NEG.
 DR RNA-binding; Nuclear protein.
 DR DOMAIN 154 235 RNA-BINDING (RRM).
 FT CONFLICT 188 188 M -> I (IN REF. 1 AND 2).
 SQ SEQUENCE 298 AA; 34616 MW; 6486AB9940B87F4 CRC64;
 Query Match 45.1%; Score 46; DB 1; Length 298;
 Best Local Similarity 50.0%; Pred. No. 2.6;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 4 EAKICHOIEYFGD 17
 DB 64 EAEVLKQVERFYFD 77
 RESULT 10
 ID TCMO_PETCR STANDARD; PRT; 506 AA.
 AC 04303;
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Trans-cinnamate 4-monooxygenase (EC 1.14.13.11) (Cinnamic acid
 4-hydroxylase) (CA4H) (C4H) (P450C4H) (Cytochrome P450 73).
 GN CYP7A10 OR CYP73.
 OS Petroselinum crispum (Parsley) (Petroselinum hortense).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Campanulids; Apiales; Apiaceae; Apioidae; apioid superclade;
 OC Apium clade; Petroselinum.
 OC NCBI_TaxID=4043;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95320184; PubMed=7597051;
 RA Logemann E., Parniske M., Hahlbrock K.;
 RT "Modes of expression and common structural features of the complete
 phenylalanine ammonia-lyase gene family in parsley.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:5905-5909(1995).
 CC -1- FUNCTION: Controls carbon flux to pigments essential for
 pollination or UV protection, to numerous phycoalexins synthesized
 by plants when challenged by pathogens, and to lignins.
 CC -1- CATALYTIC ACTIVITY: Trans-cinnamate + NADPH + O(2) = 4-
 hydroxycinnamate + NADP(+) + H(2)O.
 CC -1- PATHWAY: Lignin biosynthesis.
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
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 CC -----
 DR EMBL; L38898; AAC41660.1; -
 DR PIR; T14907; T14907.
 DR InterPro: IPR001128; Cytochrome_P450.
 DR Pfam; PF00067; P450; 1.
 DR PRINTS; PR00385; P450.
 DR PROSITE; PS00086; CYTOCHROME_P450; 1.
 RN Oxidoreductase; Monooxygenase; Heme; NADP.

FT METAL 448 448 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 SQ SEQUENCE 506 AA; 58047 MW; 32F00E959D69CFC CRC64;
 Query Match 44.1%; Score 45; DB 1; Length 506;
 Best Local Similarity 37.5%; Pred. No. 6.8;
 Matches 6; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
 QY 3 OEAKICHOIEYFGDF 18
 DB 213 ERSRLAQSFHYHGF 228
 RESULT 11
 ID ACRD_ECOLI STANDARD; PRT; 1037 AA.
 AC P24177; P76971; P77178; 046715;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable aminoglycoside efflux pump (Acriflavine resistance protein
 D).
 GN ACRD OR B2470.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OC NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12; Bertrand K.P.;
 RA Niles M.L.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 RP SEQUENCE FROM N.A.
 RA "D", Cook D.N., Alberti M., Nikaido H., Hearst J.B.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Colado-Vides J., Glaser J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97349980; PubMed=9205837;
 RA Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,
 RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
 RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
 RA Osima T., Oyama S., Saito N., Sempel G., Satoh Y., Sivasubraman S.,
 RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
 RA Yamagata S., Horiiuchi T.;
 RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
 K-12 genome corresponding to 50.0-68.8 min on the linkage map and
 analysis of its sequence features.";
 RL DNA Res. 4:91-113(1997).
 RN [5]
 RP SEQUENCE OF 998-1037 FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=92355499; PubMed=1644752;
 RA Bouvier J., Richard C., Higgins W., Bogler O., Stragier S.;
 RT "Cloning, characterization, and expression of the *dapB* gene of
 Escherichia coli.";
 RL J. Bacteriol. 174:5265-5271(1992).
 RN [6]
 RP FUNCTION.
 RX MEDLINE=20158894; PubMed=10692383;
 RA Rosenberg E.Y., Ma D., Nikaido H.;
 RT "AcrD of Escherichia coli is an aminoglycoside efflux pump.";
 RL J. Bacteriol. 182:1754-1756(2000).

FT	CONFLICT	182	183	KH -> NS (IN REF. 1).
FT	CONFLICT	283	283	A -> R (IN REF. 1).
FT	CONFLICT	329	329	K -> N (IN REF. 1).
SO	SEQUENCE	390 AA;	44884 MM;	A809288B9046A5 CRC64;
Query Match:		55.9%;	Score 57;	DB 1; Length 390;
Best Local Similarity		62.5%;	Pred. No. 0.05;	
Matches 10;	Conservative		2; Mismatches 4;	Indels 0; Gaps 0

```
QY      2 QOEAKICHQIEYFGD 17
          :||| | :|||
DB      49 KOERAIRQVEYFGD 64
```

RESULT 8	LA_AEDAL	STANDARD;	PRT;	383 AA.
LA_ID	LA_AEDAL			
AC	O26457;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	The protein homolog (La ribonucleoprotein) (La autoantigen homolog)			
OS	Aedes albopictus (Forest day mosquito).			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes.			
OX	NCBI_TaxID=7160;			
RP	[11]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=96135233; PubMed=8551578;
RT "Pardigon N., Strouse J.H.,
RL J. Virol. 70:1173-1181 (1996).
CC -1 FUNCTION: May be involved in transcription termination by RNA
CC polymerase II. Binds RNA and DNA. Binds to the 3' end of the
CC minus strand of Sindbis virus RNA. This may be significant for
CC Sindbis virus RNA replication.
CC -1 SUBCELLULAR LOCATION: Nuclear. Primarily nuclear, but significant
CC amounts are present in the cytoplasm.
CC -1 SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
CC -1 SIMILARITY: TO VERTEBRATE PROTEIN LA.
CC -----
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```

CC -----
DR EMBL; S80954; AAB35931.1; -.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS00102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; FALSE NEG.
FW K+ binding; Nuclear protein; DNA-binding.
KT DOMAIN 141 228 RNA-BINDING (RRM).
SQ SEQUENCE 383 AA; 44430 MW; 4B5CC8F21C40F452 CRC64;

```

Query Match	50.0%;	Score 51;	DB 1;	Length 383;
Best Local	Similarity	64.3%;	Pred. No. 0.51;	
Matches	9;	Conservative	1;	Mismatches 4; Indels 0; Gaps 0

```
QY      4 EAKICHQIEYFGD 17
         |||:|||||
Db      44 EASTIRQLEYYFGD 57
```

RESULT 9	
LAH1_SCHPO	STANDARD;
ID LAH1_SCHPO	PRT; 298 AA
0070E8-0123C3-0104E8	

AC P81056; U13562; U14350;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE La protein homolog (La ribonucleoprotein) (La autoantigen homolog).
GN SLAI OR SPAC57A10.10C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_taxid=4896;

RN
RP [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=98067398; PubMed=9404894;
RA van Horn D.J., Yoo C.J., Xue D., Shi H., Molin S.L.;
RT "The La protein in Schistosoma cercariae pombe: a conserved yet
RL dispensable phosphoprotein that functions in tRNA maturation."
RN RNA 3.11434-1443(1997).
RP [2]
RN
RP SEQUENCE FROM N.A.
RL Utsunomura R.R.U.;
RA Submitted (FEB-1998) to the EMBL/GenBank/DDJ databases.

RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=31849401. PubMed=11860360.

KA MEDLINE=21047401; PubMed=11033300;
RA Wood V., Gwilliam R., Rajadream M.A., Lyne M., Lyne R., Stewart A
RA Sgourous J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.
RA Holroyd S., Hornsby T., Howarth S., Huckle E. J., Hunt S., Jagels K.

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,

RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead N., Woodward I., Wolcott C., Yarrow D., Zebben I., Zimmerman B.

RA Woldward U., Volkscitil G., Aert K., Koudcn U., Gilmuplcrz D.,
RA Wcltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzvm K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.-J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.

RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Bartell B.G., Nurse P.;
"The genome sequence of *Schizosaccharomyces pombe*." ;
RT

CC -1- FUNCTION: Binds to the precursors of polymerase III RNAs.
CC Functions in tRNA maturation.
CC 1- SUBCELLULAR LOCATION: Nuclear (Probable)

CC - SIMILARITY: TO VERTEBRATE PROTEIN LA.
CC - SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
CC - SUBCELLULAR LOCATION: nuclear (cytosolic).
CC

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 CC -----
 DR EMBL; AF022949; AAB82145.1; -.
 DR EMBL; AF011371; BA024081.1; .

DR EMBL; AB011317; EMBL3501.4; -
DR EMBL; Z94864; CAB08173.1; -
DR PIR; T38937; T38937.

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CC EMBL; X68817; CAA48715.1; -

DR PIR; S33818; S33818.

DR InterPro; IPR002344; Lupsus_La.

DR InterPro; IPR006630; Lupsus_La.dom.

DR InterPro; IPR000504; RNA_rec_mot.

DR Pfam; PF05383; Rrm; 1.

DR Pfam; PF00076; Rrm; 1.

DR PRINTS; PR00302; LUPUSIA.

DR SMART; SM00715; LA; 1.

DR SMART; SM00360; RRM; 1.

DR PROSITE; PS50102; RRM; 1.

DR PROSITE; PS00030; RRM_RNP_1; 1.

DR RNA-binding; Nuclear Protein; phosphorylation.

DR RNA-binding; Nuclear Protein; phosphorylation.

FT DOMAIN 111 203 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

FT DOMAIN 196 212 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

FT DOMAIN 316 332 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

SO SEQUENCE 428 AA; 48864 MW; AEB3A38B7D2E3EC3 CRC64;

Query Match 64.7%; Score 66; DB 1; Length 428;
Best Local Similarity 78.6%; Pred. No. 0.0018;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 EAKICHOIEYFED 17
: ||| |||||
Db 14 DTKICEQIEYFED 27

RESULT 7
LA DROME STANDARD; PRT; 390 AA.

AC P40796; Q24375; Q9VIN2;
DT 01-FEB-1995 (Rel. 31, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE La protein homolog (La ribonucleoprotein) (La autoantigen homolog).
GN LA OR CG10922.

OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Canton-S; TISSUE=Ovary;
RX MEDLINE=94309632; PubMed=8035794;
RA Bai C., Li Z., Tollas P.P.;
RT "Developmental characterization of a Drosophila RNA-binding protein homologous to the human systemic lupus erythematosus-associated La/SS-B autoantigen.";
RT Mol. Cell. Biol. 14:5123-5129(1994).
RL [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=94309661; PubMed=8035818;
RA Yoo C.J., Wolin S.L.;
RT "A protein from Drosophila melanogaster and Saccharomyces cerevisiae: a yeast homolog of the La autoantigen is dispensable for growth.";
RT Mol. Cell. Biol. 14:5412-5424(1994).
RL [3]
RN SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amaratunga C., Scherer S.E., Li P.W., Hopkins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brudon R.C., Rogers J.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Balliw R.M., Basu A., Baxendale J., Bayraktaroglu I., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Betman B.P., Bhandari D., Bolshakov S.,
RA Borova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fester C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lascko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Matrei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mialshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Murry D.M., Nelson D.L.,
RA Nelson D.M., Nelson K.A., Nixon K., Nusskern D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
RA Sytkes R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -1- FUNCTION: May be involved in transcription termination by RNA polymerase III. Binds RNA and DNA. Binds to precursors of RNA development. III transcripts. May play a specialized role during fly development.
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- DEVELOPMENTAL STAGE: Expressed throughout embryonic, larval, pupal, and adult development. Expression throughout the embryo is followed by a restricted pattern of mesodermal expression that is later confined to the visceral mesoderm, gonads, gut, and salivary glands.
CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
CC -1- SIMILARITY: TO VERTEBRATE PROTEIN LA.
CC -----
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CC EMBL; U07652; AAA20518.1; -
CC EMBL; L32988; AAA21776.1; -
CC EMBL; AEO03666; AAF53885.1; -
CC PIR; A53773; A53773.
CC PIR; A53781; A53781.
CC FLYBase; FBgn0011638; La.
CC GO; GO:0008098; F:5S rRNA primary transcript binding; IDA.
CC GO; GO:0003723; F:5S rRNA binding; NAS.
CC InterPro; IPR002344; Lupsus_La.
CC InterPro; IPR006630; Lupsus_La.dom.
CC InterPro; IPR000504; RNA_rec_mot.
CC Pfam; PF05383; Rrm; 1.
CC Pfam; PF00076; Rrm; 1.
CC PRINTS; PR00302; LUPUSIA.
CC SMART; SM00715; LA; 1.
CC SMART; SM00360; RRM; 1.
CC PROSITE; PS50102; RRM; 1.
CC PROSITE; PS00030; RRM_RNP_1; 1.
CC RNA-binding; Nuclear Protein; phosphorylation.
CC RNA-binding; Nuclear Protein; phosphorylation.
FT DOMAIN 149 234 RNA-BINDING (RRM).
FT CONFLICT 169 169 A -> T (IN REF. 1).

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X67859; CAA48043.1; -
CC PIR; JCI494; JCI494.
CC InterPro; IPR002344; Lupus_La.
CC InterPro; IPR006630; Lupus_La.dom.
CC InterPro; IPR00504; RNA_rec_mot.
CC Pfam; PF05383; La; 1.
CC SMART; SM00715; LA; 1.
CC PRINTS; PR00302; LUPUSLA.
CC SMART; SM00715; LA; 1.
CC SMART; SM00360; RRM; 1.
CC PROSITE; PS50102; RRM; 1.
CC PROSITE; PS00030; RRM_RNP_1; 1.
CC RNA-binding; Nuclear protein; Phosphorylation.
CC DOMAIN 111 187 RNA-BINDING (RRM).
CC SEQUENCE 415 AA; 47777 MW; 033FD9CC1E475F98 CRC64;
SQ
Query Match 85.3%; Score 87; DB 1; Length 415;
Best Local Similarity 100.0%; Pred. No. 5.5e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 EAKICHQIEYFGDF 18
Db 14 EAKICHQIEYFGDF 28
RESULT 5
LAB_XENLA STANDARD; PRT; 427 AA.
ID LAB_XENLA
AC P28049;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Lupus La protein homolog B (La ribonucleoprotein B) (La autoantigen
DE homolog B).
GN LAB1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocyte;
RA MEDLINE=93287095; PubMed=8510143;
RA Scherly D., Stutz F., Lin-Marg N., Clarkson S.G.;
RT "La proteins from Xenopus laevis. cDNA cloning and developmental
RT expression.";
RL J. Mol. Biol. 231:196-204(1993).
CC -1- FUNCTION: La protein plays a role in the transcription of RNA
CC polymerase III. It is most probably a transcription termination
CC factor. Binds to the 3' terminus of virtually all nascent
CC polymerase III transcripts (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- DEVELOPMENTAL STAGE: Barely detectable in stage I/II oocytes,
CC accumulate in stage III/IV oocytes, then exhibit a roughly
CC constant steady state level in mature oocytes, eggs, and early
CC embryos.
CC -1- PTM: Phosphorylated (Probable).
CC -1- MISCELLANEOUS: There are two forms of La, Laa and Lab, in xenopus.
CC -1- SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN.
CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X68818; CAA48716.1; -
CC PIR; S33817; S33817.
CC InterPro; IPR002344; Lupus_La.
CC InterPro; IPR006630; Lupus_La.dom.
CC InterPro; IPR00504; RNA_rec_mot.
CC Pfam; PF05383; La; 1.
CC SMART; SM00715; LA; 1.
CC PRINTS; PR00302; LUPUSLA.
CC SMART; SM00715; LA; 1.
CC SMART; SM00360; RRM; 1.
CC PROSITE; PS50102; RRM; 1.
CC PROSITE; PS00030; RRM_RNP_1; FALSE NEG.
CC RNA-binding; Nuclear protein; Phosphorylation.
CC DOMAIN 110 202 RNA-BINDING (RRM).
CC FT DOMAIN 315 331 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
CC SEQUENCE 427 AA; 48995 MW; 45F3146F8934A355 CRC64;
SQ
Query Match 64.7%; Score 66; DB 1; Length 427;
Best Local Similarity 78.6%; Pred. No. 0.0018;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 4 EAKICHQIEYFGDF 17
Db 13 DKICQIEYFGDF 26
RESULT 6
LAA_XENLA STANDARD; PRT; 428 AA.
ID LAA_XENLA
AC P28048;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Lupus La protein homolog A (La ribonucleoprotein A) (La autoantigen
DE homolog A).
GN LAA1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocyte;
RA MEDLINE=93287095; PubMed=8510143;
RA Scherly D., Stutz F., Lin-Marg N., Clarkson S.G.;
RT "La proteins from Xenopus laevis. cDNA cloning and developmental
RT expression.";
RL J. Mol. Biol. 231:196-204(1993).
CC -1- FUNCTION: La protein plays a role in the transcription of RNA
CC polymerase III. It is most probably a transcription termination
CC factor. Binds to the 3' terminus of virtually all nascent
CC polymerase III transcripts (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- DEVELOPMENTAL STAGE: Barely detectable in stage I/II oocytes,
CC accumulate in stage III/IV oocytes, then exhibit a roughly
CC constant steady state level in mature oocytes, eggs, and early
CC embryos.
CC -1- PTM: Phosphorylated (Probable).
CC -1- MISCELLANEOUS: There are two forms of La, Laa and Lab, in xenopus.
CC -1- SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN.
CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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DR PROSITE: PS00030; RRM_RNP_1; 1.
 KW Systemic lupus erythematosus; RNA-binding; Phosphorylation;
 KW Nuclear Protein.
 FT DOMAIN 111 187 RNA-BINDING (RRM).
 FT MOD RES 366 366 PHOSPHORYLATION (BY CK2).
 SQ SEQUENCE 408 AA; 46837 MW; EC153C15F9187FC4 CRC64;
 Query Match 85.3%; Score 87; DB 1; Length 408;
 Best Local Similarity 100.0%; Pred. No. 5.4e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EAKICHOIEYFGDF 18
 DB 14 EAKICHOIEYFGDF 28

RESULT 3
 LA MOUSE STANDARD; PRT; 415 AA.
 ID LA MOUSE
 AC P32067;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Lupus la protein homolog (La ribonucleoprotein) (La autoantigen homolog).
 GN SSB OR SS-B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RX SEQUENCE FROM N.A.
 RP MEDLINE=93203630; PubMed=9454877;
 RA Topfer F., Gordon T., McCluskey J.;
 RT "Characterization of the mouse autoantigen La (SS-B). Identification of conserved RNA-binding motifs, a putative ATP binding site and reactivity of recombinant protein with poly(U) and human autoantibodies.";
 RT J. Immunol. 150:3091-3100(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12479932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda N.T., Tomihata S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullaney S.J.,
 RA Bork S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
 RA Villalón D.K., Muzny K.D., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalski U., Smallus D.E.,
 RA Schenck A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE OF 1-11 FROM N.A.
 RA Groetzl D., Bachmann M.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor forms of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S, and 7-2 RNAs.

CC -1- SUBUNIT: Interacts with DDX15 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- PTM: Phosphorylated (By similarity).
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.

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 CC EMBL; L00993; AAA39415.1; -
 CC EMBL; BC003820; AAH03820.1; -
 CC EMBL; Y07951; CAA69249.1; -
 CC MCD; MGI:98423; Ssb.
 CC GO; GO:0005634; C:nucleus; IDA.
 CC InterPro; IPR002344; Lupus_La.
 CC InterPro; IPR006630; Lupus_La_dom.
 CC InterPro; IPR000504; RNA_rec_mot.
 CC Pfam; PF05383; La; 1.
 CC Pfam; PF0076; Rrm; 1.
 CC PRINTS; PR00302; IUPUSLA.
 CC SMART; SM00715; LA; 1.
 CC SMART; SM00360; RRM; 1.
 CC DR PROSITE; PSS0102; RRM; 1.
 CC DR PROSITE; PS00030; RRM_RNP_1; 1.
 KW RNA-binding; Nuclear Protein; Phosphorylation.
 FT DOMAIN 111 187 RNA-BINDING (RRM).
 FT SEQUENCE 415 AA; 47756 MW; 2D75197692DFC933 CRC64;
 Query Match 85.3%; Score 87; DB 1; Length 415;
 Best Local Similarity 100.0%; Pred. No. 5.5e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EAKICHOIEYFGDF 18
 DB 14 EAKICHOIEYFGDF 28

RESULT 4
 LA RAT STANDARD; PRT; 415 AA.
 ID LA RAT
 AC P38656;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lupus la protein homolog (La ribonucleoprotein) (La autoantigen homolog).
 GN SSB OR SS-B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93246255; PubMed=7916708;
 RA Sensesl I., Trooster H., Bartesch H., Schwemmler M., Igloi G.L.,
 RA Bachmann M.;
 RT "Isolation of rat cDNA clones coding for the autoantigen SS-B/La: detection of species-specific variations.";
 RT Gene 126:265-268(1993).
 RL Gene 126:265-268(1993).
 CC -1- FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor forms of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S, and 7-2 RNAs.
 CC -1- SUBUNIT: Interacts with DDX15 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- PTM: Phosphorylated (By similarity).
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.

FT DOMAIN 111 187 RNA-BINDING (RM).
SQ SEQUENCE 404 AA; 46534 MW; 4EE30B5C262AD6A1 CRC64;
Query Match 85.3%; Score 87; DB 1; Length 404;
Best Local Similarity 100.0%; Pred. No. 5.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 EAKICHQIYYFGDF 18
DB 14 EAKICHQIYYFGDF 28
RESULT 2
LA HUMAN STANDARD; PRT; 408 AA.
ID LA HUMAN
AC P05455;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Lupus La protein (Sjogren syndrome type B antigen) (SS-B) (La
ribonucleoprotein) (La autoantigen).
GN SSB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89202037; PubMed=2468131;
RT Chan E.K.L., Sullivan K.F., Tan E.M.;
RT "Ribonucleoprotein SS-B/La belongs to a protein family with consensus
Nucleic Acids Res. 17:2233-2244(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89053970; PubMed=3192525;
RT Chambers J.C., Kenan D., Martin B.J., Keene J.D.;
RT "Genomic structure and amino acid sequence domains of the human La
autoantigen.";
RT J. Biol. Chem. 263:18043-18051(1988).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta, and Skeletal muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Tomshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallory S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muray D.M., Sodergren E.J., Lu X., Gibbs K.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield V.S.N., Krzywiński M.I., Skalek U., Smaluk D.E.,
RA Scheraga A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 54-408 FROM N.A.
RX MEDLINE=88199081; PubMed=2452201;
RA Scuggs A.D., Peterson M.G., McNeillage L.J., Whittingham S.,
RA Coppel R.S.;
RT "Characteristics and epitope mapping of a cloned human autoantigen
La.";
RT J. Immunol. 140:3212-3216(1988).
RN [5]

RP SEQUENCE OF 54-97 FROM N.A.
RX MEDLINE=85166283; PubMed=3856888;
RA Chambers J.C., Keene J.D.;
RT "Isolation and analysis of cDNA clones expressing human lupus La
antigen.";
RT Proc. Natl. Acad. Sci. U.S.A. 82:2115-2119(1985).
RN [6]
RP FUNCTION.
RX MEDLINE=89251617; PubMed=2470590;
RA Gottlieb E., Steltz J.A.;
RT "Function of the mammalian La protein: evidence for its action in
transcription termination by RNA polymerase III.";
RT EMBO J. 8:851-861(1989).
RN [7]
RP PHOSPHORYLATION.
RX MEDLINE=92707017; PubMed=9054510;
RA Fan H., Sakulich A.L., Goodier J.L., Zhang X., Qin J., Marrate R.J.;
RT "Phosphorylation of the human La antigen on serine 366 can regulate
recycling of RNA polymerase III transcription complexes.";
RT Cell 88:707-715(1997).
RN [8]
RP INTERACTION WITH DDX15.
RX MEDLINE=22346609; PubMed=12458796;
RA Fournaux M.A., Kolkman M.J.M., Van der Heijden A., De Jong A.S.,
RA Van Venrooij W.J., Pruijn G.J.M.;
RT "The human La (SS-B) autoantigen interacts with DDX15/hPrp43, a
putative DEAD-box RNA helicase.";
RT RNA 8:1428-1443(2002).
RN [9]
RP FUNCTION: La protein plays a role in the transcription of RNA
polymerase III. It is most probably a transcription termination
factor. Binds to the 3' termini of virtually all nascent
polymerase III transcripts. It is associated with precursor forms
of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S,
and 7-2 RNAs.
CC -1- SUBUNIT: Interacts with DDX15.
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- PTM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES ARE AT THE
C-TERMINAL PART OF THE PROTEIN.
CC -1- PTM: The N-terminus is blocked.
CC -1- DISEASE: Sera from patients with systemic lupus erythematosus
often contain antibodies that react with the normal cellular
La protein as if this antigen was foreign.
CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
CC -----
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CC -----
DR EMBL: X13697; CAA11985.1; -
DR EMBL: J04205; AAA51885.1; -
DR EMBL: BC001289; AAH01289.1; -
DR EMBL: BC020818; AAH20818.1; -
DR PIR: A31888; A31888.
DR Genew: HGNC:11316; SSB.
DR MIM: 109090; -
DR GO: GO:0030529; C:ribonucleoprotein complex; TAS.
DR GO: GO:0003729; F:RNA binding; TAS.
DR GO: GO:0000049; F:RNA binding; TAS.
DR GO: GO:0008334; P:histone mRNA metabolism; TAS.
DR GO: GO:0006400; P:RNA modification; TAS.
DR InterPro: IPR002344; Lupus_La.
DR InterPro: IPR006630; Lupus_La_dom.
DR InterPro: IPR000504; RNA_rec_mot.
DR Pfam: PF05383; La; 1.
DR Pfam: PF00076; trm; 1.
DR PRINTS: PR00302; LUPUSLA.
DR SMART: SM00715; LA; 1.
DR SMART: SM00360; RRM; 1.
DR PROSITE: PS0102; RRM; 1.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:01:41 ; Search time 7.224022 Seconds

(without alignments)
129.452 Million cell updates/sec

Title: US-09-836-073-4

Perfect score: 102

Sequence: 1 QOGEAKICHQIEYFGDF 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	85.3	404	1 LA_BOVIN	P10881 Bos taurus
2	87	85.3	408	1 LA_HUMAN	P05455 homo sapien
3	87	85.3	415	1 LA_MOUSE	P32067 mus musculu
4	87	85.3	415	1 LA_RAT	P38656 rattus norv
5	86	84.7	427	1 LAB_XENLA	P28049 xenopus lae
6	66	64.7	428	1 LA_XENLA	P28048 xenopus lae
7	57	55.9	390	1 LA_DROME	P40796 drosophila
8	51	50.0	383	1 LA_AEDAL	Q26457 aedes albop
9	46	45.1	298	1 LAH1_SCHPO	P67058 eschlosacch
10	45	44.1	505	1 TCMD_PENCR	Q43033 petroselinu
11	43.5	42.6	1037	1 ACRD_ECOLI	P24177 escherichia
12	43	42.2	926	1 MEI9_DROME	Q24087 drosophila
13	42	41.2	242	1 GINO_BACST	P27675 bacillus st
14	41	40.2	251	1 FOL2_MOUSE	P05685 mus musculu
15	41	40.2	539	1 Z173_HUMAN	Q12899 homo sapien
16	41	40.2	539	1 Z173_PANTR	Q12899 pan troglod
17	41	40.2	1220	1 DPOU_HSVB	P28856 equine herp
18	41	40.2	1221	1 V143_NPVAC	P24307 autographa
19	40.5	39.7	1173	1 GIGA_ORYSA	Q49417 oryza sativ
20	40	39.2	155	1 RS15_HALMA	P05767 halocaula
21	40	39.2	249	1 VGS1_BPT4	P17173 bacterioph
22	40	39.2	466	1 SRO9_YEAST	P25567 saccharomyc
23	40	39.2	573	1 CATT_YEAST	P68115 saccharomyc
24	40	39.2	585	1 YHO9_YEAST	P38818 saccharomyc
25	40	39.2	1107	1 MY1B_MOUSE	P46733 mus musculu
26	40	39.2	1136	1 MY1B_RAT	Q05096 rattus norv
27	39	38.2	403	1 KIM2_SHEEP	P25609 ovis aries
28	39	38.2	404	1 KIM1_HUMAN	P02534 ovis aries
29	39	38.2	412	1 KIM1_SHEEP	P02534 ovis aries
30	39	38.2	478	1 NRPA_ECOLI	P32050 escherichia
31	39	38.2	478	1 NRPA_SALTI	Q8149 salmonella
32	39	38.2	478	1 NRPA_SALTY	Q8149 salmonella
33	39	38.2	479	1 PRL2_ARATH	Q39190 arabidopsis

34	39	38.2	482	1 IPT5_HUMAN	Q13325 homo sapien
35	39	38.2	488	1 RBL_OLITU	P14959 olithodisc
36	39	38.2	507	1 NRPA_WOLSTU	Q98165 wolinnella s
37	39	38.2	755	1 SEC6_RAT	Q62825 rattus norv
38	39	38.2	756	1 SEC6_HUMAN	Q60645 homo sapien
39	39	38.2	1209	1 THR_DROME	P42286 drosophila
40	39	37.7	1070	1 P11B_RAT	Q92110 rattus norv
41	38.5	37.7	200	1 NACP_ECOLI	P33932 escherichia
42	38	37.3	281	1 Y818_PYRAE	Q82961 pyrobaculum
43	38	37.3	394	1 KIM4_HUMAN	Q76011 homo sapien
44	38	37.3	404	1 KIM5_HUMAN	Q14525 homo sapien
45	38	37.3	416	1 KIM1_HUMAN	Q15323 homo sapien

ALIGNMENTS

```

RESULT 1
LA_BOVIN          STANDARD;          PRT;          404 AA.
ID LA_BOVIN
AC P10881;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lupus La protein homolog (La ribonucleoprotein) (La autoantigen
DE homolog).
GN SSB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary;
RX MEDLINE=89202037; PubMed=2468131;
RA Chan E.K.L., Sullivan K.F., Tan E.M.;
RT "Ribonucleoprotein SS-B/La belongs to a protein family with consensus
RT sequences for RNA-binding.";
RL Nucleic Acids Res. 17:2233-2244(1989).
CC -1- FUNCTION: La protein plays a role in the transcription of RNA
CC polymerase III. It is most probably a transcription termination
CC factor. Binds to the 3' terminl of virtually all nascent
CC polymerase III transcripts. It is associated with precursor forms
CC of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S,
CC and 7-2 RNAs.
CC -1- SUBUNIT: Interacts with DDX15 (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- PTM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES ARE AT THE
CC C-TERMINAL PART OF THE PROTEIN.
CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
CC -----
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CC -----
DR EMBL; X13698; CAJ31986.1; -.
DR PIR; S03849; S03849.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR00504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
KW RNA-binding; Nuclear protein; Phosphorylation.

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C;Species: *Bacillus halodurans*
 C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C;Accession: H83743
 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A;Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
 A;Reference number: A83650, PMID:20512582; PMID:11058132
 A;Accession: H83743
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-642 <STO>
 A;Cross-references: GB:AP001509; GB:BA000004; NID:G10173176; PIDN:BA04471.1; GSPDB:GN00
 A;Experimental source: strain C-125
 C;Genetics:
 A;Gene: BH0752

Query Match 45.1%; Score 46; DB 2; Length 642;
 Best Local Similarity 56.2%; Pred. No. 14;
 Matches 9; Conservative 3; Mismatches 2; Indels 2; Gaps 1;

QY 2 QQEAKEICHOIEYFGD 17
 ::::|::|::|::|
 Db 471 QERKALVH--EYFEGD 484

RESULT 15

AE2408
 hypothetical protein alr4821 [imported] - Nostoc sp. (strain PCC 7120)
 C;Species: Nostoc sp. PCC 7120
 A;Note: Nostoc sp. strain PCC 7120 is a synonym of *Anabaena* sp. strain PCC 7120
 C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
 C;Accession: AE2408
 R;Kanehko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriyuchi
 Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
 DNA Res. 8, 205-213, 2001
 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium *Ana*
 A;Reference number: AB1807; MUID:21595285; PMID:11759840
 A;Accession: AE2408
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-352 <KUR>
 A;Cross-references: GB:BA000019; PIDN:BA876520.1; PID:G17133958; GSPDB:GN00179
 A;Experimental source: strain PCC 7120
 C;Genetics:
 A;Gene: alr4821

Query Match 44.1%; Score 45; DB 2; Length 352;
 Best Local Similarity 56.2%; Pred. No. 12;
 Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 QQEAKEICHOIEYFG 16
 ::::|::|::|::|
 Db 172 QQERAKATOLIKYYIG 187

Search completed: September 10, 2004, 18:02:28
 Job time : 15.0782 secs

RESULT 10

T00677
 hypothetical protein At2g43970 [imported] - Arabidopsis thaliana
 N:Alternate names: hypothetical protein F6B13.10
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001
 C:Accession: T00677, G84872
 R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, June 1998
 A:Description: Arabidopsis thaliana chromosome II BAC F6B13 genomic sequence.
 A:Reference number: Z14180
 A:Accession: T00677
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-529 <ROU>
 A:Cross-references: EMBL:AC004005; NID:G3212846; PID:G3212854
 A:Experimental source: cultivar Columbia
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bentto, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanhaken, S.E.; Umayam, L.; Tallon, L.; Euseb, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: G84872
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-529 <STO>
 A:Cross-references: GB:AE002093; NID:G3212854; PIDN:AAC23405.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: F6B13.10; At2g43970
 A:Map position: 2
 A:Introns: 200/3; 228/1; 259/3; 283/3; 310/2; 344/3; 367/3; 421/3

Query Match

Best Local Similarity 47.1%; Score 48; DB 2; Length 529;
 Pred. No. 5.6;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 KICHOIEYFGD 17
 ||:|:|:|:|
 DB 196 KIVNQVEYFSD 207

RESULT 11

T30953
 hypothetical protein C44B.4 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
 C:Accession: T30953
 R:Sammons, L.; Wohldmann, P.; Gillam, B. submitted to the EMBL Data Library, August 1999
 A:Description: The sequence of C. elegans cosmid C44B.
 A:Reference number: Z20945
 A:Accession: T30953
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-396 <SAM>
 A:Cross-references: EMBL:AF003140; PIDN:AAB54169.1
 A:Experimental source: strain Bristol N2; clone C44B
 C:Genetics:
 A:Map position: 1
 A:Introns: 45/1; 114/3
 A:Note: C44B.4
 C:Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology

Query Match

Best Local Similarity 46.1%; Score 47; DB 2; Length 396;
 Pred. No. 6.1;

Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 EAKICHOIEYFGD 17
 ||:|:|:|:|
 DB 13 DOKIKQVEYFGN 26

RESULT 12

T38937
 rna binding protein - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T38937
 R:Badcock, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, April 1997
 A:Reference number: Z21818
 A:Accession: T38937
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-298 <BAD>
 A:Cross-references: EMBL:Z94864; PIDN:CAB08173.1; GSPDB:GN00066; SPDB:SPAC57A10.10C
 A:Experimental source: strain 972h; cosmid G57A10
 C:Genetics:
 A:Gene: SPDB:SPAC57A10.10C
 A:Map position: 1
 A:Introns: 72/1

Query Match

Best Local Similarity 45.1%; Score 46; DB 2; Length 298;
 Pred. No. 6.7;

Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 EAKICHOIEYFGD 17
 ||:|:|:|:|
 DB 64 EAEVLKQVEYFSD 77

RESULT 13

T43542
 RNA-binding protein la homolog - fission yeast (Schizosaccharomyces pombe)
 N:Alternate names: la autoantigen; ribonucleoprotein la homolog
 C:Species: Schizosaccharomyces pombe
 C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
 C:Accession: T43542; T43325
 R:Van Horn, D.U.; Yeo, C.J.; Xue, D.; Shi, H.; Wolin, S.L. RNA 3, 1434-1443, 1997
 A:Title: The la protein in Schizosaccharomyces pombe: a conserved yet dispensable phosph
 A:Reference number: Z22560; MUID:98067398; PMID:9404894
 A:Accession: T43542
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-298 <VAN>
 A:Cross-references: EMBL:AF022949; PIDN:AAB82145.1
 R:Utsumi, R. submitted to the EMBL Data Library, February 1998
 A:Description: Screening of S. pombe cDNA library using E. coli defective in signal tran
 A:Reference number: Z22428
 A:Accession: T43325
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-298 <UTS>
 A:Cross-references: EMBL:AB011371; PIDN:BAA24981.1
 C:Genetics:
 A:Gene: slat
 C:Function:
 A:Description: the binding of the la protein to rRNA precursors is required for the endo
 C:Keywords: phosphoprotein; RNA binding

Query Match

Best Local Similarity 45.1%; Score 46; DB 2; Length 298;
 Pred. No. 6.7;

Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 EAKICHOIEYFGD 17
 ||:|:|:|:|
 DB 64 EAEVLKQVEYFSD 77

RESULT 14

H83743
 ABC transporter (permease) BH0752 [imported] - Bacillus halodurans (strain C-125)

R:Schery, D.; Stutz, F.; Lin-Marg, N.; Clarkson, S.G.
J Mol Biol. 231, 196-204, 1993
A:Title: La proteins from *Xenopus laevis*: cDNA cloning and developmental expression.
A:Reference number: S33817; MUID:93287095; PMID:8510143
A:Accession: S33818
A:Molecule type: mRNA
A:Residues: 1-428 <CCH>
A:Cross-references: EMBL:X68817; NID:G64873; PIDN:CAA48715.1; PID:G64874
C:Comment: This protein associates with a variety of small RNA molecules, most of which
act as a transcription termination factor.
C:Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology
C:Keywords: phosphoprotein; RNA binding
F:112-178/Domain: ribonucleoprotein repeat homology <SRM>
F:113-118/Region: RNA-binding RNP2 motif
F:151-158/Region: RNA-binding RNP1 motif
F:428-428/Domain: phosphorylated #status predicted <PHY>

Query Match 64.7%; Score 66; DB 1; Length 428;
Best Local Similarity 78.6%; Pred. No. 0.005;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 EAKICHOIEYFGD 17
DB 14 DTKICEQIEYFGD 27

RESULT 6
La/SS-B homolog D-1a - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jul-2000
C:Accession: A53773
R:Bal, C.; Li, Z.; Tolias, P.P.
Mol. Cell. Biol. 14, 5123-5129, 1994
A:Title: Developmental characterization of a *Drosophila* RNA-binding protein homologous to
A:Reference number: A53773; MUID:94309632; PMID:8035794
A:Accession: A53773
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-390 <BAI>
A:Cross-references: GB:U07652; NID:G464019; PIDN:AAA20518.1; PID:G464020
C:Genetics:
A:Gene: FlyBase:La
A:Cross-references: FlyBase:FBgn0011638
C:Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology
C:Keywords: leucine zipper; RNA binding

Query Match 55.9%; Score 57; DB 2; Length 390;
Best Local Similarity 62.5%; Pred. No. 0.14;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 QOEAKICHOIEYFGD 17
DB 49 KQERAILRQVEYFGD 64

RESULT 7
A53781
ribonucleoprotein la - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 20-Sep-1999
C:Accession: A53781
R:Yoo, C.U.; Molin, S.L.
Mol. Cell. Biol. 14, 5412-5424, 1994
A:Title: La proteins from *Drosophila melanogaster* and *Saccharomyces cerevisiae*: a yeast
A:Reference number: A53781; MUID:94309661; PMID:8035818
A:Accession: A53781
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-390 <YOO>
A:Cross-references: GB:U32988; NID:G488469; PID:G488470
C:Genetics:
A:Gene: FlyBase:La

A:Cross-references: FlyBase:FBgn0011638
C:Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology
C:Keywords: RNA binding

Query Match 55.9%; Score 57; DB 2; Length 390;
Best Local Similarity 62.5%; Pred. No. 0.14;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 QOEAKICHOIEYFGD 17
DB 49 KQERAILRQVEYFGD 64

RESULT 8
H89777
capsular polysaccharide synthesis enzyme CapSP [imported] - *Staphylococcus aureus* (stra
C:Species: *Staphylococcus aureus*
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: H89777
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogur
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H89777
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-391 <KUR>
A:Cross-references: GB:BA000018; PID:G13700080; PIDN:BA841379.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: capP
C:Superfamily: lipopolysaccharide biosynthesis protein bplD

Query Match 51.0%; Score 52; DB 2; Length 391;
Best Local Similarity 60.0%; Pred. No. 0.91;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 QOEAKICHOIEYFG 16
DB 362 QASRRICEAIEYFG 376

RESULT 9
T32701
hypothetical protein C14C6.12 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T32701
R:David, M.; Wohldmann, P.; Bauer, C.; Antoniou, B.
submitted to the EMBL Data Library, December 1997
A:Description: The sequence of C. elegans cosmid C14C6.
A:Reference number: Z21210
A:Accession: T32701
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-166 <DAV>
A:Cross-references: EMBL:AF039051; PIDN:AB94258.1; GSPDB:GN00023; CESP:C14C6.12
A:Experimental source: strain Bristol N2; clone C14C6
C:Genetics:
A:Gene: CESP:C14C6.12
A:Map position: 5
A:Introns: 42/1; 156/3

Query Match 49.0%; Score 50; DB 2; Length 166;
Best Local Similarity 58.8%; Pred. No. 0.83;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 QOEAKICHOIEYFGD 18
DB 77 QDVKKICNVIEYMTGDF 93

A:Reference number: S03848; MWID:89202037; PMID:2468131
 A:Accession: S03848
 A:Molecule type: mRNA
 A:Residues: 1-408 <CH2>
 A:Cross-references: EMBL:X13697; NID:g36414; PIDN:CAA31985.1; PID:g36415
 R:Chambers, J.C.; Keene, J.D.
 Proc. Natl. Acad. Sci. U.S.A. 82, 2115-2119, 1985
 A:Title: Isolation and analysis of cDNA clones expressing human lupus La antigen.
 A:Reference number: A22956; MWID:85166283; PMID:3856888
 A:Accession: A22956
 A:Molecule type: mRNA
 A:Residues: 45-97, 'LK' <CH3>
 A:Cross-references: GB:J04205
 A:Note: this sequence has been revised in reference A31888
 R:Nyman, U.; Ringertz, N.R.; Petersson, I.
 Immunol. Lett. 22, 65-72, 1989
 A:Title: Demonstration of an amino terminal La epitope recognized by human anti-La sera.
 A:Reference number: A61051; MWID:89379261; PMID:2476379
 A:Accession: A61051
 A:Status: not compared with conceptual translation
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-19, 'E', '21-47' <NYM>
 R:Stungess, A.D.; Peterson, M.G.; McNeillage, L.J.; Whittingham, S.; Coppel, R.L.
 J. Immunol. 140, 3212-3218, 1988
 A:Title: Characteristics and epitope mapping of a cloned human autoantigen La.
 A:Reference number: S11013; MWID:88199081; PMID:2452201
 A:Accession: S11013
 A:Molecule type: mRNA
 A:Residues: 'E', '55-287', 'V', '289-408' <STU>
 A:Cross-references: EMBL:M20328; NID:g337456; PIDN:AAA36577.1; PID:g337457
 R:Kobayashi, H.; Yamamoto, K.; Fujii, H.; Miura, H.; Miyasaka, N.; Nishioke, K.; Miyamoto, U.
 Clin. Invest. 85, 1566-1574, 1990
 A:Title: Fine epitope mapping the human SS-B/La protein: Identification of a distinct autoantigen.
 A:Reference number: I55553; MWID:90337237; PMID:1692037
 A:Accession: I55553
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 81-107 <RES>
 A:Cross-references: GB:M35261; NID:g338491; PIDN:AAA36652.1; PID:g338495
 A:Accession: I70205
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 174-224 <RE2>
 A:Cross-references: GB:M35263; NID:g338492; PIDN:AAA36653.1; PID:g338496
 A:Accession: I70206
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 279-342 <RE3>
 A:Cross-references: GB:M35262; NID:g338493; PIDN:AAA36654.1; PID:g338497
 A:Comment: This protein associates with a variety of small RNA molecules, most of which act as a transcription termination factor.
 C:Gene: GDB:SSB
 A:Gene: GDB:SSB
 A:Cross-references: GDB:125359; OMIM:109090
 A:Map position: 2
 A:Introns: 22/3; 57/2; 115/3; 151/3; 185/2; 209/2; 223/3; 264/3; 380/2
 C:Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
 C:Keywords: phosphoprotein; RNA binding
 F:112-176/Domain: ribonucleoprotein repeat homology <RNM>
 F:113-118/Region: RNA-binding RNP2 motif
 F:151-158/Region: RNA-binding RNP1 motif
 F:228-408/Domain: phosphorylated #status experimental <PHY>

Query Match 85.3%; Score 87; DB 1; Length 408;
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EAKICHOIEYFGDF 18
 :|||||
 :|||||

DB 14 EAKICHOIEYFGDF 28

RESULT 3

JCI494
 N:Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 24-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
 C:Accession: JCI494; S25145
 R:Semel, I.; Troester, H.; Bartsch, H.; Schwemmler, M.; Igloi, G.L.; Bachmann, M.
 Gene 126, 265-268, 1993
 A:Title: Isolation of rat cDNA clones coding for the autoantigen SS-B/La. Detection of s
 A:Reference number: JCI494; MWID:93246255; PMID:7916708
 A:Accession: JCI494
 A:Molecule type: mRNA
 A:Residues: 1-415 <SEM>
 A:Cross-references: GB:X67859; NID:g55778; PIDN:CAA48043.1; PID:g55779
 A:Experimental source: liver
 C:Comment: This protein associates with a variety of small RNA molecules, most of which act as a transcription termination factor.
 C:Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
 C:Keywords: phosphoprotein; RNA binding
 F:112-176/Domain: ribonucleoprotein repeat homology <RNM>
 F:113-118/Region: RNA-binding RNP2 motif
 F:151-158/Region: RNA-binding RNP1 motif
 F:227-415/Domain: phosphorylated #status predicted <PHY>

Query Match 85.3%; Score 87; DB 1; Length 415;
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EAKICHOIEYFGDF 18
 :|||||
 :|||||

DB 14 EAKICHOIEYFGDF 28

RESULT 4
 S33817
 ribonucleoprotein La-B - African clawed frog
 N:Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
 C:Accession: S33817; S28544
 R:Scherry, D.; Stutz, F.; Lin-Mary, N.; Clarkson, S.G.
 J. Mol. Biol. 231, 196-204, 1993
 A:Title: La proteins from Xenopus laevis. cDNA cloning and developmental expression.
 A:Reference number: S33817; MWID:93287095; PMID:8510143
 A:Accession: S33817
 A:Molecule type: mRNA
 A:Residues: 1-427 <SCH>
 A:Cross-references: EMBL:X68918; NID:g64875; PIDN:CAA48716.1; PID:g64876
 C:Comment: This protein associates with a variety of small RNA molecules, most of which act as a transcription termination factor.
 C:Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
 C:Keywords: phosphoprotein; RNA binding
 F:111-177/Domain: ribonucleoprotein repeat homology <RNM>
 F:112-117/Region: RNA-binding RNP2 motif
 F:150-157/Region: RNA-binding RNP1 motif
 F:227-427/Domain: phosphorylated #status predicted <PHY>

Query Match 64.7%; Score 66; DB 1; Length 427;
 Best Local Similarity 78.6%; Pred. No. 0.005;
 Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 EAKICHOIEYFGDF 17
 :|||||
 :|||||

DB 13 DKICHOIEYFGDF 26

RESULT 5

S33818
 ribonucleoprotein La-A - African clawed frog
 N:Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
 C:Accession: S33818; S28545

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:33:11 ; Search time 14.0782 Seconds
(without alignments)
122.988 Million cell updates/sec

Title: US-09-836-073-4

Perfect score: 102

Sequence: 1 QOQEKICHQIEYFGDF 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR 78: *
2: PIR3: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	85.3	404	1 S03849	ribonucleoprotein
2	87	85.3	408	1 A31888	ribonucleoprotein
3	87	85.3	415	1 UC1494	ribonucleoprotein
4	66	64.7	427	1 S33817	ribonucleoprotein
5	66	64.7	428	1 S33818	ribonucleoprotein
6	57	55.9	390	2 A53773	La/SS-B homolog D-
7	57	55.9	390	2 A53781	ribonucleoprotein
8	52	51.0	391	2 H89777	capsular polysacch
9	50	49.0	166	2 T32701	hypothetical prote
10	48	47.1	529	2 T00677	hypothetical prote
11	47	46.1	396	2 T30953	hypothetical prote
12	46	45.1	298	2 T38937	rna binding protei
13	46	45.1	298	2 T43542	RNA-binding protei
14	46	45.1	642	2 H83743	ABC transporter (p
15	45	44.1	352	2 A2408	hypothetical prote
16	45	44.1	506	2 T14907	trans-cinnamate 4-
17	45	44.1	566	2 C82379	response regulator
18	43.5	42.6	788	2 A71076	hypothetical prote
19	43.5	42.6	1037	2 B65022	acridiflavin resista
20	43.5	42.6	1037	2 D91045	amloglycoside eff
21	43.5	42.6	1037	2 G85889	hypothetical prote
22	43	42.2	658	2 D96656	hypothetical prote
23	43	42.2	658	2 T19487	hypothetical prote
24	43	42.2	926	2 S58936	metotic recombinat
25	43	42.2	1131	2 T15617	hypothetical prote
26	42	41.2	242	2 A42478	glutamine transpor
27	42	41.2	401	2 AC2207	L-cysteine/cystine
28	42	41.2	416	2 S60034	keratin Hal' type
29	42	41.2	424	2 T46197	hypothetical prote

30	42	41.2	449	2 G84091	hypothetical prote
31	42	41.2	505	2 B90181	Na+/H+ antiporter
32	42	41.2	506	2 T41623	probable protein k
33	42	41.2	515	2 T43152	hypothetical prote
34	41.5	40.7	1428	2 T13926	probable protein p
35	41	40.2	51	2 G81188	hypothetical prote
36	41	40.2	172	2 F75491	conserved hypothet
37	41	40.2	175	2 S23687	erythrocyte membra
38	41	40.2	251	2 B40969	folate-binding pro
39	41	40.2	319	2 AF0228	probable transpos
40	41	40.2	469	2 C70357	hypothetical prote
41	41	40.2	506	2 F85016	probable RING zinc
42	41	40.2	704	2 AE2107	serine/threonine k
43	41	40.2	845	2 T34064	hypothetical prote
44	41	40.2	1220	1 DJBEC3	DNA-directed DNA p
45	41	40.2	1220	2 T42573	DNA-directed DNA p

ALIGNMENTS

RESULT 1
S03849
ribonucleoprotein Ia - bovine
N;Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1990 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C;Accession: S03849
R;Chan, E.K.L.; Sullivan, K.F.; Tan, E.M.
Nucleic Acids Res. 17, 2233-2244, 1989
A;Title: Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences
A;Reference number: S03848; MUID:89202037; PMID:2468131
A;Accession: S03849
A;Molecule type: mRNA
A;Residues: 1-404 <CHA>
A;Cross-references: EMBL:X13698; NID:g755; PIDD:CAA31986.1; PID:g756
A;Note: part of this sequence was confirmed by protein sequencing
C;Comment: This protein associates with a variety of small RNA molecules, most of which
act as a transcription termination factor.
C;Superfamily: ribonucleoprotein Ia; ribonucleoprotein repeat homology
C;Keywords: blocked amino end; phosphoprotein; RNA binding
F;112-178/Domain: ribonucleoprotein repeat homology <RRM>
F;113-118/Region: RNA-binding RNP2 motif
F;151-158/Region: RNA-binding RNP1 motif
F;228-404/Domain: phosphorylated #status predicted <PHY>

Query Match 85.3%; Score 87; DB 1; Length 404;
Best Local Similarity 100.0%; Pred. No. 1.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EAKICHQIEYFGDF 18
DB 14 EAKICHQIEYFGDF 28

RESULT 2
A31888
ribonucleoprotein Ia - human
N;Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B; Sjogren syndrome antigen
C;Species: Homo sapiens (man)
C;Date: 21-May-1990 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C;Accession: A31888; S03848; A22956; A61051; S11013; I55553; I70205; I70206; A31273
R;Chambers, J.C.; Kenan, D.; Martin, B.U.; Keene, J.D.
J. Biol. Chem. 263, 18043-18051, 1988
A;Title: Genomic structure and amino acid sequence domains of the human La autoantigen.
A;Reference number: A31888; MUID:89053970; PMID:3192525
A;Accession: A31888
A;Molecule type: mRNA
A;Residues: 1-408 <CHA>
A;Cross-references: GB:U04205; NID:g178686; PIDD:AAA51885.1; PID:g178687
R;Chan, E.K.L.; Sullivan, K.F.; Tan, E.M.
Nucleic Acids Res. 17, 2233-2244, 1989
A;Title: Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences

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RN [1] SEQUENCE FROM N.A.
RP STRAIN=Becker;
RX MEDLINE=96178981; PubMed=8606192;
RA Sau S., Lee C.Y.;
RT "Cloning of type 8 capsule genes and analysis of gene clusters for the
RT production of different capsular polysaccharides in Staphylococcus
RT aureus.";
RL J. Bacteriol. 178:2118-2126(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Becker;
RX MEDLINE=97197525;
RA Sau S., Sun J., Lee C.Y.;
RT "Molecular characterization and transcriptional analysis of type 8
RT capsule genes in Staphylococcus aureus";
RL J. Bacteriol. 179:1614-1621(1997).
DR EMBL; U73374; ABA9445.1; -.
DR HSSP; P27828; 1P6D.
DR GO; GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity; IEA.
DR GO; GO:0009103; F:11policysaccharide biosynthesis; IEA.
DR GO; GO:0006047; F:UDP-N-acetylglucosamine metabolism; IEA.
DR InterPro; IPR003331; Epimerase_2.
DR Pfam; PF02350; Epimerase 2; 1.
DR TIGRFAMs; TIGR00236; wecB; 1.
SQ SEQUENCE 391 AA; 44247 MW; 1E8D9FA95C76FD CRC64;

Query Match 46.9%; Score 46; DB 2; Length 391;
Best Local Similarity 63.6%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 KICHOIQYFG 16
: || |::|||
Db 366 RICEAIEYFG 376

RESULT 11
ID P95709 PRELIMINARY; PRT; 391 AA.
AC P95709;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE CapsP.
GN CAPSP.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Reynolds and Newman;
RX MEDLINE=97388587; PubMed=9245821;
RA Sau S., Bhasin N., Mann E.R., Lee J.C., Foster T.J., Lee C.Y.;
RT "The Staphylococcus aureus allelic genetic loci for serotype 5 and 8
RT capsule expression contain the type-specific genes flanked by common
RT gene.";
RL Microbiology 143:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Reynolds and Newman;
RX MEDLINE=98101481; PubMed=9440531;
RA Kiser K.B., Lee J.C.;
RT "Staphylococcus aureus cap50 and cap5p genes functionally complement
RT mutations affecting enterobacterial common-antigen biosynthesis in
RT Escherichia coli";
RL J. Bacteriol. 180:403-406(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Reynolds and Newman;
RX MEDLINE=98125727; PubMed=9466251;
RA Bhasin N., Albus A., Michon F., Livolsi P.J., Park J.-S., Lee J.C.;
RT "Identification of a gene essential for O-acetylation of the
RT Staphylococcus aureus type 5 capsular polysaccharide";

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RL Mol. Microbiol. 27:9-21 (1998) .
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Reynolds and Newman;
RA Baggia N., Mann E.R., Foster T.J., Lee J.C.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81973; AAC46099.1; -.
DR HSSP; P27828; 1F6D.
DR GO; GO:0008761; P:UDP-N-acetylglucosamine 2-epimerase activity; IEA.
DR GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
DR GO; GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.
DR InterPro; IPR003331; Epimerase_2.
DR Pfam; PF02350; Epimerase 2; 1.
DR TIGRFAMs; TIGR00236; wecB; 1.
SQ SEQUENCE 391 AA; 44328 MW; B0105F690DB7CFLD CRC64;
QY Query Match 46.9%; Score 46; DB 2; Length 391;
Best Local Similarity 63.6%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
DB 366 RICEAIIEYFG 376
QY 6 KICHIQIYFG 16
: || | : || |
: || | : || |
DB 366 RICEAIIEYFG 376
RESULT 12
Q99X57 PRELIMINARY; PRT; 391 AA.
ID Q99X57;
AC Q99X57;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Capsular polysaccharide synthase enzyme Cap5P.
GN CAP OR SAV0164 OR SA0159.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699) , and
OS Staphylococcus aureus (strain N315) .
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158878, 158879;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Ijari J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Matsuyama A., Murakami H., Hoshoyama A.,
RA Mizutani-Oi Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hiraoka H., Kohara S., Goto S., Yabuzaki J.,
RA Kaneshima M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240 (2001) .
DR EMBL; AP003358; BAB56326.1; -.
DR EMBL; AP003129; BAB41379.1; -.
DR PIR; H89777; H89777.
DR HSSP; P27828; 1F6D.
DR GO; GO:0008761; P:UDP-N-acetylglucosamine 2-epimerase activity; IEA.
DR GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
DR GO; GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.
DR InterPro; IPR003331; Epimerase_2.
DR Pfam; PF02350; Epimerase 2; 1.
DR TIGRFAMs; TIGR00236; wecB; 1.
KW Complete proteome.
SQ SEQUENCE 391 AA; 44372 MW; DDDF5FA715BCCECC CRC64;
QY Query Match 46.9%; Score 46; DB 16; Length 391;
Best Local Similarity 63.6%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
DB 366 RICEAIIEYFG 376

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AC 07X050;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DE OSJNB0046p18.10 protein.
DE OSJNB0046p18.10.
OC Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriactoidae; Oryzaceae; Oryza.
OX NCBI_TaxId=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Fu G., Wang S.Y., Ren S.X., Lv G., Lin W., Gu W.Q., Zhu G.F., Tu Y.F.,
RA Jia J., Yin H.F., Zhang Y., Cai Z., Chen J., Kang H., Chen X.Y.,
RA Shao Y., Sun Y., Hu Q.P., Zhang X.L., Zhang W., Wang L.J., Ding C.W.,
RA Sheng H.H., Gu J.L., Chen S.T., Ni L., Zhu F.H., Han B., Feng Q.,
RA Huang Y.C., Li Y., Zhu J.J., Zhao Q., Hu X., Liu Y.L., Mu J., Yu Z.,
RA Chen L., Fan D.L., Wang Q.J., Zhang L., Lu Y.Q., Yu S.L., Liu X.H.,
RA Lu T.T., Zhang Y.J., Lu Y., Li C., Li T., Zhang Y., Hu H., Jia P.X.,
RA Qian Y.M., Ying X., Zhou B., Chen Z.H., Hao P., Zhang U., Wu M.,
RA Zhang R.Q., Guan J.P., Hong G.F.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL60630; CA03294.1; -
SQ SEQUENCE 863 AA; 96838 MW; 8ACE2362CCF2F296 CRC64;

Query Match
Best Local Similarity 48.0%; Score 47; DB 10; Length 863;
Matches 6; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

OY 3 L0AKICHOIYYFG 16
Db 380 LOSQVCHERRYFVG 393

RESULT 8
ID 080WCO; PRELIMINARY; PRT; 141 AA.
AC 080WCO;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Similar to Ras, guanylate releasing protein 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Mammary gland;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeng B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish J.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo W.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Murzyn D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton B., Kettelman W., Madan A., Roditsky S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Schermer A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.

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RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051474; AAH51474.1; -.
DR GO; GO:0005085; P:guanylate nucleotide exchange factor activity; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR000651; RASGEFN.
DR InterPro; IPR008937; Ras GER.
DR SMART; SM00229; RASGEFN_1.
DR PROSITE; PS00212; RASGER_NTER; 1.
SQ SEQUENCE 141 AA; 16186 MW; 242C314B00AD9191 CRC64;

Query Match
Best Local Similarity 46.9%; Score 46; DB 11; Length 141;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

OY 2 AL0AKICHOIYYFGQF 18
Db 70 SLQMTCHLVRYWISAF 86

RESULT 9
ID 08NYN8; PRELIMINARY; PRT; 381 AA.
AC 08NYN8;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Capsular polysaccharide synthesis enzyme Cap8P.
GN CAP8P OR MW0139.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=196620;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).
DR EMBL; AP004822; BAB94004.1; -.
DR GO; GO:0008761; P:UDP-N-acetylglucosamine 2-epimerase activity; IEA.
DR GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
DR GO; GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.
DR InterPro; IPR003311; Epimerase_2.
DR Pfam; PF02350; Epimerase 2; 1.
DR TIGRPFAM; TIGR00236; wecB; 1.
KW complete proteome.
SQ SEQUENCE 381 AA; 43106 MW; 125E4D5D1904779C CRC64;

Query Match
Best Local Similarity 46.9%; Score 46; DB 16; Length 381;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 6 KICHOIYYFG 16
Db 356 RICEAIEYFVG 366

RESULT 10
ID P72382; PRELIMINARY; PRT; 391 AA.
AC P72382;
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Cap8P.
GN CAP8P.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;

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RESULT 5
ID Q7ZT10 PRELIMINARY; PRT; 401 AA.
AC Q7ZT10;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Similar to sjogren syndrome antigen B (Autoantigen Ia).
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC045392; AA045392.1; -.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003723; F:RNA binding; IEA.
DR InterPro: IPR002344; Lupus_La.
DR InterPro: IPR006630; Lupus_La_dom.
DR InterPro: IPR000504; RNA_rec_mot.
DR Pfam: PF00076; Rrm_1.
DR PRINTS: PR00302; LUPUSLA.
DR SMART: SM00715; LA_1.
DR SMART: SM00360; RRM_1.
DR PROSITE: PS50102; RRM_1.
DR PROSITE: PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 401 AA; 46138 MW; 2EF02FDD3916291 CRC64;

Query Match 51.0%; Score 50; DB 13; Length 401;
Best Local Similarity 57.1%; Pred. No. 3.6;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 LQAKICHQIQYFGF 16
Db 10 LKKVIAEQIEYFG 23

RESULT 6
ID Q9UL65 PRELIMINARY; PRT; 671 AA.
AC Q9UL65; 000538;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Guanine exchange factor MCG7 isoform 1 (F25B3.3 Kinase like
DE protein).
GN CALDAG-GEFI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20493616; PubMed=10918068;
RA Clyde-Smith J., Silins G., Gartside M., Grimmond S., Etheridge M.,
RA Apolloni A., Hayward N., Hancock J.F.;
RT Characterization of RasGRP2, a Plasma Membrane-targeted, Dual
RT Specificity Ras/Rap Exchange Factor.;
RL J. Biol. Chem. 275:32260-32267(2000).
RN [2]
RP SEQUENCE OF 63-671 FROM N.A.
RC MEDLINE=98001089; PubMed=9341881;
RA Kedra D., Seroussi E., Fransson I., Trifunovic J., Clark M.,
RA Lagercrantz J., Blennow E., Mehlin H., Dumanski J.;
RT "The germinal center kinase gene and a novel CDC25-like gene are
RT located in the vicinity of the PYGM gene on 11q13.";
RL Hum. Genet. 100:611-619(1997).
RN [3]

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RP SEQUENCE OF 63-671 FROM N.A.
RX MEDLINE=99007305; PubMed=9789079;
RA Kawasaki H., Spriggett G.M., Toki S., Canales J.J., Harlan P.,
RA Blumenstiel J.P., Chen E.J., Bany I.A., Mochizuki N., Ashbacher A.,
RA Matsuda M., Housman D.E., Graybiel A.M.;
RT "A Rap guanine nucleotide exchange factor enriched highly in the basal
RT ganglia.";
RN [4]
RP SEQUENCE OF 63-671 FROM N.A.
RC Kawasaki H., Housman D.E., Graybiel A.M.;
RA Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 63-671 FROM N.A.
RC Kawasaki H., Housman D.E., Graybiel A.M.;
RA Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 63-671 FROM N.A.
RA Kawasaki H., Spriggett G.M., Toki S., Canales J.J., Blumenstiel J.P.,
RA Chen E.J., Bany I.A., Mochizuki N., Ashbacher A., Matsuda M.,
RA Housman D.E., Graybiel A.M.;
RT "A Novel Rap Guanine Nucleotide Exchange Factor Enriched in the Basal
RT Ganglia.";
RN [7]
RP SEQUENCE OF 63-671 FROM N.A.
RA Silins G.U., Grimmond S., Hayward N.;
RT Characterisation of a Novel Nucleotide Exchange Factor.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF043722; AAF07219.1; -.
DR EMBL: Y12336; CAAT73005.1; -.
DR EMBL: U78170; AAD12741.1; -.
DR EMBL: AF081194; AAC79698.1; -.
DR EMBL: AF043723; AAF07220.1; -.
DR HSP; P28867; IPTQ.
DR Genew; HGNC:9879; RasGRP2.
DR GO: GO:0005509; F:calcium ion binding; IEA.
DR GO: GO:0019992; F:diacylglycerol binding; IEA.
DR GO: GO:0005085; F:guanyl-nucleotide exchange factor activity; IEA.
DR GO: GO:0008289; F:lipid binding; TAS.
DR GO: GO:0007165; P:signal transduction; TAS.
DR InterPro: IPR002219; DAG_PE-bind.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000651; RasGEFN.
DR InterPro: IPR001895; RasGEF_CDC25.
DR Pfam: PF00130; DAG_PE-bind; 1.
DR Pfam: PF00036; ehand; 2.
DR Pfam: PF00617; RasGEF; 1.
DR SMART: SM00109; Cl_1.
DR SMART: SM00147; RasGEF; 1.
DR SMART: SM00229; RasGEFN; 1.
DR PROSITE: PS00479; DAG_PE_BIND_DOM_1; 1.
DR PROSITE: PS50081; DAG_PE_BIND_DOM_2; 1.
DR PROSITE: PS00018; EF_HAND; 2.
DR PROSITE: PS50009; RasGEF_CAT; 1.
DR PROSITE: PS50212; RasGEF_NTER; 1.
DR Calcium; Calcium-binding; Phorbol-ester binding.
KV SEQUENCE 671 AA; 75547 MW; 67B7BD2B4FAED4D CRC64;

Query Match 48.0%; Score 47; DB 4; Length 671;
Best Local Similarity 41.2%; Pred. No. 19;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 2 ALQAKICHQIQYFGF 18
Db 132 SLQYKCHLVRYWISAF 148

RESULT 7
ID Q7XQ50 PRELIMINARY; PRT; 863 AA.

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DR GO:0005634; C.nucleus; IDA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; rtm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
SQ SEQUENCE 381 AA; 43891 MW; 2E2DEF1452C0F0E9 CRC64;

Query Match
Best Local Similarity 84.7%; Score 83; DB 11; Length 381;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ALOAKICHOIQYFQGF 18
DB 12 ALEAKICHOIEYFGDF 28

RESULT 2
Q8BTU4 PRELIMINARY; PRT; 415 AA.
ID Q8BTU4;
AC Q8BTU4;
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Sjogren syndrome antigen B.
GN SSB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12468851;
RA The PANOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK086677; BAC040498.1; -.
DR MGD; MGI:98423; Ssb.
DR GO:0005634; C.nucleus; IDA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; rtm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 415 AA; 47657 MW; A7545C7686AC8363 CRC64;

Query Match
Best Local Similarity 84.7%; Score 83; DB 11; Length 415;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ALOAKICHOIQYFQGF 18
DB 12 ALEAKICHOIEYFGDF 28

RESULT 3
Q8QHT5 PRELIMINARY; PRT; 206 AA.
ID Q8QHT5;
AC Q8QHT5;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Untranslated region binding-protein.

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GN UBP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA L'Ecuver T.J., Fang H.-L.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF467897; AAL76269.1; -.
DR GO:0005634; C.nucleus; IEA.
DR GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; rtm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 206 AA; 23992 MW; 965B62F7DFFB90E9 CRC64;

Query Match
Best Local Similarity 63.3%; Score 62; DB 13; Length 206;
Matches 10; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 LOAKICHOIQYFQGF 16
DB 13 LESKICQOIEYFQGF 26

RESULT 4
Q7ZTK2 PRELIMINARY; PRT; 427 AA.
ID Q7ZTK2;
AC Q7ZTK2;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Similar to lupus LA protein homolog B.
DR EMBL; BC046654; AAH46654.1; -.
DR GO:0005634; C.nucleus; IEA.
DR GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rtm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 2.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 427 AA; 48996 MW; 1E7CD82D8AB9C69A CRC64;

Query Match
Best Local Similarity 60.2%; Score 59; DB 13; Length 427;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 LOAKICHOIQYFQGF 16
DB 12 LDTKICQOIEYFQGF 25

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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:29:01 : Search time 41.229 Seconds
(without alignments)
137.751 Million cell updates/sec

Title: US-09-836-073-3

Perfect score: 98
Sequence: 1 AALQAKICHQIQYFQGF 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_TREMBL_25:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*
16: sp_virus:*
17: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	84.7	381	11	Q9CYB9 mus musculus
2	83	84.7	415	11	Q8BTU4 mus musculus
3	62	60.3	206	13	Q8OH15 gallus galli
4	59	60.2	427	13	Q7ZTK2 xenopus lae
5	50	51.0	401	13	Q7ZT10 brachydanio
6	47	48.0	671	4	Q9UL65 homo sapien
7	47	48.0	863	10	Q7XQ50 oryza sativ
8	46	46.9	141	11	Q8MWC0 mus musculus
9	46	46.9	381	16	Q8NVM8 staphylococ
10	46	46.9	391	2	P72382 staphylococ
11	46	46.9	391	2	P95709 staphylococ
12	46	46.9	391	16	Q99X57 staphylococ
13	46	46.9	608	11	Q9QUC9 mus musculus
14	45	45.9	568	16	Q9K17 vibrio chol
15	45	45.9	928	10	Q9LJ02 oryza sativ
16	44	44.9	239	10	Q9SMD8 laminiaria d

17	44	44.9	1676	8	Q85FR6 cyanidiosch
18	43	43.9	337	2	Q8RX98 mycoplasma
19	42.5	43.4	577	16	Q97DB6 clostridium
20	42	42.9	179	5	Q814P8 plasmodium
21	42	42.9	188	5	Q81094 plasmodium
22	42	42.9	244	5	Q81M79 plasmodium
23	42	42.9	396	5	Q01806 caenorhabdi
24	42	42.9	478	16	Q87GS8 vibrio para
25	42	42.9	541	16	Q9ZKY5 helicobacte
26	42	42.9	542	16	Q25534 helicobacte
27	42	42.9	547	10	Q7XVC6 oryza sativ
28	42	42.9	658	10	Q9CAN3 arabidopsis
29	42	42.9	1017	11	Q80Z25 mus musculu
30	42	42.9	1220	12	Q39272 equine hep
31	42	42.9	1249	12	Q65152 african swi
32	42	42.9	1560	10	Q7XTP9 oryza sativ
33	42	42.9	2644	4	Q13535 homo sapien
34	41	41.8	259	3	Q9P5X3 neurospora
35	41	41.8	271	16	Q8CTY0 staphylococ
36	41	41.8	296	5	Q9W129 drosophila
37	41	41.8	336	2	Q50359 mycoplasma
38	41	41.8	336	16	Q98QD2 mycoplasma
39	41	41.8	366	2	Q85787 mycoplasma
40	41	41.8	369	2	Q30382 mycoplasma
41	41	41.8	369	2	Q9R8C2 mycoplasma
42	41	41.8	369	16	Q98BP1 mycoplasma
43	41	41.8	399	2	Q85799 mycoplasma
44	41	41.8	411	10	Q9FL36 arabidopsis
45	41	41.8	422	10	Q94A38 arabidopsis

ALIGNMENTS

RESULT 1
Q9CYB9 PRELIMINARY; PRT; 381 AA.
ID Q9CYB9
AC Q9CYB9;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Sjogren eyndrome antigen B.
GN SSB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiraldi L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guernicich S., Hill D., Hofmann M., Hume D.A., Kaniwa M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima Y., Mazarelli J., Mommaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilting L.,
RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.",
RL Nature 409:685-690(2001).
DR EMBL; AK017822; BAB30957.1; -
MGD; MGI:98423; Ssb.

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FT METAL 18 18 IRON (HEME AXIAL LIGAND).
 FT METAL 80 80 IRON (HEME AXIAL LIGAND).
 SQ SEQUENCE 104 AA; 11209 MW; 1B5F2A7B657CD36F CRC64;

QY 2 ALQAKICHQIQ 12
 DB 108 ALQOQCCHQIR 118

Query Match 39.8%; Score 39; DB 1; Length 104;
 Best Local Similarity 75.0%; Pred. No. 8.3;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Search completed: September 10, 2004, 17:53:03
 Job time : 8.24022 secs

QY 4 QAKICHQI 11
 DB 13 QCKICHQV 20

RESULT 15

ZEB2_MAIZE
 ID ZEB2_MAIZE STANDARD; PRT; 183 AA.
 AC P08031;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Zein-beta precursor (Zein 2) (16 kDa) (Zein ZC1).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=87248094; PubMed=3596247;
 RA Prat S., Perez-Grau L., Puigdomenech P.;
 RT "Multiple variability in the sequence of a family of maize endosperm
 RT proteins";
 RL Gene 52:41-49(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA STRAIN=cv. W64A; TISSUE=Endosperm;
 RX MEDLINE=91057131; PubMed=2243787;
 RA Reina M., Guillen P., Ponte I., Boronat A., Palau J.;
 RT "DNA sequence of the gene encoding the Zci protein from Zea mays W64
 RT A.";
 RL Nucleic Acids Res. 18:6425-6425(1990).
 CC -1- FUNCTION: Zeins are major seed storage proteins.
 CC -1- SUBCELLULAR LOCATION: Endosperm protein bodies.
 CC -1- SIMILARITY: TO GLUTENIN 2.
 CC -----
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 DR EMBL; M16460; AAA33523.1; -;
 DR EMBL; X53515; CAA37595.1; -;
 DR PIR; B29017; B29017.
 DR MaizeDB; 58053; -;
 DR InterPro; IPR003612; AAI.
 DR InterPro; IPR001954; G1a_glutenin.
 DR InterPro; IPR000480; Glutelin.
 DR Pfam; PF00234; tryp_alpha_amy1; 1.
 DR PRINTS; PR00208; GLIADGLUTEN.
 DR PRINTS; PR00211; GLUTELIN.
 DR SMART; SM00499; AAI; 1.
 DR Seed storage protein; Repeat; Multigene family; signal.
 FT SIGNAL 1 19
 FT CHAIN 1 183 ZEIN-BETA.
 FT SEQUENCE 183 AA; 19558 MW; 3965BBBC1151F45A CRC64;
 SQ

Query Match 39.8%; Score 39; DB 1; Length 183;
 Best Local Similarity 63.6%; Pred. No. 15;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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DR EMBL; X62826; CAA58033.1; -
 DR EMBL; AB022217; BAB02756.1; ALT SEQ.
 DR EMBL; AY054181; AAL06842.1; ALT_INIT.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; WD40; 7.
 DR PRINTS; PR00320; GPROTEINBRPT.
 DR PRODOM; PD000018; WD40; 2.
 DR SMART; SM00320; WD40; 7.
 DR PROSITE; PS00678; WD_REPEATS_1; 2.
 DR PROSITE; PS00682; WD_REPEATS_2; 4.
 DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
 KW Repeat; WD repeat.
 FT REPEAT 168 198 WD 1.
 FT REPEAT 210 240 WD 2.
 FT REPEAT 252 282 WD 3.
 FT REPEAT 293 323 WD 4.
 FT REPEAT 335 364 WD 5.
 FT REPEAT 377 406 WD 6.
 FT REPEAT 426 456 WD 7.
 SQ SEQUENCE 479 AA; 53568 MW; 3019864AER80670 CRC64;

Query Match
 Best Local Similarity 40.8%; Score 40; DB 1; Length 479;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 KICHOIQYFG 16
 Db 48 RLCHKIQVAFG 58

RESULT 13
 TCPT_VIBCH STANDARD; PRT; 503 AA.
 AC TCPT_VIBCH Q9KTR0;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Toxin coregulated pilus biosynthesis protein T (TCP pilus
 DE biosynthesis protein tcpt).
 GN TCPT OR VC0835.
 OS Vibrio cholerae.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 CC Vibrionaceae; Vibrio.
 OX NCBI_TaxId=666;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=classical Inaba Z17561 / Serotype O1;
 RA Heidelberg J.F., Bisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bae S., Olin H., Dragoi I., Sellers P.,
 RA McDonald L., Uetakeback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Frazer C.M.;
 RA "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 RT cholerae.";

RL Nature 406:477-483 (2000).
 CC - FUNCTION: INVOLVED IN THE TRANSLOCATION OF THE TCPA PILIN.
 CC - SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC - SIMILARITY: BELONGS TO THE PILE/OUTE/EXSE/XPSE/XCPR FAMILY.
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DR EMBL; X64098; CAA45462.1; -
 DR EMBL; AE004168; AAF93998.1; -
 DR PIR; F82275; F82275.
 DR TIGR; VC0835; -
 DR InterPro; IPR001482; GSPFI_E.
 DR Pfam; PR00437; GSPFI_E; 1.
 DR PRODOM; PD000739; GSPFI_E; 1.
 DR PROSITE; PS00662; T2SP_E; 1.
 KW Transport; ATP-binding; Complete proteome.
 KW NP BIND 236 243 ATP (POTENTIAL).
 FT CONFLICT 137 137 A -> S (IN REF. 1).
 SQ SEQUENCE 503 AA; 57276 MW; ED3FDF8F579F918 CRC64;

Query Match
 Best Local Similarity 40.3%; Score 39.5; DB 1; Length 503;
 Matches 7; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

Qy 3 LQKICHOQ-IQYFQ 17
 Db 471 LKGVCHETVLMFQ 486

RESULT 14
 CY2_RHOVA STANDARD; PRT; 104 AA.
 AC P00082;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cytochrome C2.
 OS Rhodocrobium vanielii.
 CC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 CC Rhodocyclaceae; Rhodocrobium.
 OX NCBI_TaxId=1069;
 OX [1]
 RP SEQUENCE.
 RC STRAIN=ATCC 17100;
 RA MEDLINE=76102814; PubMed=174109;
 RA Ambler R.P., Meyer T.E., Kamen M.D.;
 RT "Primary structure determination of two cytochromes C2: close
 RT similarity to functionally unrelated mitochondrial cytochrome C.";
 RL Proc. Natl. Acad. Sci. U.S.A. 73:472-475 (1976).
 CC - FUNCTION: CYTOCHROME C2 IS FOUND MAINLY IN PURPLE, NONSULFUR,
 CC PHOTOSYNTHETIC BACTERIA WHERE IT FUNCTIONS AS THE ELECTRON DONOR
 CC TO THE OXIDIZED BACTERIOCHLOROPHYLL IN THE PHOTOPHOSPHORYLATION
 CC PATHWAY. HOWEVER, IT MAY ALSO HAVE A ROLE IN THE RESPIRATORY CHAIN
 CC AND IS FOUND IN SOME NONPHOTOSYNTHETIC BACTERIA.
 CC - PTM: Binds 1 heme group per molecule.
 DR PIR; A00074; CCR02.
 DR HSSP; P00083; ICR7.
 DR InterPro; IPR003088; Cyt_C1.
 DR InterPro; IPR002327; Cyt_C1AB.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR Pfam; PR00034; Cytochrome C; 1.
 DR PRINTS; PR00604; CYTCHEMCTAB.
 DR PRODOM; PD000375; Cyt_C1AB; 1.
 DR PROSITE; PS00190; CYTOCHROME C; 1.
 KW Electron transport; Photosynthesis; Heme.
 FT BINDING 14 14 HEME (COVALENT).
 FT BINDING 17 17 HEME (COVALENT).
 FT BINDING 17 17 HEME (COVALENT).

YB14 SCHPO STANDARD; PRT; 646 AA.
 ID YB14 SCHPO
 AC 013659;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Putative GTP-binding protein CIB3.04c.
 GN SPAC1B3.04c.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 NCBI_Taxid=4896;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Scouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Voicakeart G., Aert R., Robben J., Grymptre B.,
 RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Leirich H., Reinhardt R., Pohl T.M.,
 RA Beyer P., Zimmermann W., Wedler H., Mambo R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hunt S.M.,
 RA Lucas M., Rocher M., Galliard C., Tallada V.A., Garzon A., Rhode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forberg S.L.,
 RA Carrutell L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880(2002).
 CC -1- SIMILARITY: Belongs to the GTP-binding elongation factor family.
 CC Lepa subfamily.
 CC -----
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 CC -----
 CC EMBL: Z98598; CAB1233.1; -
 CC PIR: T38022.
 CC HSP: P13551; IFNM.
 CC Genedb_Spombe: SPAC1B3.04c; -
 CC InterPro: IPR000795; EF_GTPbind.
 CC InterPro: IPR000640; EFG_C.
 CC InterPro: IPR009022; EFG_III_V.
 CC InterPro: IPR004161; EFTU_D2.
 CC InterPro: IPR006297; LepA.
 CC InterPro: IPR005225; Small_GTP.
 CC InterPro: IPR009000; Translat_factor.
 CC Pfam: PF00679; EFG_C.1.
 CC Pfam: PF00009; GTP_EFTU.1.
 CC Pfam: PF0144; GTP_EFTU_D2.1.
 CC PRINTS: PR00315; E1ONGATNCT.
 CC TIGRFAMs: TIGR00393; LepA.1.
 CC TIGRFAMs: TIGR00231; small1.GTP.1.
 CC PROSITE: PS00301; EFACOR_GTP.1.
 CC Hypothetical protein: GTP-binding.

FT NE_BIND 65 72 GTP (POTENTIAL).
 FT NE_BIND 130 134 GTP (POTENTIAL).
 FT NE_BIND 184 187 GTP (POTENTIAL).
 SQ SEQUENCE 646 AA; 72683 MW; F9FA9498D384503E CRC64;
 Query Match 41.8%; Score 41; DB 1; Length 646;
 Best Local Similarity 46.7%; Freq. No. 25;
 Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 Qy 3 LQAKICHOIQYFQ 17
 Db 108 VKAQTSMIYYHGO 122
 RESULT 12
 PRL2_ARATH STANDARD; PRT; 479 AA.
 ID PRL2_ARATH
 AC Q39190; Q94007; Q9LUR9;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Pp1/pp2A phosphatases pleiotropic regulator PRL2.
 GN PRL2 OR AT3G16550 OR MGL6.11.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Magnoliophyta; Eudicotyledons; core eudicots; rosids;
 OC Asterids II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_Taxid=3702;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=98438452; PubMed=9765207;
 RA Nemeth K., Salchert K., Putnocky P., Bhalerao R., Koncz-Kalman Z.,
 RA Stankovic-Stangeland B., Bako L., Mathur J., Okresz L., Stabel S.,
 RA Geigenberger P., Sitt M., Redei G.P., Schell J., Koncz C.;
 RT "Pleiotropic control of glucose and hormone responses by PRL1, a
 RT nuclear WD protein, in Arabidopsis.";
 RL Genes Dev. 12:3059-3073(1998).
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20277480; PubMed=10819329;
 RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
 RT features of the regions of 4,504,864 bp covered by sixty P1 and TAC
 RT clones.";
 RL DNA Res. 7:131-135(2000).
 [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=22954850; PubMed=14593172;
 RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J., Cheuk R.F.,
 RA Soultzwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
 RA Kalish-Newman G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
 RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Tortum M.J.,
 RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Anestri P.,
 RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.V., Carninci P.,
 RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gujral M., Hansen N.F.,
 RA Hayashizaki Y., Johnson-Hopson C., Hsu V.W., Iida K., Karnes M.,
 RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
 RA Kantiya A., Meyers C., Nakajima M., Narisaka M., Seki M., Sakurai T.,
 RA Satou M., Tamse R., Vaysberg M., Wallenberg E.K., Wong C., Yamamura Y.,
 RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RT "Empirical analysis of transcriptional activity in the Arabidopsis
 RT genome.";
 RL Science 302:842-846(2003).
 CC -1- FUNCTION: Pleiotropic regulator of Pp1 and Pp2A phosphatases.
 CC -1- SIMILARITY: Contains 7 WD repeats.
 CC -1- SIMILARITY: Belongs to the WD-repeat PRL1/PRL2 family.
 CC -1- CAUTION: Ref.2 sequence differs from that shown due to erroneous
 CC gene model prediction.
 CC -1- CAUTION: It is uncertain whether Met-1 or Met-3 is the initiator.

QY 2 ALOAKICHOIYFGOF 18
 DB 8 AVMLKIRPIDYFSOF 24

RESULT 9
 IFITS_HUMAN STANDARD; PRT; 482 AA.

AC Q13325;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Interferon-induced protein with tetratricopeptide repeats 5 (IFIT-5)
 DE (Retinotic acid- and interferon-inducible 58 kDa protein).
 GN IFIT5 OR R158.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98114590; PubMed=9398535;
 RA Nifkura T., Hirata R., Weil S.C.;
 RT "A novel interferon-inducible gene expressed during myeloid
 differentiation";
 RL Blood Cells Mol. Dis. 23:337-349(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreeas, and Spleen;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschuld S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Mariani K., Farmer A.A., Rubin G.M., Hong L.,
 Staudenroth M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ustin T.B., Toshynski S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallary S.J.,
 Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultyn S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 Butcherfield V.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- INDUCTION: By Interferons.
 CC -1- SIMILARITY: Belongs to the IFIT family.
 CC -1- SIMILARITY: Contains 8 TPR repeats.
 CC -----
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 CC -----
 CC EMBL, U34605; AA04934.1; -
 DR EMBL, BC025786; AA025786.1; -
 DR PIR, G02058; G02058.
 DR Genem; HGNC:13328; IFIT5.
 DR InterPro; IPR008940; Pfam; PF001440; TPR.
 DR InterPro; IPR001440; TPR.
 DR Pfam; PF001440; TPR.
 DR SMART; SM00028; TPR; 5.
 DR Repeat; TPR repeat; Interferon induction.
 FT REPEAT 51 84 TPR 1.
 FT REPEAT 94 127 TPR 2.

FT REPEAT 138 173 TPR 3.
 FT REPEAT 181 214 TPR 4.
 FT REPEAT 249 282 TPR 5.
 FT REPEAT 338 371 TPR 6.
 FT REPEAT 376 410 TPR 7.
 FT REPEAT 435 468 TPR 8.
 SQ SEQUENCE 482 AA; 55846 MW; 8045BC100384BE05 CRC64;

Query Match
 Best Local Similarity 42.9%; Score 42; DB 1; Length 482;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 9 HOIYOYFGOF 18
 DB 376 HOIHYGRF 385

RESULT 10
 DPOL_HSVB STANDARD; PRT; 1220 AA.

AC P28858;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE DNA polymerase (EC 2.7.7.7).
 GN 30.
 OS Equine herpesvirus type 1 (strain Abap) (EHV-1).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicellovirinae.
 OX NCBI_TaxID=31520;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92295566; PubMed=1318606;
 RA Telford E.A.R., Watson M.S., McBride K., Davison A.J.;
 RT "The DNA sequence of equine herpesvirus-1";
 RL Virology 189:304-316(1992).
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
 + (DNA)(N).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: Belongs to the DNA polymerase type-B family.
 CC -----
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 CC -----
 CC EMBL, M86664; AA02465.1; -
 DR PIR, D36798; D36798.
 DR InterPro; IPR006172; DNA_pol_B.
 DR InterPro; IPR006134; DNA_pol_B_dom.
 DR InterPro; IPR006133; DNA_pol_B_exo.
 DR Pfam; PF00136; DNA_pol_B_1.
 DR Pfam; PF00136; DNA_pol_B_1.
 DR Pfam; PF00136; DNA_pol_B_1.
 DR PRINTS; PR00104; DNA_pol_B_exo; 1.
 DR PRINTS; PR00106; DNAPOLB.
 DR SMART; SM00486; POLB; 1.
 DR PROSITE; PS00116; DNA_POLYMERASE_B; 1.
 KW Transferrase; DNA-directed DNA polymerase; DNA replication;
 KW DNA-binding; Nuclear protein.
 SQ SEQUENCE 1220 AA; 135956 MW; 858C14DCCCT1A65B CRC64;

Query Match
 Best Local Similarity 42.9%; Score 42; DB 1; Length 1220;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 ICHOIYFG 16
 DB 248 VCHTLYYFG 257

RESULT 11

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DR EMBL; X68817; CAA48715.1; -.

DR PIR; S33818; S33818.

DR InterPro; IPR002344; Lupus_La.

DR InterPro; IPR006630; Lupus_La.dom.

DR InterPro; IPR000504; RNA_rec_mot.

DR Pfam; PF05383; La; 1.

DR Pfam; PF00076; rrm; 1.

DR PRINTS; PR00302; LUPUSLA.

DR SMART; SM00715; LA; 1.

DR SMART; SM00360; RRM; 1.

DR PROSITE; PS00102; RRM_1.

DR PROSITE; PS00030; RRM_RNP_1; 1.

DR RNA-binding; Nuclear Protein; Phosphorylation.

FT DOMAIN 111 203 RNA-BINDING (RRM).

FT DOMAIN 196 212 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

FT DOMAIN 316 332 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

SQ SEQUENCE 428 AA; 48864 MW; AEB3A38B7D2B3EC3 CRC64;

Query Match 56.1%; Score 55; DB 1; Length 428;
Best Local Similarity 81.8%; Pred. No. 0.061;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 KICHOIQYFYG 16
DB 16 KICEQIEYFYG 26

RESULT 7

LA_AEDAL STANDARD; PRT; 383 AA.

ID LA_AEDAL Q26457;

AC 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE La protein homolog (La ribonucleoprotein) (La autoantigen homolog).

OS Aedes albopictus (Forest day mosquito).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Aedes.

OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes.

OX NCBI_TaxID=7160;

RN [1]

RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.

RX MEDLINE=96135233; PubMed=8551578;

RA Parignon N., Straus J.H.;

RT "Mosquito homolog of the La autoantigen binds to Sindbis virus RNA.";

RT J. Virol. 70:1173-1181(1996).

CC -1- FUNCTION: May be involved in transcription termination by RNA polymerase III. Binds RNA and DNA. Binds to the 3' end of the minus strand of Sindbis virus RNA. This may be significant for Sindbis virus RNA replication.

CC -1- SUBCELLULAR LOCATION: Nuclear. Primarily nuclear, but significant amounts are present in the cytoplasm.

CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.

CC -1- SIMILARITY: TO VERTEBRATE PROTEIN LA.

CC -----

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CC -----

DR EMBL; S80954; AAB35931.1; -.

DR InterPro; IPR002344; Lupus_La.

DR InterPro; IPR006630; Lupus_La.dom.

DR InterPro; IPR000504; RNA_rec_mot.

DR Pfam; PF05383; La; 1.

DR Pfam; PF00076; rrm; 1.

DR PRINTS; PR00302; LUPUSLA.

DR SMART; SM00715; LA; 1.

DR SMART; SM00360; RRM; 1.

DR PROSITE; PS00102; RRM; 1.

DR PROSITE; PS00030; RRM_RNP_1; FALSE NEG.

KW RNA-binding; Nuclear Protein; DNA-Binding.

FT DOMAIN 141 228 RNA-BINDING (RRM).

FT DOMAIN 171 178 ATP (POTENTIAL).

SQ SEQUENCE 383 AA; 44430 MW; 4E5CC8F21C40F452 CRC64;

Query Match 43.9%; Score 43; DB 1; Length 383;
Best Local Similarity 50.0%; Pred. No. 6.5;
Matches 7; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 LQAKICHOIQYFYG 16
DB 43 LEASTIROLEYFYG 56

RESULT 8

EX5A_BUCAL STANDARD; PRT; 602 AA.

ID EX5A_BUCAL AC P57530;

AC 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Exodeoxyribonuclease V alpha chain (EC 3.1.11.5).

GN RECD OR BU455.

OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum symbiotic bacterium).

OS Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; OC Enterobacteriaceae; Buchnera.

OX NCBI_TaxID=118099;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Tokyo 1998;

RX MEDLINE=20445173; PubMed=10993077;

RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;

RT "Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. APS.";

RT Nature 407:81-86(2000).

CC -1- FUNCTION: EXHIBITS SEVERAL CATALYTIC ACTIVITIES, INCLUDING ATP-DEPENDENT UNWINDING AND DNA-DEPENDENT ATPASE ACTIVITIES. STRAND CLEAVAGE OCCURS 5' TO 3' DURING THE UNWINDING OF DUPLEX DNA AT CHI SEQUENCES, WHICH LOCALLY STIMULATE RECOMBINATION (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: Exonucleolytic cleavage (in the presence of ATP) in either 5'- to 3'- or 3'- to 5'-direction to yield 5'-phosphooligonucleotides.

CC -1- SUBUNIT: Consist of three subunits; recB, recC and recD (by similarity).

CC -----

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CC -----

DR EMBL; AP001119; BAB13153.1; -.

DR InterPro; IPR003593; AAA_ATPase.

DR InterPro; IPR006344; RecD.

DR SMART; SM00382; AAA; 1.

DR TIGRFAMs; TIGR01447; recD; 1.

DR Hydroxylase; Nuclease; Exonuclease; Helicase; ATP-binding; KW DNA repair; Complete proteome.

FT NP BIND 171 178 ATP (POTENTIAL).

FT NP BIND 171 178 ATP (POTENTIAL).

SQ SEQUENCE 602 AA; 69494 MW; 340FPAE3BBA456059 CRC64;

Query Match 43.9%; Score 43; DB 1; Length 602;
Best Local Similarity 47.1%; Pred. No. 10;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

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DR EMBL; L00993; AAA39415.1; -
 DR EMBL; BC003820; AAH03820.1; -
 DR EMBL; Y07951; CAA69249.1; -
 DR MGD; MGI:98423; Ssb.
 DR GO; GO:0005634; C.nucleus; IDA.
 DR InterPro; IPR002344; Lupus_La.
 DR InterPro; IPR006630; Lupus_La.dom.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF05383; La; 1.
 DR Pfam; PF00076; xrm; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PS50102; RRM; 1.
 DR PROSITE; PS00030; RRM_RNP_1; 1.
 DR RNA-binding; Nuclear protein; Phosphorylation.
 DR RNA-binding; Nuclear protein; RNA-BINDING (RRM).
 FT DOMAIN 111 187
 SQ SEQUENCE 415 AA; 4756 MW; 2D75197692FDC933 CRC64;

Query Match 84.7%; Score 83; DB 1; Length 415;
 Best Local Similarity 82.4%; Pred. No. 8.4e-07;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 ALOAKICHQIQYFGQF 18
 Db 12 ALBAKICHOIEYFGDF 28

RESULT 5
 LAB_XENLA STANDARD; PRT; 427 AA.
 ID LAB_XENLA
 AC P28049;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Lupus La protein homolog B (La ribonucleoprotein B) (La autoantigen
 DE homolog B).
 GN LAB1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Oocyte;
 RA MEDLINE=93287095; PubMed=8510143;
 RA Scherly D., Stutz F., Lin-Marg N., Clarkson S.G.;
 RT "La proteins from Xenopus laevis. cDNA cloning and developmental
 RT expression.";
 RL J. Mol. Biol. 231:196-204 (1993).
 CC -!- FUNCTION: La protein plays a role in the transcription of RNA
 CC polymerase III. It is most probably a transcription termination
 CC factor. Binds to the 3' termin of virtually all nascent
 CC polymerase III transcripts (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -!- DEVELOPMENTAL STAGE: Barely detectable in stage I/II oocytes,
 CC accumulate in stage III/IV oocytes, then exhibit a roughly
 CC constant steady state level in mature oocytes, eggs, and early
 CC embryos.
 CC -!- PTM: Phosphorylated (Probable).
 CC -!- MISCELLANEOUS: There are two forms of La, Laa and Lab, in xenopus.
 CC -!- SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN.
 CC -!- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
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DR EMBL; X68818; CAA48716.1; -
 DR PIR; S33817; S33817.
 DR InterPro; IPR002344; Lupus_La.
 DR InterPro; IPR006630; Lupus_La.dom.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF05383; La; 1.
 DR Pfam; PF00076; xrm; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PS50102; RRM; 1.
 DR PROSITE; PS00030; RRM_RNP_1; FALSE NEG.
 DR RNA-binding; Nuclear protein; Phosphorylation.
 DR RNA-binding; Nuclear protein; RNA-BINDING (RRM).
 FT DOMAIN 110 202
 SQ SEQUENCE 427 AA; 48995 MW; 45F3146F8934A355 CRC64;

Query Match 60.2%; Score 59; DB 1; Length 427;
 Best Local Similarity 71.4%; Pred. No. 0.012;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 LQAKICHQIQYFG 16
 Db 12 LDTKICEQIEYFG 25

RESULT 6
 LAa_XENLA STANDARD; PRT; 428 AA.
 ID LAa_XENLA
 AC P28048;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Lupus La protein homolog A (La ribonucleoprotein A) (La autoantigen
 DE homolog A).
 GN LAa1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Oocyte;
 RA MEDLINE=93287095; PubMed=8510143;
 RA Scherly D., Stutz F., Lin-Marg N., Clarkson S.G.;
 RT "La proteins from Xenopus laevis. cDNA cloning and developmental
 RT expression.";
 RL J. Mol. Biol. 231:196-204 (1993).
 CC -!- FUNCTION: La protein plays a role in the transcription of RNA
 CC polymerase III. It is most probably a transcription termination
 CC factor. Binds to the 3' termin of virtually all nascent
 CC polymerase III transcripts (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -!- DEVELOPMENTAL STAGE: Barely detectable in stage I/II oocytes,
 CC accumulate in stage III/IV oocytes, then exhibit a roughly
 CC constant steady state level in mature oocytes, eggs, and early
 CC embryos.
 CC -!- PTM: Phosphorylated (Probable).
 CC -!- MISCELLANEOUS: There are two forms of La, Laa and Lab, in xenopus.
 CC -!- SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN.
 CC -!- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
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DR PROSITE: PS00030; RRM_RNP_1; 1.
 KW Systemic lupus erythematosus; RNA-binding; Phosphorylation;
 KM Nuclear protein.
 FT DOMAIN 111 187 RNA-BINDING (RRM).
 FT MOD_RES 366 366 PHOSPHORYLATION (BY CK2).
 SQ SEQUENCE 408 AA; 46837 MW; EC153C15F9187FC4 CRC64;

Query Match 88.8%; Score 87; DB 1; Length 408;
 Best Local Similarity 83.3%; Pred. No. 1,7e-07;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AALQAKICHQIYYFGQF 18
 |||:|||||:|||||
 DB 11 AALEAKICHQIYYFGDF 28

RESULT 3

LA_RAT STANDARD; PRT; 415 AA.

AC P38656;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lupus La protein homolog (La ribonucleoprotein) (La autoantigen
 DE homolog).
 GN SSB OR SS-B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93246255; PubMed=7916708;
 RA Samesi I., Troester H., Bartsch H., Schwemle M., Igloi G.L.,
 RA Bachmann M.;
 RT "Isolation of rat cDNA clones coding for the autoantigen SS-B/La:
 RT detection of species-specific variations";
 RL Gene 1261265-266(1993).

CC -1- FUNCTION: La protein plays a role in the transcription of RNA
 CC polymerase III. It is most probably a transcription termination
 CC factor. Binds to the 3' termini of virtually all nascent
 CC polymerase III transcripts. It is associated with precursor forms
 CC of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S,
 CC and 7-2 RNAs.

CC -1- SUBUNIT: Interacts with DDX15 (By similarity).

CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).

CC -1- PTM: Phosphorylated (By similarity).

CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.

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CC -----
 CC EMBL: X67859; CAA48043.1; -.
 CC PIR: JCI494; JCI494.
 CC InterPro: IPR002344; Lupus_La.
 CC InterPro: IPR006630; Lupus_La_dom.
 CC InterPro: IPR005054; RNA_rec_mot.
 CC Pfam: PF05383; La; 1.
 CC Pfam: PF00076; rrm; 1.
 CC PRINTS: PRO0302; LUPUSLA.
 CC SMART: SM00715; LA; 1.
 CC SMART: SM00360; RRM; 1.
 CC PROSITE: PS0102; RRM; 1.
 CC PROSITE: PS00030; RRM_RNP_1; 1.
 CC RRNA-binding; RRM_Nuclear protein; Phosphorylation.
 CC DOMAIN 111 187 RNA-BINDING (RRM).
 CC SEQUENCE 415 AA; 47777 MW; 033PF9CC1E475F98 CRC64;

Query Match 88.8%; Score 87; DB 1; Length 415;
 Best Local Similarity 83.3%; Pred. No. 1,7e-07;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AALQAKICHQIYYFGQF 18
 |||:|||||:|||||
 DB 11 AALEAKICHQIYYFGDF 28

RESULT 4

LA_MOUSE STANDARD; PRT; 415 AA.

AC P32067;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Lupus La protein homolog (La ribonucleoprotein) (La autoantigen
 DE homolog).
 GN SSB OR SS-B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93203630; PubMed=8454877;
 RA Topfer F., Gordon T., McCluskey J.;
 RT "Characterization of the mouse autoantigen La (SS-B). Identification
 RT of conserved RNA-binding motifs; a putative ATP binding site and
 RT reactivity of recombinant protein with poly(U) and human
 RT autoantibodies";
 RL J. Immunol. 150:3091-3100(1993).

CC -1- FUNCTION: La protein plays a role in the transcription of RNA
 CC polymerase III. It is most probably a transcription termination
 CC factor. Binds to the 3' termini of virtually all nascent
 CC polymerase III transcripts. It is associated with precursor forms
 CC of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S,
 CC and 7-2 RNAs.

CC -1- SUBUNIT: Interacts with DDX15 (By similarity).

CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).

CC -1- PTM: Phosphorylated (By similarity).

CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.

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CC -----
 CC EMBL: X67859; CAA48043.1; -.
 CC PIR: JCI494; JCI494.
 CC InterPro: IPR002344; Lupus_La.
 CC InterPro: IPR006630; Lupus_La_dom.
 CC InterPro: IPR005054; RNA_rec_mot.
 CC Pfam: PF05383; La; 1.
 CC Pfam: PF00076; rrm; 1.
 CC PRINTS: PRO0302; LUPUSLA.
 CC SMART: SM00715; LA; 1.
 CC SMART: SM00360; RRM; 1.
 CC PROSITE: PS0102; RRM; 1.
 CC PROSITE: PS00030; RRM_RNP_1; 1.
 CC RRNA-binding; RRM_Nuclear protein; Phosphorylation.
 CC DOMAIN 111 187 RNA-BINDING (RRM).
 CC SEQUENCE 415 AA; 47777 MW; 033PF9CC1E475F98 CRC64;

FT DOMAIN 111 187 RNA-BINDING (RM).
 SQ. SEQUENCE 404 AA; 46534 MW; 4EE30B5C262AD6A1 CRC64;
 Query Match 88.8%; Score 87; DB 1; Length 404;
 Best Local Similarity 83.3%; Pred. No. 1.7e-07;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AALQAKICHQIQYFGQF 18
 |||:|||||:|||||
 DB 11 AALEAKICHQIEYFGEF 28

RESULT 2
 LA HUMAN STANDARD; PRT; 408 AA.
 ID P05455;
 AC 01-NOV-1988 (Rel. 09, Created)
 DT 01-JUL-1989 (Rel. 11, Last annotation update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Lupus La protein (S)ogen syndrome type B antigen (SS-B) (La
 ribonucleoprotein) (La autoantigen).
 GN SSB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Eureleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RX MEDLINE=89202037; PubMed=2468131;
 RT "Chan E.K.L., Sullivan K.F., Tan E.M.;
 "Ribonucleoprotein SS-B/La belongs to a protein family with consensus
 sequences for RNA-binding.";
 RT Nucleic Acids Res. 17:2233-2244(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89053970; PubMed=3192525;
 RT Chambers J.C., Keman D., Martin B.J., Keene J.D.;
 "Genomic structure and amino acid sequence domains of the human La
 autoantigen.";
 RT J. Biol. Chem. 263:18043-18051(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta, and Skeletal muscle;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stappleton W., Soares M.B., Bonaldo M.F., Cassavani T.L., Scheetz T.E.,
 Brownstein M.J., Ueda T.B., Tomihata S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.B., Peters G.J., Abramson R.D., Mulyan S.J.,
 Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Morley J.C., McKernan K.J., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalón D.K., Muzny D.M., Sedergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Heintz B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butlerfield V.S.N., Krzywicki M.I., Skalka U., Smilg D.E.,
 Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE OF 54-408 FROM N.A.
 RX MEDLINE=88199081; PubMed=2455201;
 RA Scuzes A.D., Peterson M.G., McNeillage L.J., Whittingham S.,
 Coppel R.S.;
 "Characteristics and epitope mapping of a cloned human autoantigen
 La.";
 RT J. Immunol. 140:3212-3216(1988).
 RN [5]

RP SEQUENCE OF 54-97 FROM N.A.
 RX MEDLINE=85166283; PubMed=3856888;
 RA Chambers J.C., Keene J.D.;
 RT "Isolation and analysis of cDNA clones expressing human lupus La
 antigen.";
 RT Proc. Natl. Acad. Sci. U.S.A. 82:2115-2119(1985).
 RN [6]
 RP FUNCTION.
 RX MEDLINE=89251617; PubMed=2470590;
 RA Gottlieb E., Steltz J.A.;
 RT "Function of the mammalian La protein: evidence for its action in
 transcription termination by RNA polymerase III.";
 RT EMBO J. 8:851-861(1989).
 RN [7]
 RP PHOSPHORYLATION.
 RX MEDLINE=97207017; PubMed=9054510;
 RA Fan H., Sakulich A.L., Goodier J.L., Zhang X., Qin J., Marate R.J.;
 RT "Phosphorylation of the human La antigen on serine 366 can regulate
 recycling of RNA polymerase III transcription complexes.";
 RT Cell 88:707-715(1997).
 RN [8]
 RP INTERACTION WITH DDIX15.
 RX MEDLINE=22346609; PubMed=12458796;
 RA Fournaux M.A., Kolman M.J.M., Van der Heijden A., De Jong A.S.,
 Van Venrooij W.J., Pruyn G.J.M.;
 RT "The human La (SS-B) autoantigen interacts with DDIX15/hPrp43, a
 putative DEAD-box RNA helicase.";
 RT RNA 8:1428-1443(2002).
 CC -1- FUNCTION: La protein plays a role in the transcription of RNA
 polymerase III transcripts. It is most probably a transcription termination
 factor. Binds to the 3' terminus of virtually all nascent
 polymerase III transcripts. It is associated with precursor forms
 of RNA polymerase III transcripts including crRNA and 4.5S, 5S, 7S,
 and 7-2 RNAs.
 CC -1- SUBUNIT: Interacts with DDIX15.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- PTM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES ARE AT THE
 C-TERMINAL PART OF THE PROTEIN.
 CC -1- PTM: The N-terminus is blocked.
 CC -1- DISEASE: Sera from patients with systemic lupus erythematosus
 often contain antibodies that react with the normal cellular
 La protein as if this antigen was foreign.
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
 CC -----
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 CC -----
 DR EMBL; X13697; CAA11985.1; -
 DR EMBL; J04205; AAA51885.1; -
 DR EMBL; BC001289; AAH01289.1; -
 DR EMBL; BC020818; AAH20818.1; -
 DR PIR; A31888; A31888.
 DR Genew; HGNC:11316; SSB.
 DR MIM; 109090; -
 DR GO; GO:0030529; C:ribonucleoprotein complex; TAS.
 DR GO; GO:0003729; F:RNA binding; TAS.
 DR GO; GO:0000449; F:RNA binding; TAS.
 DR GO; GO:0008334; P:histone mRNA metabolism; TAS.
 DR GO; GO:0006400; P:RNA modification; TAS.
 DR InterPro; IPR002344; Lupus La.
 DR InterPro; IPR006630; Lupus La dom.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF00076; xrm; 1.
 DR Pfam; PF00076; xrm; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR SMART; SMO0715; LA; 1.
 DR SMART; SMO0360; RRM; 1.
 DR PROSITE; PS50102; RRM; 1.

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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:01:41 ; Search time 7.24022 Seconds
(without alignments)
129.452 Million cell updates/sec

Title: US-09-836-073-3

Perfect score: 98
Sequence: 1 AALQAKICHQIQYFGQF 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	88.8	404	1	LA_BOVIN
2	87	88.8	404	1	LA_BOVIN
3	87	88.8	404	1	LA_BOVIN
4	83	84.7	415	1	LA_RAT
5	83	84.7	415	1	LA_MOUSE
6	55	60.2	427	1	LA_XENLA
7	55	60.2	427	1	LA_XENLA
8	43	43.9	383	1	LA_AEDAL
9	43	43.9	383	1	LA_AEDAL
10	42	42.9	482	1	LA_HUMAN
11	42	42.9	482	1	LA_HUMAN
12	41	41.8	1220	1	LA_HUMAN
13	39.5	40.3	503	1	LA_HUMAN
14	39	39.8	104	1	LA_HUMAN
15	39	39.8	183	1	LA_HUMAN
16	39	39.8	390	1	LA_HUMAN
17	39	39.8	397	1	LA_HUMAN
18	39	39.8	631	1	LA_HUMAN
19	39	39.8	735	1	LA_HUMAN
20	39	39.8	926	1	LA_HUMAN
21	39	39.8	1221	1	LA_HUMAN
22	38.5	39.3	940	1	LA_HUMAN
23	38.5	39.3	977	1	LA_HUMAN
24	38.5	39.3	977	1	LA_HUMAN
25	38.5	39.3	977	1	LA_HUMAN
26	38	38.8	251	1	LA_HUMAN
27	38	38.8	305	1	LA_HUMAN
28	38	38.8	786	1	LA_HUMAN
29	38	38.8	1088	1	LA_HUMAN
30	38	38.8	1107	1	LA_HUMAN
31	38	38.8	1136	1	LA_HUMAN
32	38	38.8	1189	1	LA_HUMAN
33	38	38.8	1596	1	LA_HUMAN

34	37	37.8	227	1	MOAR_KLEAE
35	37	37.8	231	1	MTNA_BACSU
36	37	37.8	243	1	SDGF_RAT
37	37	37.8	309	1	FDHE_PSEAE
38	37	37.8	359	1	CKR3_MOUSE
39	37	37.8	357	1	CARA_BUCBP
40	37	37.8	433	1	THIC_FUSNN
41	37	37.8	463	1	Y863_SYNY3
42	37	37.8	464	1	CASB_KLEOX
43	37	37.8	466	1	SRO9_YEAST
44	37	37.8	480	1	GIGA_RHTR
45	37	37.8	487	1	GATB_CHLVC

ALIGNMENTS

RESULT 1	ID	LA_BOVIN	STANDARD	PRT	404 AA.
AC	P10881				
DT	01-JUL-1989 (Rel. 11, Created)				
DT	01-JUL-1989 (Rel. 11, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Lupus La protein homolog (La ribonucleoprotein) (La autoantigen homolog)				
DE	SSB.				
OS	Bos taurus (Bovine).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
OC	Bovidae; Bovinae; Bos.				
OX	NCBI_TaxID=9913;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Pituitary;				
RX	MEDLINE=89202037; PubMed=2468131;				
RA	Chan E.K.L., Sullivan K.F., Tan E.M.;				
RT	"Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences for RNA-binding."				
RL	Nucleic Acids Res. 17:2233-2244(1989).				
CC	-1- FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' terminus of virtually all nascent polymerase III transcripts. It is associated with precursor forms of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S, and 7-2 RNAs.				
CC	-1- SUBUNIT: Interacts with DDX15 (By similarity).				
CC	-1- SUBCELLULAR LOCATION: Nuclear (Probable).				
CC	-1- PM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES ARE AT THE C-TERMINAL PART OF THE PROTEIN.				
CC	-1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ebi.ac.uk/announcements or send an email to license@ebi.ac.uk).				
CC	EMBL: X13698; CAA31986.1; -				
DR	PIR: S03849; S03849.				
DR	InterPro: IPR002344; Lupus La.				
DR	InterPro: IPR006630; Lupus La dom.				
DR	InterPro: IPR005054; RNA_rec_mot.				
DR	Pfam: PF05383; La; 1.				
DR	Pfam: PF00076; rrm; 1.				
DR	PRINTS: PR00302; LupusLa.				
DR	SMART: SM00715; LA; 1.				
DR	SMART: SM00360; RRM; 1.				
DR	PROSITE: PS50102; RRM; 1.				
DR	PROSITE: PS00030; RRM_RNP_1; 1.				
KW	RNA-binding; Nuclear protein; Phosphorylation.				

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Matches 5; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 3 LQAKICHQIQYRQGF 18
| : : | : : | : |

Db 520 LKTRVCNLSLKYSAMP 535

RESULT 15

DJBEC3

DNA-directed DNA polymerase (EC 2.7.7.7) - equine herpesvirus 1 (strain Ab4p)

C;Species: equine herpesvirus 1

A;Note: host Equus caballus (domestic horse)

C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 27-Oct-2003

C;Accession: D36798

R;RefSeq: E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.

submitted to GenBank, March 1992

A;Description: The DNA sequence of equine herpesvirus-1.

A;Reference number: A36805

A;Accession: D36798

A;Molecule type: DNA

A;Residues: 1-1220 <TEL>

A;Cross-references: GB:M86664; NID:G330791; PIDN:AAB02465.1; PID:G330822

R;RefSeq: E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J.

Virology 189, 304-316, 1992

A;Title: The DNA sequence of equine herpesvirus-1.

A;Reference number: A41831; MUID:92295566; PMID:1318606

A;Contents: annotation; possible protein-coding frames

A;Note: neither amino acid nor nucleotide sequence is given

C;Genetics:

A;Gene: 30

C;Superfamily: DNA polymerase

C;Keywords: DNA binding; DNA replication; nucleotidyltransferase

Query Match Similarity 42.9%; Score 42; DB 1; Length 1220;

Best Local Similarity 60.0%; Pred. No. 63;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 ICHQIQYRFG 16
| : : | : : | : |

Db 248 VCHTTLTYFG 257

Search completed: September 10, 2004, 18:02:27
Job time : 16.0782 secs

RESULT 10

T30953

hypothetical protein C44E4.4 - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*

C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000

C/Accession: T30953
 R:Sammons, L.; Wohldmann, P.; Gilling, B.

submitted to the EMBL Data Library, August 1999

A>Description: The sequence of *C. elegans* cosmid C44E4.

A:Reference number: Z20945

A:Accession: T30953

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-396 <SAM>

A:Cross-references: EMBL:AF003140; PIDN:AA54169.1

A:Experimental source: strain Bristol N2; clone C44E4

C:Genetics:

A:Map position: 1

A:introns: 45/1; 114/3

A>Note: C44E4.4

C:Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology

Query Match 42.9%; Score 42; DB 2; Length 396;
 Best Local Similarity 63.6%; Pred. No. 21;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 6 KICHQIYVFG 16
 |||::|||
 DB 15 KIHKQLEYFG 25

RESULT 11

G02058

retinoid acid- and interferon-inducible 58K protein R158 - human
 C:Species: *Homo sapiens* (man)

C>Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 29-Sep-1999

C/Accession: G02058

R:Well, S.C.

submitted to the EMBL Data Library, August 1995

A:Reference number: H00758

A:Accession: G02058

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-482 <WEI>

A:Cross-references: EMBL:U34605; NID:g1144510; PIDN:AAA4934.1; PID:g1144511

C:Superfamily: interferon-induced 56K protein

Query Match 42.9%; Score 42; DB 2; Length 482;
 Best Local Similarity 60.0%; Pred. No. 26;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 9 HOIOYVFG 18
 |||::|||
 DB 376 HOIHVYGRF 385

RESULT 12

H71887

hypothetical protein jhp0797 - *Helicobacter pylori* (strain J99)
 C:Species: *Helicobacter pylori*

A:Variety: strain J99

C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 28-Jul-2000

C/Accession: H71887

R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;

; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;

Nature 397, 176-180, 1999

A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path

A:Reference number: A71800; MUID:99120557; PMID:9923682

A:Accession: H71887

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-541 <ARN>

A:Cross-references: GB:AE001509; GB:AE001439; NID:g4155350; PIDN:AAD06373.1; PID:g415536

A:Experimental source: strain J99

C:Genetics:

A:Gene: jhp0797

C:Superfamily: *Helicobacter pylori* hypothetical protein jhp0797

Query Match 42.9%; Score 42; DB 2; Length 541;
 Best Local Similarity 50.0%; Pred. No. 29;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 AALQKICHQIQ 12
 |||::|||
 DB 123 AEVDKICHQVE 134

RESULT 13

G64627

hypothetical protein HP0863 - *Helicobacter pylori* (strain 26695)
 C:Species: *Helicobacter pylori*

C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 28-Jul-2000

C/Accession: G64627

R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.

son, J.D.; Kelley, J.M.; Cotton, M.D.; Woldman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.

Nature 386, 539-547, 1997

A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.

A:Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.

A:Reference number: A64520; MUID:97394467; PMID:9252185

A:Accession: G64627

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-542 <TON>

A:Cross-references: GB:AE000596; GB:AE000511; NID:g2313982; PIDN:AAD07917.1; PID:g231400

C:Superfamily: *Helicobacter pylori* hypothetical protein jhp0797

Query Match 42.9%; Score 42; DB 2; Length 542;
 Best Local Similarity 50.0%; Pred. No. 29;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 AALQKICHQIQ 12
 |||::|||
 DB 123 AEVDKICHQVE 134

RESULT 14

D96656

hypothetical protein Fl6M19.21 [imported] - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C/Accession: D96656

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luhrs, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Talon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.

A:Reference number: A66141; MUID:21016719; PMID:11130712

A:Accession: D96656

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-658 <STO>

A:Cross-references: GB:AE005173; NID:g6598840; PIDN:AA18695.1; GSPDB:GN00141

C:Genetics:

A:Gene: Fl6M19.21

A:Map position: 1

Query Match 42.9%; Score 42; DB 2; Length 658;
 Best Local Similarity 31.2%; Pred. No. 35;

R.Scherly, D.; Sprutz, F.; Lin-Marg, N.; Clarkson, S.G.
J. Mol. Biol. 231, 196-204, 1993
A:Title: La proteins from *Xenopus laevis*. cDNA cloning and developmental expression.
A:Reference number: S33817; MUID:93287095; PMID:8510143
A:Accession: S33818
A:Molecule type: mRNA
A:Residues: 1-428 <SC>
A:Cross-references: EMBL:X68817; NID:G64873; PIDN:CAA48715.1; PID:G64874
A:Comment: This protein associates with a variety of small RNA molecules, most of which
act as a transcription termination factor.
C:Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology
C:Keywords: phosphoprotein; RNA binding
F:112-178/Domain: ribonucleoprotein repeat homology <RRM>
F:113-118/Region: RNA-binding RNP2 motif
F:151-158/Region: RNA-binding RNP1 motif
F:228-428/Domain: phosphorylated status predicted <PHY>

Query Match 56.1%; Score 55; DB 1; Length 428;
Best Local Similarity 81.8%; Pred. No. 0.13;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 KICHOIQYFG 16
DB 16 KICEQIEYFG 26
||| ||| |||
||| ||| |||

RESULT 6
H89777
capsular polysaccharide synthesis enzyme CapsP [imported] - *Staphylococcus aureus* (strain
C:Species: *Staphylococcus aureus*
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: H89777
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H89777
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-391 <KUR>
A:Cross-references: GB:BA000018; PID:G1370080; PIDN:BA41379.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: capsP
C:Superfamily: lipopolysaccharide biosynthesis protein bp1d

Query Match 46.9%; Score 46; DB 2; Length 391;
Best Local Similarity 63.6%; Pred. No. 4.3;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 KICHOIQYFG 16
DB 366 RICAEIYFG 376
||| ||| |||
||| ||| |||

RESULT 7
C82379
response regulator VC1086 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)
C:Species: *Vibrio cholerae*
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 28-Apr-2003
C:Accession: C82379
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.D.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A:Reference number: A82035; MUID:2040683; PMID:10952301
A:Accession: C82379
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-568 <HEI>

A:Cross-references: GB:AE004434; GB:AE003853; NID:G9658531; PIDN:AAF6979.1; GSPDB:GN00
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1086
A:Map position: 2
C:Superfamily: response regulator, Hnr type; response regulator homology

Query Match 45.9%; Score 45; DB 2; Length 568;
Best Local Similarity 42.9%; Pred. No. 9.1;
Matches 6; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 3 LQAKICHOIQYFG 16
DB 156 LMEEMCHQYEHFG 169
||| ||| |||
||| ||| |||

RESULT 8
A84983
exodeoxyribonuclease V (EC 3.1.11.5) 67 kD polypeptide [imported] - *Buchnera* sp. (strain
C:Species: *Buchnera* sp.
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 27-Nov-2001
C:Accession: A84983
R:Shigenobu, S.; Matanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A:Title: Genome sequence of the endocellular bacterial symbiont of aphids *Buchnera* sp.
A:Reference number: A84930; MUID:20445173; PMID:10993077
A:Accession: A84983
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-602 <STO>
A:Cross-references: GB:AP000398; GSPDB:GN00144
A:Experimental source: strain APS
C:Genetics:
A:Gene: recD; BU455
C:Superfamily: exodeoxyribonuclease V 67k chain
C:Keywords: hydrolase

Query Match 43.9%; Score 43; DB 2; Length 602;
Best Local Similarity 47.1%; Pred. No. 21;
Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 ALQAKICHOIQYFG 18
DB 8 AVKLKIRPIDFYSG 24
||| ||| |||
||| ||| |||

RESULT 9
D97337
mismatch repair protein Muts-like ATPase [imported] - *Clostridium acetobutylicum*
C:Species: *Clostridium acetobutylicum*
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: D97337
R:Nolling, U.; Breton, G.; Omejchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C1
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: D97337
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-577 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK81487.1; PID:G1502659; GSPDB:GN00168
A:Experimental source: *Clostridium acetobutylicum* ATCC624
C:Genetics:
A:Gene: CAC3563

Query Match 43.4%; Score 42.5; DB 2; Length 577;
Best Local Similarity 38.1%; Pred. No. 25;
Matches 8; Conservative 6; Mismatches 2; Indels 5; Gaps 1;

QY 3 LQAKICHOIQY-----YFG 18
DB 53 MKAKIHKLNYERFRKRWGEF 73
||| ||| |||
||| ||| |||

A:Reference number: S03848; UID:89202037; PMID:2468131
 A:Accession: S03848
 A:Molecule type: mRNA
 A:Residues: 1-408 <CH2>
 A:Cross-references: EMBL:X13697; NID:936414; PID:CAA31985.1; PID:936415
 R:Chambers, J.C.; Keene, J.D.
 Proc. Natl. Acad. Sci. U.S.A. 82, 2115-2119, 1985
 A:Title: Isolation and analysis of cDNA clones expressing human lupus Ia antigen.
 A:Reference number: A22956; UID:85166283; PMID:3856888
 A:Accession: A22956
 A:Molecule type: mRNA
 A:Residues: 45-97, 'LK' <CH3>
 A:Cross-references: GB:J04205
 A:Note: This sequence has been revised in reference A31888
 R:Nyman, U.; Ringertz, N.R.; Petersson, I.
 Immunol. Lett. 22, 65-72, 1989
 A:Title: Demonstration of an amino terminal Ia epitope recognized by human anti-Ia sera.
 A:Reference number: A61051; UID:89379261; PMID:2476379
 A:Accession: A61051
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-19, 'E', 21-47 <NYM>
 R:Sturges, A.D.; Peterson, M.G.; McNeilage, L.J.; Whittingham, S.; Coppel, R.L.
 J. Immunol. 140, 3212-3218, 1988
 A:Title: Characteristics and epitope mapping of a cloned human autoantigen Ia.
 A:Reference number: S11013; UID:88199081; PMID:2452201
 A:Accession: S11013
 A:Molecule type: mRNA
 A:Residues: 'E', 55-287, 'V', 289-408 <STU>
 A:Cross-references: EMBL:M0328; NID:9337456; PID:AAA36577.1; PID:9337457
 R:Kohanka, H.; Yamamoto, K.; Fujii, H.; Mura, H.; Miyasaka, N.; Nishioaka, K.; Miyamoto, J.
 Clin. Invest. 85, 1566-1574, 1990
 A:Title: Fine epitope mapping the human SS-B/La protein: Identification of a distinct autoantigen.
 A:Reference number: I55553; UID:90237237; PMID:1692037
 A:Accession: I55553
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 81-107 <RES>
 A:Cross-references: GB:M3561; NID:9338491; PID:AAA36652.1; PID:9338495
 A:Accession: I70205
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 174-224 <RES2>
 A:Cross-references: GB:M3563; NID:9338492; PID:AAA36653.1; PID:9338496
 A:Accession: I70206
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 279-342 <RES3>
 A:Cross-references: GB:M3562; NID:9338493; PID:AAA36654.1; PID:9338497
 A:Comment: This protein associates with a variety of small RNA molecules, most of which act as a transcription termination factor.
 C:Genetics:
 A:Gene: GDB:SSB
 A:Cross-references: GDB:125359; OMIM:109090
 A:Map position: 2
 A:Introns: 22/3; 57/2; 115/3; 151/3; 185/2; 209/2; 223/3; 264/3; 380/2
 C:Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
 C:Keywords: phosphoprotein; RNA binding
 F:112-178/Domain: ribonucleoprotein repeat homology <RRM>
 F:113-118/Region: RNA-binding RNP2 motif
 F:151-158/Region: RNA-binding RNP1 motif
 F:228-408/Domain: phosphorylated #status experimental <PHY>

Query Match 88.8%; Score 87; DB 1; Length 408;
 Best Local Similarity 83.3%; Pred. No. 3.7e-07;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AALQAKICHQIQYFGQF 18
 |||:|||||:|||||
 Db 11 AALEAKICHQIEYFGDF 28

RESULT 3

JC1494
 N:Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 24-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
 C:Accession: JC1494; S25145
 R:Semel, I.; Troester, H.; Bartsch, H.; Schwemmler, M.; Igloi, G.L.; Bachmann, M.
 Gene 126, 265-268, 1993
 A:Title: Isolation of rat cDNA clones coding for the autoantigen SS-B/La: Detection of a
 A:Reference number: JC1494; UID:93246255; PMID:7916708
 A:Accession: JC1494
 A:Molecule type: mRNA
 A:Residues: 1-415 <SEM>
 A:Cross-references: GB:X67859; NID:955778; PID:CAA48043.1; PID:955779
 A:Experimental source: liver
 A:Comment: This protein associates with a variety of small RNA molecules, most of which act as a transcription termination factor.
 C:Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
 C:Keywords: phosphoprotein; RNA binding
 F:112-178/Domain: ribonucleoprotein repeat homology <RRM>
 F:113-118/Region: RNA-binding RNP2 motif
 F:151-158/Region: RNA-binding RNP1 motif
 F:227-415/Domain: phosphorylated #status predicted <PHY>

Query Match 88.8%; Score 87; DB 1; Length 415;
 Best Local Similarity 83.3%; Pred. No. 3.8e-07;
 Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AALQAKICHQIQYFGQF 18
 |||:|||||:|||||
 Db 11 AALEAKICHQIEYFGDF 28

RESULT 4

S33817
 N:Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
 C:Accession: S33817; S28544
 R:Schertly, D.; Stutz, F.; Lin-Marq, N.; Clarkson, S.G.
 J. Mol. Biol. 231, 196-204, 1993
 A:Title: La proteins from Xenopus laevis. cDNA cloning and developmental expression.
 A:Reference number: S33817; UID:93287095; PMID:8510143
 A:Accession: S33817
 A:Molecule type: mRNA
 A:Residues: 1-427 <SCH>
 A:Cross-references: EMBL:X68818; NID:964875; PID:CAA48716.1; PID:964876
 A:Comment: This protein associates with a variety of small RNA molecules, most of which act as a transcription termination factor.
 C:Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
 C:Keywords: phosphoprotein; RNA binding
 F:111-177/Domain: ribonucleoprotein repeat homology <RRM>
 F:112-117/Region: RNA-binding RNP2 motif
 F:150-157/Region: RNA-binding RNP1 motif
 F:227-427/Domain: phosphorylated #status predicted <PHY>

Query Match 60.2%; Score 59; DB 1; Length 427;
 Best Local Similarity 71.4%; Pred. No. 0.027;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 LQAKICHQIQYFG 16
 |||:|||||:|||||
 Db 12 LDTKICEQIEYFG 25

RESULT 5

S33818
 N:Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
 C:Accession: S33818; S28545

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:33:11 ; Search time 14.0782 Seconds
(without alignments)
122.988 Million cell updates/sec

Title: US-09-836-073-3

Perfect score: 98
Sequence: 1 AALQAKICHQIYFFGQF 18

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.78.*

1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	88.8	404	1	S03849
2	87	88.8	408	1	A31888
3	87	88.8	415	1	JC1494
4	59	60.2	427	1	S33817
5	55	56.1	428	1	S33818
6	46	46.9	391	2	H89777
7	45	45.9	391	2	C82379
8	43	43.9	602	2	A84983
9	42.5	43.4	577	2	D97337
10	42	42.9	396	2	T30953
11	42	42.9	482	2	G02058
12	42	42.9	541	2	H71887
13	42	42.9	542	2	G64627
14	42	42.9	658	2	D96656
15	42	42.9	1220	1	DJBEC3
16	42	42.9	1220	1	T42573
17	42	41.8	259	2	T49596
18	41	41.8	336	2	S49396
19	41	41.8	336	2	B90566
20	41	41.8	369	2	G90596
21	41	41.8	646	2	T38022
22	40	40.8	120	2	AT1482
23	40	40.8	133	2	A83987
24	40	40.8	175	2	S23697
25	40	40.8	380	2	UC5217
26	40	40.8	598	2	T05888
27	40	40.8	658	2	T19487
28	39.5	40.3	163	2	H87733
29	39.5	40.3	503	2	F82275

30	39.5	40.3	503	2	JN0524	lept protein - Vib
31	39	39.8	104	1	CCRD2	cytochrome c2 - Rh
32	39	39.8	166	2	T32701	hypothetical prote
33	39	39.8	183	2	B29017	zein Zc1 - maize
34	39	39.8	346	2	A82659	two-component syst
35	39	39.8	388	2	AF0183	probable exported
36	39	39.8	390	2	A53773	La/SS-B homolog D-
37	39	39.8	390	2	A53781	ribonucleoprotein
38	39	39.8	461	2	T27651	hypothetical prote
39	39	39.8	487	2	T27653	hypothetical prote
40	39	39.8	505	2	B90181	Na+/H+ antiporter
41	39	39.8	506	2	F85016	probable RING zinc
42	39	39.8	529	2	T00677	hypothetical prote
43	39	39.8	631	2	S36505	E1 protein - human
44	39	39.8	696	2	F83886	penicillin-binding
45	39	39.8	735	2	T41187	hypothetical prote

ALIGNMENTS

RESULT 1

S03849
ribonucleoprotein La - bovine
N/Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
C/Species: Bos primigenius taurus (cattle)
C/Date: 31-Dec-1990 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C/Accession: S03849
R/Chan, E.K.L.; Sullivan, K.F.; Tan, E.M.
Nucleic Acids Res. 17, 2233-2244, 1989
A/Title: Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences
A/Reference number: S03848; MUID:89202037; PMID:2468131
A/Accession: S03849

A/Molecule type: mRNA
A/Residues: 1-404 <CH>
A/Cross-references: EMBL:X13698; NID:9755; PIDD:CAA31986.1; PID:9756

A/Note: part of this sequence was confirmed by protein sequencing
C/Comment: This protein associates with a variety of small RNA molecules, most of which

act as a transcription termination factor.
C/Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology

C/Keywords: blocked amino end; phosphoprotein; RNA binding
F/112-178/Domain: ribonucleoprotein repeat homology <RHM>
F/113-118/Region: RNA-binding RNP2 motif
F/151-158/Region: RNA-binding RNP1 motif
F/228-404/Domain: phosphorylated #status predicted <PHX>

Query Match	Score	DB 1;	Length	404;
Best Local Similarity	88.8%;	Pred. No.	3.7e-07;	
Matches 15; Conservative	2;	Mismatches	1;	Indels 0; Gaps 0;
Db	11	AALQAKICHQIYFFGQF 18		
		: :		
		11 AALEKICHQIYFFGQF 28		

RESULT 2

A31888
ribonucleoprotein La - human
N/Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B; Sjogren syndrome antigen
C/Species: Homo sapiens (man)
C/Date: 21-May-1990 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C/Accession: A31888; S03848; A22956; A61051; S11013; I55553; I70205; I70206; A31273
R/Chan, E.K.L.; Kenan, D.; Martin, B.J.; Keene, J.D.
J. Biol. Chem. 263, 18043-18051, 1988
A/Title: Genomic structure and amino acid sequence domains of the human La autoantigen
A/Reference number: A31888; MUID:89053970; PMID:3192525
A/Accession: A31888

A/Molecule type: mRNA
A/Residues: 1-408 <CH>

A/Cross-references: GB:J04205; NID:9178686; PIDD:AAA51885.1; PID:9178687
R/Chan, E.K.L.; Sullivan, K.F.; Tan, E.M.
Nucleic Acids Res. 17, 2233-2244, 1989

A/Title: Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences

SPECTES=S.aureus (strain Mu50), and S.aureus (strain N315);
 RX MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekintzu K., Hirakawa H., Kohara S., Goto S., Yabuzaki J.,
 RA Kanetsu M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RT Lancel 357:1225-1240(2001).
 DR EMBL: AP003358; BAB56326.1; -
 DR EMBL: AP003329; BAB4139.1; -
 DR PIR: H89777; H89777.
 DR HSP: P27828; 1F6D.
 DR GO: GO:0008761; P:UDP-N-acetylglucosamine 2-epimerase activity; IEA.
 DR GO: GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
 DR GO: GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.
 DR InterPro: IPR003331; Epimerase_2.
 DR Pfam: PF02350; Epimerase_2; 1.
 DR TIGRFAMs: TIGR00236; wecB; 1.
 KM Complete proteome.
 SQ SEQUENCE 391 AA; 44372 MW; DDDF5FA715BCCECC CRC64;
 Query Match 52.1%; Score 50; DB 16; Length 391;
 Best Local Similarity 72.7%; Pred. No. 5.4;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 6 QICQIQIEYFG 16
 DB 366 RICEAIEYFG 376

RESULT 12
 Q9FL36 PRELIMINARY; PRT; 411 AA.
 AC Q9FL36;
 DT 01-MAR-2001 (TREMBlrel. 16; Created)
 DT 01-MAR-2001 (TREMBlrel. 16; Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25; Last annotation update)
 DE Similarity to RNA-binding protein.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=Columbia;
 RX MEDLINE=96344145; PubMed=9679202;
 RA Kaneko T., Kocant H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence
 RT features of the regions of 1,381,565 bp covered by twenty one
 RT physically assigned P1 and TAC clones.";
 RL DNA Res. 5:131-145(1998).
 DR EMBL: AB010638; BAB11080.1; -
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003723; F:RNA binding; IEA.
 DR InterPro: IPR002344; Lupus_La.
 DR InterPro: IPR006630; Lupus_La_dom.
 DR Pfam: PF05383; La; 1.
 DR Pfam: PF00076; rrm; 1.
 DR PRINTS: PR00302; LUPUSLA.
 DR SMART: SM00715; LA; 1.
 DR SMART: SM00360; RRM; 1.
 DR PROSITE: PS50102; RRM; 1.
 SQ SEQUENCE 411 AA; 45655 MW; A2EF62EB5B89B099 CRC64;
 Query Match 49.0%; Score 47; DB 10; Length 411;
 Best Local Similarity 53.3%; Pred. No. 18;

Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 3 LEAQICQIEYFG 17
 DB 92 LNKQIRQVEYFSD 106

RESULT 13
 ID Q94A38 PRELIMINARY; PRT; 422 AA.
 AC Q94A38;
 DT 01-DEC-2001 (TREMBlrel. 19; Created)
 DT 01-DEC-2001 (TREMBlrel. 19; Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25; Last annotation update)
 DE A75946250/MPL12.3.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TaxID=3702;
 RN RP SEQUENCE FROM N.A.
 RA Shin P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
 RA Ban J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,
 RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamita A.,
 RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
 RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
 RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,
 RT "Arabidopsis cDNA clones" to the EMBL/GenBank/DBJ databases.
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Shin P., Bowser L., Carninci P.,
 RA Chan M.M., Chang C.H., Dale J.M., Deng J.M., Hayashizaki Y.,
 RA Hsuan V.W., Ishida J., Jones T., Kamita A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
 RA Nguyen M., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M.,
 RA Southwick A., Tang C.C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
 RA Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A.,
 Ecker J.R.;
 RT "Arabidopsis ORF clones" to the EMBL/GenBank/DBJ databases.
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY050403; AA91419.1; -
 DR EMBL: BT000588; AA118157.1; -
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003723; F:RNA binding; IEA.
 DR InterPro: IPR002344; Lupus_La.
 DR InterPro: IPR006630; Lupus_La_dom.
 DR InterPro: IPR000504; RNA_rec_mot.
 DR Pfam: PF05383; La; 1.
 DR Pfam: PF00076; rrm; 1.
 DR PRINTS: PR00302; LUPUSLA.
 DR SMART: SM00715; LA; 1.
 DR SMART: SM00360; RRM; 1.
 DR PROSITE: PS50102; RRM; 1.
 SQ SEQUENCE 422 AA; 46842 MW; 4EC4BBF1E068F0E CRC64;
 Query Match 49.0%; Score 47; DB 10; Length 422;
 Best Local Similarity 53.3%; Pred. No. 18;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 3 LEAQICQIEYFG 17
 DB 103 LNKQIRQVEYFSD 117

RESULT 14
 Q87GS8 PRELIMINARY; PRT; 478 AA.
 AC Q87GS8;
 DT 01-JUN-2003 (TREMBlrel. 24; Created)

RT acquired MSA";
 RL Lancer 359:1819-1827(2002).
 DR EMBL; AB004822; BAB94004.1; -
 DR GO; GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity; IEA.
 DR GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
 DR GO; GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.
 DR InterPro; IPR003331; Epimerase_2.
 DR Pfam; PF02350; Epimerase_2; 1.
 DR TIGRFAMs; TIGR00236; wecB; 1.
 DR Complete proteome.
 KW SEQUENCE 381 AA; 43106 MW; 125E4D5D1904779C CRC64;

Query Match 52.1%; Score 50; DB 16; Length 381;
 Best Local Similarity 72.7%; Pred. No. 5.2;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 6 QICQOIIEYFG 16
 DB 356 RICEAIEYFG 366

RESULT 9

ID P72382 PRELIMINARY; PRT; 391 AA.
 AC P72382;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE CAPSP.
 GN CAPSP.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_Taxid=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Becker;
 RX MEDLINE=96178981; PubMed=8606197;
 RA Sau S., Lee C.Y.;
 RT "Cloning of type 8 capsule genes and analysis of gene clusters for the
 RT production of different capsular polysaccharides in Staphylococcus
 RT aureus";
 RT J. Bacteriol. 178:2118-2126(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Becker;
 RX MEDLINE=97197525;
 RA Sau S., Sun J., Lee C.Y.;
 RT "Molecular characterization and transcriptional analysis of type 8
 RT capsule genes in Staphylococcus aureus";
 RT J. Bacteriol. 179:1614-1621(1997).
 RL EMBL; U73374; AAB49445.1; -
 DR HSSP; P27828; 1F6D.
 DR GO; GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity; IEA.
 DR GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
 DR GO; GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.
 DR InterPro; IPR003331; Epimerase_2.
 DR Pfam; PF02350; Epimerase_2; 1.
 DR TIGRFAMs; TIGR00236; wecB; 1.
 DR Complete proteome.
 KW SEQUENCE 391 AA; 44247 MW; 1E8D9FAA9BC76F0D CRC64;

Query Match 52.1%; Score 50; DB 2; Length 391;
 Best Local Similarity 72.7%; Pred. No. 5.4;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 6 QICQOIIEYFG 16
 DB 366 RICEAIEYFG 376

RESULT 10

ID P95709 PRELIMINARY; PRT; 391 AA.
 AC P95709;
 RN [1]
 RP SEQUENCE FROM N.A.

DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE CAPSP.
 GN CAPSP.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_Taxid=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Reynolds and Newman;
 RX MEDLINE=97188587; PubMed=9245821;
 RA Sau S., Bhasin N., Mann E.R., Lee J.C., Foster T.J., Lee C.Y.;
 RT "The Staphylococcus aureus allelic genetic loci for serotype 5 and 8
 RT capsule expression contain the type-specific genes flanked by common
 RT genes";
 RT J. Microbiol. 143:0-0(0).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Reynolds and Newman;
 RX MEDLINE=98101481; PubMed=9440531;
 RA Kiser K.B., Lee J.C.;
 RT "Staphylococcus aureus cap50 and cap5 genes functionally complement
 RT mutations affecting enterobacterial common-antigen biosynthesis in
 RT Escherichia coli";
 RT J. Bacteriol. 180:403-406(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Reynolds and Newman;
 RX MEDLINE=98125727; PubMed=9466251;
 RA Bhasin N., Albus A., Michon F., Livolsi P.J., Park J.-S., Lee J.C.;
 RT "Identification of a gene essential for O-acetylation of the
 RT Staphylococcus aureus type 5 capsular polysaccharide";
 RT Mol. Microbiol. 27:9-21(1998).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Reynolds and Newman;
 RA Baga N., Mann E.R., Foster T.J., Lee J.C.;
 RT Submitted (DEC-1996) to the EMBL/Genbank/DBJ databases.
 RL EMBL; U81973; AAC46099.1; -
 DR HSSP; P27828; 1F6D.
 DR GO; GO:0008761; F:UDP-N-acetylglucosamine 2-epimerase activity; IEA.
 DR GO; GO:0009103; P:lipopolysaccharide biosynthesis; IEA.
 DR GO; GO:0006047; P:UDP-N-acetylglucosamine metabolism; IEA.
 DR InterPro; IPR003331; Epimerase_2.
 DR Pfam; PF02350; Epimerase_2; 1.
 DR TIGRFAMs; TIGR00236; wecB; 1.
 DR Complete proteome.
 KW SEQUENCE 391 AA; 44328 MW; B0105F690DB7CFID CRC64;

Query Match 52.1%; Score 50; DB 2; Length 391;
 Best Local Similarity 72.7%; Pred. No. 5.4;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 6 QICQOIIEYFG 16
 DB 366 RICEAIEYFG 376

RESULT 11

ID Q99X57 PRELIMINARY; PRT; 391 AA.
 AC Q99X57;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Capsular polysaccharide synthesis enzyme CapSP.
 GN CAP OR SA0164 OR SA0159.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_Taxid=158878; 158879;
 RN [1]
 RP SEQUENCE FROM N.A.

```
RESULT 5
Q87T10 PRELIMINARY; PRT; 401 AA.
ID Q87T10
AC Q87T10;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
DE Similar to Sjogren syndrome antigen B (Autoantigen La).
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC045392; AAI45392.1; -.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003723; F:RNA binding; IEA.
DR InterPro: IPR002344; Lupus_La.
DR InterPro: IPR006630; Lupus_La_dom.
DR InterPro: IPR000504; RNA_rec_mot.
DR Pfam: PF00076; rrm; 1.
DR PRINTS: PR00302; LUPUSLA.
DR SMART: SM00715; LA; 1.
DR SMART: SM00360; RRM; 1.
DR PROSITE: PSS0102; RRM; 1.
DR PROSITE: PSS0030; RRM_RNP_1; 1.
SQ SEQUENCE 401 AA; 46138 MW; 2EF032FDD3916291 CRC64;

Query Match 62.5%; Score 60; DB 13; Length 401;
Best Local Similarity 66.7%; Pred. No. 0.12;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 LEAQICQIIEYFGD 17
DB 10 LEKVAEQIIEYFGD 24

RESULT 6
Q87S15 PRELIMINARY; PRT; 390 AA.
ID Q87S15
AC Q87S15;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
DE A122034P.
GN LA OR CG10922.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Aspayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA Guerge R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phuanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Cejnkner S.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY075257; AAL68124.1; -.
DR FLYBase: FBgn0011638; La.
DR GO: GO:0008058; F:5S rRNA primary transcript binding; IDA.
DR GO: GO:0003723; F:RNA binding; NAS.
DR InterPro: IPR002344; Lupus_La.
DR InterPro: IPR006630; Lupus_La_dom.
DR InterPro: IPR000504; RNA_rec_mot.
DR Pfam: PF05383; LA; 1.
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DR Pfam: PF00076; rrm; 1.
DR PRINTS: PR00302; LUPUSLA.
DR SMART: SM00715; LA; 1.
DR SMART: SM00360; RRM; 1.
DR PROSITE: PSS0102; RRM; 1.
DR PROSITE: PSS0030; RRM_RNP_1; 1.
SQ SEQUENCE 390 AA; 44869 MW; 797FDE26B903C909 CRC64;

Query Match 54.2%; Score 52; DB 5; Length 390;
Best Local Similarity 64.3%; Pred. No. 2.5;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 EAQICQIIEYFGD 17
DB 51 ERAIIRQVEYFGD 64

RESULT 7
Q81MP9 PRELIMINARY; PRT; 481 AA.
ID Q81MP9
AC Q81MP9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
DE Hypothetical protein.
GN OSJNBA001114.12.
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Wing R.A., Yu Y., Soderlund C., Chen M., Kim H.-R., Rambo T.,
RA Sasaki C., Henry D., Oates R., Simmons J.;
RT "Rice Genomic Sequence";
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC105730; AAM51838.1; -.
DR Gramene: Q81MP9; -.
DR InterPro: IPR006630; Lupus_La_dom.
DR Pfam: PF05383; LA; 1.
DR SMART: SM00715; LA; 1.
DR KMW Hypothetical protein.
SQ SEQUENCE 481 AA; 49959 MW; 6EA2BED31191362 CRC64;

Query Match 54.2%; Score 52; DB 10; Length 481;
Best Local Similarity 60.0%; Pred. No. 3.1;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 LEAQICQIIEYFGD 17
DB 307 LRRAELKQIIEYFGD 321

RESULT 8
Q8NTY8 PRELIMINARY; PRT; 381 AA.
ID Q8NTY8
AC Q8NTY8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, last annotation update)
DE Capsular polysaccharide synthesis enzyme Cap8P.
GN CAP8P OR MW0139.
OS Staphylococcus aureus (strain MW).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=2204717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
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DR GO; GO:0005634; C:nucleus; IDA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
SQ SEQUENCE 381 AA; 43891 MW; 2E2DEF1452C0F0E9 CRC64;

Query Match
Best Local Similarity 86.5%; Score 83; DB 11; Length 381;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ALEAQCQIQIEYFGDF 18
DB 12 ALEAKICHOIEYFGDF 28

RESULT 2
ID Q8BTU4 PRELIMINARY; PRT; 415 AA.
AC Q8BTU4;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Sjogren syndrome antigen B.
GN SSB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NOD; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANOM Consortium.
RA The RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573 (2002).
DR EMBL; AK086677; BAC040498.1; -.
DR MGD; MGI:98423; Ssb.
DR GO; GO:0005634; C:nucleus; IDA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 415 AA; 47657 MW; A7545C7686AC8363 CRC64;

Query Match
Best Local Similarity 86.5%; Score 83; DB 11; Length 415;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ALEAQCQIQIEYFGDF 18
DB 12 ALEAKICHOIEYFGDF 28

RESULT 3
ID Q8QHT5 PRELIMINARY; PRT; 206 AA.
AC Q8QHT5;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Untranslated region binding-protein.
```

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GN UBP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopteria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA L'Ecuuyer T.J., Fang H.-L.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF467897; AAL76269.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 206 AA; 23992 MW; 965B62F7DFE980E9 CRC64;

Query Match
Best Local Similarity 72.9%; Score 70; DB 13; Length 206;
Matches 12; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 LEAQCQIQIEYFGD 17
DB 13 LESKICQIQIEYFGN 27

RESULT 4
ID Q7ZTK2 PRELIMINARY; PRT; 427 AA.
AC Q7ZTK2;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Similar to lupus LA protein homolog B.
DR EMBL; BC046654; AAH46654.1; -.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003723; F:RNA binding; IEA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 1.
DR PRINTS; PR00302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 2.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 427 AA; 48996 MW; 1E7CD82D8AB9C69A CRC64;

Query Match
Best Local Similarity 70.8%; Score 68; DB 13; Length 427;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 LEAQCQIQIEYFGD 17
DB 12 LDTKICQIQIEYFGD 26
```

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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:29:01 / Search time 41.229 Seconds
(without alignments)
137.751 Million cell updates/sec

Title: US-09-836-073-2

Perfect score: 96
Sequence: 1 AALEAQICQIEYFGDF 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database:

SPTREMBL.25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	86.5	381	11 Q9CYB9	Q9CYB9 mus musculus
2	83	86.5	415	11 Q8BTU4	Q8BTU4 mus musculus
3	70	72.9	206	13 Q8QHT5	Q8QHT5 gallus galli
4	68	70.8	427	13 Q7ZPK2	Q7ZPK2 xenopus lae
5	60	62.5	401	13 Q7ZNT0	Q7ZNT0 brachydanio
6	52	54.2	390	5 Q8T8V5	Q8T8V5 drosophila
7	52	54.2	481	10 Q8LMP9	Q8LMP9 oryza sativ
8	50	52.1	381	16 Q8NTN8	Q8NTN8 staphylococ
9	50	52.1	391	2 P723B2	P723B2 staphylococ
10	50	52.1	391	2 P95709	P95709 staphylococ
11	50	52.1	391	16 Q9X57	Q9X57 staphylococ
12	47	49.0	411	10 Q9FJ36	Q9FJ36 arabidopsis
13	47	49.0	422	10 Q94A38	Q94A38 arabidopsis
14	47	49.0	478	16 Q87G58	Q87G58 vibrio para
15	45.5	47.4	928	10 Q9L02	Q9L02 oryza sativ
16	45	46.9	396	5 Q01806	Q01806 caenorhabdi

17	45	46.9	688	5 Q9YBE6	Q9YBE6 drosophila
18	45	46.9	826	10 Q940X9	Q940X9 arabidopsis
19	44	45.8	389	10 Q8S0T8	Q8S0T8 oryza sativ
20	44	45.8	506	10 Q9M143	Q9M143 arabidopsis
21	44	45.8	898	10 Q8LRF3	Q8LRF3 oryza sativ
22	44	45.8	1126	5 Q8EPR0	Q8EPR0 cryptospori
23	44	45.8	1126	5 Q7YXV0	Q7YXV0 cryptospori
24	44	45.8	1126	5 Q44678	Q44678 caenorhabdi
25	43	44.8	111	17 Q978R4	Q978R4 thermoplasma
26	43	44.8	119	10 Q9ZP89	Q9ZP89 neurospora
27	43	44.8	181	16 Q8Z279	Q8Z279 streptococu
28	43	44.8	271	16 Q8Z2F4	Q8Z2F4 streptococu
29	43	44.8	355	10 Q8RYB4	Q8RYB4 phytophthor
30	43	44.8	506	10 Q84TQ4	Q84TQ4 amma majus
31	43	44.8	545	10 Q80567	Q80567 arabidopsis
32	42	43.8	151	5 Q86WR7	Q86WR7 plasmodium
33	42	43.8	159	16 Q97LL1	Q97LL1 clostridium
34	42	43.8	186	11 Q8VDM3	Q8VDM3 mus musculu
35	42	43.8	214	11 Q9CS12	Q9CS12 mus musculu
36	42	43.8	239	3 Q9P8N6	Q9P8N6 cochlidiolu
37	42	43.8	269	5 Q8MYR3	Q8MYR3 drosophila
38	42	43.8	328	4 Q9NW12	Q9NW12 homo sapien
39	42	43.8	342	11 Q9CUD5	Q9CUD5 mus musculu
40	42	43.8	482	16 Q8YCX0	Q8YCX0 bruceella su
41	42	43.8	482	16 Q8G0Z3	Q8G0Z3 bruceella su
42	42	43.8	575	4 Q8NAP2	Q8NAP2 homo sapien
43	42	43.8	669	16 Q8XRQ1	Q8XRQ1 ralsstonia s
44	42	43.8	965	5 Q9VAM5	Q9VAM5 drosophila
45	42	43.8	1064	16 Q8FHH0	Q8FHH0 corynebacte

ALIGNMENTS

RESULT 1
Q9CYB9 PRELIMINARY, PRT; 381 AA.
AC Q9CYB9; 01-JUN-2001 (TREMREL. 17, Created)
DT 01-JUN-2001 (TREMREL. 17, Last sequence update)
DT 01-OCT-2003 (TREMREL. 25, Last annotation update)
DE Sjogren syndrome antigen B.
GN SSB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Koehl P., Lewis S., Matsuo Y., Nikaido I., Nobile G., Quackenbush J.,
RA Schirml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Maehio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whitlaker C., Wilming L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA "Haseizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK017822; BAB30957.1; -;
DR MGD; MGI:98423; SSB.

RP VARIANT GALACTOSEMIA THR-28.
 RX MEDLINE=99452591; PubMed=10521295;
 RA Kalydjieva L., Perez-Izraun A., Angelicheva D., Onengut S., Dye D.,
 Rossard N.U., Jordanova A., Savov A., Yanakiev P., Kremensky I.,
 Radeva B., Hallmayer J., Markov A., Nedkova V., Tounnev I., Aneva L.,
 RA Gitzelmann R.;
 RT "A founder mutation in the G6Pase gene is responsible for galactokinase
 deficiency in Roma (Gypsies)."
 RL Am. J. Hum. Genet. 65:1299-1307(1999).
 RN [6]
 RP VARIANT GALACTOSEMIA VAL-198.
 RX MEDLINE=21152290; PubMed=11231902;
 RA Okano Y., Asada M., Fujimoto A., Otake A., Murayama K., Hsiao K.-J.,
 Choeh K., Yang Y., Cao Q., Reichardt J.K.V., Nihira S., Imamura T.,
 Yamano T.;
 RT "A genetic factor for age-related cataract: identification and
 characterization of a novel galactokinase variant, 'Osaka,' in
 Asians.";
 RL Am. J. Hum. Genet. 68:1036-1042(2001).
 CC -1- FUNCTION: Major enzyme for galactose metabolism.
 CC -1- CATALYTIC ACTIVITY: ATP + D-galactose = ADP + D-galactose 1-
 CC phosphate.
 CC -1- PATHWAY: Galactose metabolism; first step.
 CC -1- DISEASE: Defects in GALK1 are the cause of galactosemia II
 [MIM:230200], an autosomal recessive deficiency characterized by
 congenital cataracts during infancy and presenile cataracts in the
 adult population. The cataracts are secondary to accumulation of
 galactitol in the lenses.
 CC -1- SIMILARITY: Belongs to the GMP kinase family. GALK subfamily.
 CC -----
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 CC -----
 CC EMBL: U26401; AAA96147.1; -;
 CC EMBL: L76927; AAB51607.1; -;
 CC EMBL: BC001166; AAH01166.1; -;
 CC Genew; HGNC:4118; GALK1.
 CC MIM: 60413; -;
 CC MIM: 230200; -;
 DR GO: GO:0005737; C:cytoplasm; TAS.
 DR GO: GO:0004335; F:galactokinase activity; TAS.
 DR GO: GO:0006012; P:galactose metabolism; TAS.
 DR InterPro: IPR000705; Galactokinase.
 DR InterPro: IPR006204; GMP kinase.
 DR InterPro: IPR006203; GMPkinse ATP.
 DR InterPro: IPR006206; Mv_galkinase.
 DR Pfam: PF00288; GMP_kinases; 1.
 DR PRINTS: PR00473; GALTOKINASE.
 DR PRINTS: PR00960; LMBPROTEIN.
 DR PRINTS: PR00959; MEYGALKINASE.
 DR TIGRFAMs: TIGR00131; gal_kin; 1.
 DR PROSITE: PS00106; GALACTOKINASE; 1.
 DR PROSITE: PS00627; GMP_KINASES ATP; 1.
 KM Transferrase; Kinase; Galactose metabolism; ATP-binding;
 KM Disease mutation.
 FT NP_BIND 134 144 ATP (POTENTIAL).
 FT NP_BIND 28 28 P -> T (in galactosemia II).
 FT VARIANT 32 32 /FtId=VAR_008514.
 FT VARIANT 32 32 V -> M (in galactosemia II).
 FT VARIANT 198 198 A -> V (in galactosemia II; mild
 deficiency; Osaka).
 FT SEQUENCE 392 AA; 42272 MW; 8D7CF8FDB0B4718 CRC64;
 SQ

Query Match 45.8%; Score 44; DB 1; Length 392;
 Best Local Similarity 57.1%; Pred. No. 4.3;

Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 2 ALEAGICQIEYVF 15
 DB 164 AARQVCCQAEHSF 177

RESULT 14
 VP45_ARATH
 ID VP45_ARATH STANDARD; PRT; 569 AA.
 AC 049018; 080650;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Vacuolar protein-sorting protein 45 homolog (AtVP45).
 GN VP45 OR ATIG7140 OR T14N5.2.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=98289086; PubMed=9625693;
 RA Bassham D.C., Raikhel N.V.;
 RT "An Arabidopsis VP45p homolog implicated in protein transport to the
 vacuole.";
 RL Plant Physiol. 117:407-415(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016719; PubMed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 White O., Alonso J., Altafi H., Arujo R., Bowman C.L., Brooks S.Y.,
 Bucher E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
 Dunn P., Egu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
 Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 Kim C.J., Koo H.L., Kremenetskaia I., Kurcz D.B., Khan A., Lam B.,
 Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marzilli A.,
 Millescher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 Pail G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 Sun H., Tallon L.U., Tambunga G., Toriumi M.U., Town C.D., Walker M.,
 Utechtack T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,
 Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 thaliana.";
 RL Nature 408:816-820(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=22954850; PubMed=14593172;
 RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
 Soutwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
 Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
 Kautin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
 Miranda M., Quesh H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
 Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Anarai Y.,
 Arakawa T., Bahr J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
 Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
 Hayashizaki Y., Johnson-Hopson C., Huan V.W., Iida K., Kaneko M.,
 Khan S., Koseme E., Ishida J., Jiang P.X., Jones T., Kawai J.,
 Kaniya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
 Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
 Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RT "Empirical analysis of transcriptional activity in the Arabidopsis
 genome.";
 RL Science 302:842-846(2003).
 RN [4]
 INTERACTIONS WITH SYP21, SYP22, SYP31, SYP41, SYP42, SYP61, VTI11 AND

SQ SEQUENCE 487 AA; 54571 MW; 7D4E0E7760A0AF7 CRC64;
 Query Match 46.9%; Score 45; DB 1; Length 487;
 Best Local Similarity 69.2%; Pred. No. 3.7;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 ALEAQCQOIEYV 14
 Db 228 ALEAERQIEAY 240
 RESULT 12
 GALT_CANFA STANDARD; PRT; 392 AA.
 ID GALT_CANFA
 AC 09GK4;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Galactokinase (EC 2.7.1.6) (Galactose kinase).
 GN GALK1.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxId=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sidjanin D.J.;
 RT "Identification and analysis of canine galactokinase (GALK1) cDNA";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=22508185; PubMed=12620391;
 RA Sidjanin D.J., Miller B., Kijas J., McElwee J., Pillardy J., Malek J.,
 RA Pai G., Feldblyum T., Fraser C., Acland G., Aguirre G.;
 RT "Radiation hybrid map, physical map, and low-pass genomic sequence of
 RT the canine prcd region on CPA9 and comparative mapping with the
 RT syntenic region on human chromosome 17";
 RL Genomics 81:138-148(2003);
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Graves K.T., Emis R.B.;
 RT "Exon scan of the canine galactokinase (GALK1) gene in dog breeds
 RT affected with juvenile cataract";
 RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Major enzyme for galactose metabolism.
 CC -1- CATALYTIC ACTIVITY: ATP + D-galactose = ADP + D-galactose 1-
 CC phosphate.
 CC -1- PATHWAY: Galactose metabolism; first step.
 CC -1- SIMILARITY: Belongs to the GHMP kinase family. Galk subfamily.
 CC
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 CC
 CC EMBL; AF215513; AAC3832.1; -;
 CC EMBL; AF454963; AA015527.1; -;
 CC EMBL; AY267338; AAP31026.1; -;
 CC InterPro; IPR000705; Galactokinase.
 CC InterPro; IPR001174; Galk_kinase.
 CC InterPro; IPR006204; GHMP_kinase.
 CC InterPro; IPR006203; GHMP_kinase ATP.
 CC InterPro; IPR006206; Mv_galk_kinase.
 CC Pfam; PF00288; GHMP_kinases.1.
 CC PRINTS; PR00473; GALTCTOKINASE.
 CC PRINTS; PR00960; LMPPROTEIN.
 CC PRINTS; PR00959; MEVGALKINASE.
 CC TIGRFAM; TIGR00131; gal_kin.1.
 CC PROSITE; PS00106; GALACTOKINASE; 1.
 CC PROSITE; PS00627; GHMP_KINASES_ATP; 1.
 DR

KW Transferase; Kinase; Galactose metabolism; ATP-binding.
 FT NP_BIND 134 144 ATP (POTENTIAL).
 SQ SEQUENCE 392 AA; 42120 MW; 8FD5BCF3AB4386BF CRC64;
 Query Match 45.8%; Score 44; DB 1; Length 392;
 Best Local Similarity 57.1%; Pred. No. 4.3;
 Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 2 ALEAQCQOIEYV 15
 Db 164 AARAQVCOAHSF 177
 RESULT 13
 GALT_HUMAN STANDARD; PRT; 392 AA.
 ID GALT_HUMAN
 AC P51570;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Galactokinase (EC 2.7.1.6) (Galactose kinase).
 GN GALK1 OR GALK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANT GALACTOSEMIA MET-32.
 RA MEDLINE=95400298; PubMed=7670469;
 RA Stambolian D., Ai Y., Sidjanin D., Nesburn K., Sathe G., Rosenberg M.,
 RA Bergsma D.J.;
 RT "Cloning of the galactokinase cDNA and identification of mutations in
 RT two families with cataracts";
 RL Nat. Genet. 10:307-312(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=97064967; PubMed=8908517;
 RA Bergsma D.J., Ai Y., Skach W.R., Nesburn K., Anioia E.,
 RA van Horn S., Stambolian D.;
 RT "Fine structure of the human galactokinase GALK1 gene";
 RL Genome Res. 6:980-985(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Burow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ushed T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.T., Skalska U., Smalls D.E.,
 RA Scherch A., Schein J.E., Jones S.J.W., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=95352063; PubMed=7542884;
 RA Ai Y., Bergsma D.J., Stambolian D.;
 RT "Comparison of the enzymatic activities of human galactokinase GALK1
 RT and a related human galactokinase protein GK2";
 RL Biochem. Biophys. Res. Commun. 212:687-691(1995).
 RN [5]

DR PIR: T43542; T43542.
 DR GenDB_Spombe: SPAC57A10.10c; -
 DR InterPro: IPR002344; Lupus_La.
 DR InterPro: IPR006630; Lupus_La_dcm.
 DR InterPro: IPR000504; RNA_rec_moc.
 DR Pfam: PF03383; La; 1.
 DR Pfam: PF00076; rrm; 1.
 DR PRINTS: PR00302; LUPUSLA.
 DR SMART: SM00715; La; 1.
 DR SMART: SM00360; RRM; 1.
 DR PROSITE: PS0102; RRM; 1.
 DR PROSITE: PS00030; RRM_RNP_1; FALSE_NEG.
 DR RNA-Binding: Nuclear Protein.
 DR RNA-Binding: Nuclear Protein.
 FT DOMAIN 154 235 RNA-BINDING (RRM).
 FT CONFICT 188 188 M->I (IN REF. 1 AND 2).
 SQ SEQUENCE 298 AA; 34616 MW; 6466AB9940B87F4 CRC64;
 Query Match 51.0%; Score 49; DB 1; Length 298;
 Best Local Similarity 50.0%; Pred. No. 0.42;
 Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 4 EAQICQIEYFSD 17
 Db 64 EAEVLKQVEYFSD 77
 RESULT 10
 TCMO_PETCR STANDARD; PRT; 506 AA.
 AC Q43033;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Trans-cinnamate 4-monooxygenase (EC 1.14.13.11) (Cinnamic acid
 4-hydroxylase) (CA4H) (C4H) (P450CA4H) (Cytochrome P450 73).
 GN CYP73A10 OR CYP73.
 OS Petroselinum crispum (Parsley) (Petroselinum hortense).
 OC Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Campanulids; Apiales; Apiaceae; Apioidae; apioid superclade;
 OC Apium clade; Petroselinum.
 OX NCBI_TaxID=4043;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95320184; PubMed=7597051.
 RA Logemann E., Parniske M., Hahlbrock K.;
 RT "Modes of expression and common structural features of the complete
 phenylalanine ammonia-lyase gene family in parsley.";
 RT Proc. Natl. Acad. Sci. U.S.A. 92:5905-5909(1995).
 RL
 CC -1- FUNCTION: Controls carbon flux to pigments essential for
 CC pollination or UV protection, to numerous phytoalexins synthesized
 CC by plants when challenged by pathogens, and to lignins.
 CC -1- CATALYTIC ACTIVITY: Trans-cinnamate + NADPH + O(2) = 4-
 CC hydroxycinnamate + NADP(+) + H(2)O.
 CC -1- PATHWAY: Lignin biosynthesis.
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
 CC
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 CC
 DR EMBL: L38898; AAC41660.1; -
 DR PIR: T14907; T14907.
 DR InterPro: IPR001128; Cytochrome_P450.
 DR Pfam: PF00067; P450; 1.
 DR PRINTS: PR00385; P450.
 DR PROSITE: PS00086; CYTOCHROME_P450; 1.
 KM Oxidoreductase; Monooxygenase; Heme; NADP.

FT METAL 448 448 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
 SQ SEQUENCE 506 AA; 58047 MW; 32F0EB959D69CF CRC64;
 Query Match 49.0%; Score 47; DB 1; Length 506;
 Best Local Similarity 50.0%; Pred. No. 1.7;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 5 AQICQIEYFSD 18
 Db 215 SRAQSFYFHDGF 228
 RESULT 11
 GATB_CHLVCV STANDARD; PRT; 487 AA.
 ID GATB_CHLVCV
 AC 982386;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Aspartyl/glutamyl-L-Asn(Gln) amidotransferase subunit B
 DE (EC 6.3.5.-) (Asp/Glu-ADT subunit B).
 GN GATB OR CCA00289
 OS Chlamydomonas reinhardtii.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomonadales.
 OX NCBI_TaxID=83557;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GPIC.
 RX MEDLINE=22569155; PubMed=12682364;
 RA Read T.D., Myers G.S., Brunham R.C., Nelson W.C., Paulsen I.T.,
 RA Heidelberg J., Holtzapple E., Khouri H., Fedorova N.B., Carty H.A.,
 RA Mayhew L.A., Haft D.H., Peterson J., Beaman M.J., White O.,
 RA Salzberg S.L., Hest R.-C., McClarty G., Rank R.G., Bavoil P.M.,
 RA Fraser C.M.;
 RT "Genome sequence of Chlamydomonas reinhardtii (Chlamydia psittaci GPIC):
 RT examining the role of niche-specific genes in the evolution of the
 RT Chlamydiaceae.";
 RT Nucleic Acids Res. 31:2134-2147(2003).
 RL
 CC -1- FUNCTION: Allows the formation of correctly charged Asn-tRNA(Asn)
 CC or Gln-tRNA(Gln) through the transamidation of misacylated Asp-
 CC tRNA(Asn) or Glu-tRNA(Gln) in organisms which lack either or both
 CC of asparaginyl-tRNA or glutamyl-tRNA synthetases. The reaction
 CC takes place in the presence of glutamine and ATP through an
 CC activated phospho-Asp-tRNA(Asn) or phospho-Glu-tRNA(Gln) (By
 CC similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + L-glutamyl-L-tRNA(Gln) + L-glutamine = ADP
 CC + phosphatate + L-glutamyl-L-tRNA(Gln) + L-glutamate.
 CC -1- CATALYTIC ACTIVITY: ATP + L-aspartyl-L-tRNA(Asn) + L-glutamine = ADP
 CC + phosphatate + L-asparaginyl-L-tRNA(Asn) + L-glutamate.
 CC -1- SUBUNIT: Heterotrimer of A, B and C subunits (By similarity).
 CC -1- SIMILARITY: Belongs to the gatB/gatC family. GatB subfamily.
 CC
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 CC
 DR EMBL: AE016995; AAP05038.1; -
 DR TIGR: CCA00289; -
 DR HAMAP: MF 00121; -; 1.
 DR InterPro: IPR004413; GatB.
 DR InterPro: IPR006107; GatB_cent.
 DR InterPro: IPR006075; GatB_N.
 DR InterPro: IPR003789; GatB_Yqey.
 DR Pfam: PF01162; GatB; 1.
 DR Pfam: PF02934; GatB_N; 1.
 DR Pfam: PF02637; GatB_Yqey; 1.
 DR TIGRPFAMs: TIGR00133; gatB; 1.
 DR PROSITE: PS01234; GATB; 1.
 KM Protein biosynthesis; Ligase; Complete proteome.

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DR EMBL; L00993; AAA39415.1; -
 DR EMBL; BC003820; AAH03820.1; -
 DR EMBL; Y07951; CAA69249.1; -
 DR MGD; MGI:98423; Sab.
 DR GO; GO:0005634; C:nucleus; IDA.
 DR InterPro; IPR002344; Lupus_La_dom.
 DR InterPro; IPR006630; Lupus_La_dom.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF05383; La; 1.
 DR Pfam; PF00076; rrm; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PS0102; RRM; 1.
 DR PROSITE; PS0030; RRM_RNP_1; 1.
 DR RNA-binding; Nuclear protein; Phosphorylation.
 DR RNA-binding; Nuclear protein; RNA-BINDING (RRM).
 FT DOMAIN 111 187
 SQ SEQUENCE 415 AA; 4756 MW; 2D75197692FDC933 CRC64;

Query Match 86.5%; Score 83; DB 1; Length 415;
 Best Local Similarity 88.2%; Pred. No. 6.2e-07;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ALEAQCQQLIEYFGDF 18
 Db 12 ALEAKICHOIEYFGDF 28

RESULT 5
 LAB_XENLA STANDARD; PRT; 427 AA.
 AC P28049;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Lupus La protein homolog B (La ribonucleoprotein B) (La autoantigen
 DE homolog B).
 GN LAB1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Oocyte;
 RX MEDLINE=93287095; PubMed=8510143;
 RA Scherly D., Stutz F., Lin-Marg N., Clarkson S.G.;
 RT "La proteins from Xenopus laevis. cDNA cloning and developmental
 expression.";
 RL J. Mol. Biol. 231:196-204(1993).
 CC -1- FUNCTION: La protein plays a role in the transcription of RNA
 CC polymerase III. It is most probably a transcription termination
 CC factor. Binds to the 3' termin of virtually all nascent
 CC polymerase III transcripts (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- DEVELOPMENTAL STAGE: Barely detectable in stage I/II oocytes,
 CC accumulate in stage III/IV oocytes, then exhibit a roughly
 CC constant steady state level in mature oocytes, eggs, and early
 CC embryos.
 CC -1- PTM: Phosphorylated (Probable).
 CC -1- MISCELLANEOUS: There are two forms of La, Laa and Lab, in xenopus.
 CC -1- SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN.
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
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DR EMBL; X68818; CAA48716.1; -
 DR PIR; S33817; S33817.
 DR InterPro; IPR002344; Lupus_La.
 DR InterPro; IPR006630; Lupus_La_dom.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF05383; La; 1.
 DR Pfam; PF00076; rrm; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PS0102; RRM; 1.
 DR PROSITE; PS0030; RRM_RNP_1; FALSE NEG.
 DR RNA-binding; Nuclear protein; Phosphorylation.
 DR RNA-binding; Nuclear protein; RNA-BINDING (RRM).
 FT DOMAIN 110 202
 SQ SEQUENCE 427 AA; 48995 MW; 45F3146F8934A355 CRC64;

Query Match 70.8%; Score 68; DB 1; Length 427;
 Best Local Similarity 73.3%; Pred. No. 0.00028;
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 LEAQCQQLIEYFGD 17
 Db 12 LDTKICQQLIEYFGD 26

RESULT 6
 LAa_XENLA STANDARD; PRT; 428 AA.
 AC P28048;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Lupus La protein homolog A (La ribonucleoprotein A) (La autoantigen
 DE homolog A).
 GN LAa1.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Oocyte;
 RX MEDLINE=93287095; PubMed=8510143;
 RA Scherly D., Stutz F., Lin-Marg N., Clarkson S.G.;
 RT "La proteins from Xenopus laevis. cDNA cloning and developmental
 expression.";
 RL J. Mol. Biol. 231:196-204(1993).
 CC -1- FUNCTION: La protein plays a role in the transcription of RNA
 CC polymerase III. It is most probably a transcription termination
 CC factor. Binds to the 3' termin of virtually all nascent
 CC polymerase III transcripts (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- DEVELOPMENTAL STAGE: Barely detectable in stage I/II oocytes,
 CC accumulate in stage III/IV oocytes, then exhibit a roughly
 CC constant steady state level in mature oocytes, eggs, and early
 CC embryos.
 CC -1- PTM: Phosphorylated (Probable).
 CC -1- MISCELLANEOUS: There are two forms of La, Laa and Lab, in xenopus.
 CC -1- SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN.
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
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DR PROSITE: PS00030; RRM_RNP_1; 1.
 KM Systemic lupus erythematosus; RNA-binding; Phosphorylation;
 KW Nucleic protein.
 FT DOMAIN 111 187 RNA-BINDING (RRM).
 FT MOD RES 366 366 PHOSPHORYLATION (BY CK2).
 SQ SEQUENCE 408 AA; 46837 MW; EC153C15F9187FC4 CRC64;

Query Match 90.6%; Score 87; DB 1; Length 408;
 Best Local Similarity 88.9%; Pred. No. 1.2e-07;
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AALEAQICQIEYFGDF 18
 DB 11 AALEAKICQIEYFGDF 28

RESULT 3
 ID LA RAT STANDARD; PRT; 415 AA.
 AC P38656;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lupus La protein homolog (La ribonucleoprotein) (La autoantigen
 DE homolog)
 GN SSB OR SS-B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93246255; PubMed=7916708;
 RA Samsel I., Troester H., Bartsch H., Schwemle M., Igloi G.L.,
 RA Bachmann M.;
 RT "Isolation of rat cDNA clones coding for the autoantigen SS-B/La:
 RT detection of species-specific variations";
 RL Gene 1261265-268(1993).
 CC -1- FUNCTION: La protein plays a role in the transcription of RNA
 CC polymerase III. It is most probably a transcription termination
 CC factor. Binds to the 3' termini of virtually all nascent
 CC polymerase III transcripts. It is associated with precursor forms
 CC of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S,
 CC and 7-2 RNAs.
 CC -1- SUBUNIT: Interacts with DDX15 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
 CC -----
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 CC -----
 CC EMBL: X67859; CAA48043.1; -.
 DR PIR: JCI494; JCI494.
 DR InterPro: IPR002344; Lupus_La.
 DR InterPro: IPR006630; Lupus_La_dom.
 DR InterPro: IPR005054; RNA_rec_mot.
 DR Pfam: PF05383; La; 1.
 DR Pfam: PF00076; rrm; 1.
 DR PRINTS: PR00302; LUPUSLA.
 DR SMART: SMO0215; LA; 1.
 DR SMART: SMO0360; RRM; 1.
 DR PROSITE: PS50102; RRM_1.
 DR PROSITE: PS00030; RRM_RNP_1; 1.
 KW RNA-binding; Nuclear protein; Phosphorylation.
 FT DOMAIN 111 187 RNA-BINDING (RRM).
 SQ SEQUENCE 415 AA; 47777 MW; 033FD9CC1E475F98 CRC64;

Query Match 90.6%; Score 87; DB 1; Length 415;
 Best Local Similarity 88.9%; Pred. No. 1.2e-07;
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AALEAQICQIEYFGDF 18
 DB 11 AALEAKICQIEYFGDF 28

RESULT 4
 ID LA MOUSE STANDARD; PRT; 415 AA.
 AC P32067;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Lupus La protein homolog (La ribonucleoprotein) (La autoantigen
 DE homolog).
 GN SSB OR SS-B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93203630; PubMed=8454877;
 RA Topfer F., Gordon T., McCluskey J.;
 RT "Characterization of the mouse autoantigen La (SS-B). Identification
 RT of conserved RNA-binding motifs, a putative ATP binding site and
 RT reactivity of recombinant protein with poly(U) and human
 RT autoantibodies";
 RL J. Immunol. 150:3091-3100(1993).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC STRAIN=FVB/N; TISSUE=Mammary gland;
 CC MEDLINE=22388257; PubMed=12477932;
 CC Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 CC Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 CC Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 CC Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haefl F.,
 CC Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 CC Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 CC Brownstein M.J., Ueclin T.B., Toshiyuki S., Carninci P., Prange C.,
 CC Rana S.S., Loguelfano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 CC Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 CC Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 CC Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 CC Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 CC Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 CC Blakeley A.C., Grimwood J., Schmutz J., Myers R.M.,
 CC Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 CC Schenck A., Schein J.E., Jones S.J.W., Maira M.A.,
 CC "Generation and initial analysis of more than 15,000 full-length
 CC human and mouse cDNA sequences";
 CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC [3]
 CC SEQUENCE OF 1-11 FROM N.A.
 CC Groelz D., Bachmann M.;
 CC submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: La protein plays a role in the transcription of RNA
 CC polymerase III. It is most probably a transcription termination
 CC factor. Binds to the 3' termini of virtually all nascent
 CC polymerase III transcripts. It is associated with precursor forms
 CC of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S,
 CC and 7-2 RNAs.
 CC -1- SUBUNIT: Interacts with DDX15 (By similarity).
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- PTM: Phosphorylated (By similarity).
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

FT DOMAIN 111 187 RNA-BINDING (RRM).
 SQ SEQUENCE 404 AA; 46534 MW; 4EE20B5C262AD6A1 CRC64;
 Query Match 90.6%; Score 87; DB 1; Length 404;
 Best Local Similarity 88.9%; Pred. No. 1.2e-07;
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AALBAQICQOIEYFQDF 18
 |||||
 DB 11 AALBAKICQOIEYFQDF 28

RESULT 2
 ID LA HUMAN STANDARD; PRT; 408 AA.
 AC P05455;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Lupus La protein (Sjogren syndrome type B antigen) (SS-B) (La
 DE ribonucleoprotein) (La autoantigen).
 GN SSB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN 11
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89202037; PubMed=2468131;
 RA Chan E.K.L., Sullivan K.F., Tan E.M.;
 RT "Ribonucleoprotein SS-B/La belongs to a protein family with consensus
 RT sequences for RNA-binding.";
 RL Nucleic Acids Res. 17:2233-2244(1989).
 RN 12
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89053970; PubMed=3192525;
 RA Chambers J.C., Kenan D., Martin B.J., Keene J.D.;
 RT "Genomic structure and amino acid sequence domains of the human La
 RT autoantigen.";
 RL J. Biol. Chem. 263:18043-18051(1988).
 RN 13
 RP SEQUENCE FROM N.A.
 RC TISSUE-Placenta, and Skeletal muscle;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Rahney J., Heilón B., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield J.S.N., Krzywicki M.I., Skalka U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN 14
 RP SEQUENCE OF 54-408 FROM N.A.
 RX MEDLINE=88199081; PubMed=2452201;
 RA Sturgees A.D., Peterson M.G., McNeillage L.J., Whittingham S.,
 RA Coppel R.S.;
 RT "Characteristics and epitope mapping of a cloned human autoantigen
 RT La.";
 RL J. Immunol. 140:3212-3216(1988).
 RN 15

RP SEQUENCE OF 54-97 FROM N.A.
 RX MEDLINE=85166283; PubMed=3856888;
 RA Chambers J.C., Keene J.D.;
 RT "Isolation and analysis of cDNA clones expressing human lupus La
 RT antigen.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:2115-2119(1985).
 RN 16
 RP FUNCTION.
 RX MEDLINE=89251617; PubMed=24705590;
 RA Gottlieb E., Steltz J.A.;
 RT "Function of the mammalian La protein: evidence for its action in
 RT transcription termination by RNA polymerase III.";
 RL EMBO J. 8:851-861(1989).
 RN 17
 RP PHOSPHORYLATION.
 RX MEDLINE=97207017; PubMed=9054510;
 RA Fan H., Sakulich A.L., Goodier J.L., Zhang X., Qin J., Marale R.J.;
 RT "Phosphorylation of the human La antigen on serine 366 can regulate
 RT recycling of RNA polymerase III transcription complexes.";
 RL Cell 88:707-715(1997).
 RN 18
 RP INTERACTION WITH DDx15.
 RX MEDLINE=22346609; PubMed=12458796;
 RA Fouraux M.A., Kolman M.J.M., Van der Heijden A., De Jong A.S.,
 RA Van Venrooij W.J., Pruijn G.J.M.;
 RT "The human La (SS-B) autoantigen interacts with DDx15/hPrp43, a
 RT putative DEAD-box RNA helicase.";
 RL RNA 8:1428-1443(2002).
 CC -1- FUNCTION: La protein plays a role in the transcription of RNA
 CC polymerase III. It is most probably a transcription termination
 CC factor. Binds to the 3' terminus of virtually all nascent
 CC polymerase III transcripts. It is associated with precursor forms
 CC of RNA polymerase III transcripts including tRNA and 4.5S, 5S, 7S,
 CC and 7-2 RNAs.
 CC -1- SUBUNIT: Interacts with DDx15.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- PTM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES ARE AT THE
 CC C-TERMINAL PART OF THE PROTEIN.
 CC -1- PTM: The N-terminus is blocked.
 CC -1- DISEASE: Sera from patients with systemic lupus erythematosus
 CC often contain antibodies that react with the normal cellular
 CC La protein as if this antigen was foreign.
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
 CC
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 CC
 CC EMBL; X13697; CAA11985.1; -
 CC EMBL; J04205; AAA15885.1; -
 CC EMBL; BC001289; AAH01289.1; -
 CC EMBL; BC020818; AAH20818.1; -
 CC PIR; A31888; A31888.
 CC GeneW; HGNC:11316; SSB.
 CC MIM; 109090; -
 CC GO; GO:0030529; Ribonucleoprotein complex; TAS.
 CC GO; GO:0003729; rRNA binding; TAS.
 CC GO; GO:0000049; rRNA binding; TAS.
 CC GO; GO:0008334; Histone mRNA metabolism; TAS.
 CC GO; GO:0006400; rRNA modification; TAS.
 CC InterPro; IPR002344; Lupus La.
 CC InterPro; IPR006630; Lupus La dom.
 CC InterPro; IPR000504; RNA_rec_mot.
 CC Pfam; PF05383; La; 1.
 CC Pfam; PF00076; trm; 1.
 CC PRINTS; PR00302; LUPUSLA.
 CC SMART; SM00715; LA; 1.
 CC SMART; SM00360; RRM; 1.
 CC PROSITE; PSS0102; RRM; 1.
 DR

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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:01:41 ; Search time 7.24022 Seconds
(without alignments)
129.452 Million cell updates/sec

Title: US-09-836-073-2

Perfect score: 96
Sequence: 1 AALEAQICQIEYFGDF 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	90.6	404	1	LA_BOVIN
2	87	90.6	404	1	LA_BOVIN
3	87	90.6	415	1	LA_RAT
4	83	86.5	415	1	LA_MOUSE
5	68	70.8	427	1	LAB_XENLA
6	64	66.7	428	1	LAB_XENLA
7	56	58.3	383	1	LA_AEDAL
8	52	54.2	390	1	LA_DROME
9	49	51.0	298	1	LAHI_SCHPO
10	47	46.9	506	1	TCMO_PETCR
11	45	46.0	487	1	GATB_CHICV
12	44	45.8	392	1	GALI_CANFA
13	44	45.8	392	1	GALI_HUMAN
14	43	44.8	569	1	VP45_ARATH
15	41	42.7	466	1	SRO9_YEAST
16	40	41.7	175	1	IPYR_PSEPK
17	40	41.7	176	1	IPYR_HABIN
18	40	41.7	292	1	IPYR_HABIN
19	40	41.7	292	1	IPYR_HABIN
20	40	41.7	292	1	IPYR_HABIN
21	40	41.7	292	1	IPYR_HABIN
22	40	41.7	389	1	EP1G_DAUCU
23	40	41.7	391	1	GALI_MOUSE
24	40	41.7	505	1	TCMO_ARATH
25	40	41.7	505	1	TCMO_CICAR
26	40	41.7	505	1	TCMO_GLYEC
27	40	41.7	505	1	TCMO_HELTU
28	40	41.7	505	1	TCMO_PEA
29	40	41.7	505	1	TCMO_PHAU
30	40	41.7	505	1	TCMO_ZINEL
31	40	41.7	506	1	TCMO_MEDSA
32	40	41.7	506	1	TCMO_RUTGR
33	40	41.7	506	1	TCMO_SOVRN

34	40	41.7	646	1	YE14_SCHPO
35	40	41.7	755	1	SEC6_RAT
36	40	41.7	756	1	SEC6_HUMAN
37	40	41.7	1180	1	C4AA_BACTI
38	40	41.7	1418	1	CELL_CAREL
39	40	41.7	2032	1	TRPG_CAREL
40	40	41.1	367	1	TRPB_NITEU
41	39	40.6	363	1	LE3A_ASPENG
42	39	40.6	475	1	VG41_BP74
43	39	40.6	482	1	LBP_RABIT
44	39	40.6	490	1	IFTA_HUMAN
45	39	40.6	1164	1	RPO2_COMPX

ALIGNMENTS

RESULT 1	LA_BOVIN	STANDARD	PRT	404 AA.
AC	P10881			
DT	01-JUL-1989 (Rel. 11, Created)			
DT	01-JUL-1989 (Rel. 11, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Lapus La protein homolog (La ribonucleoprotein) (La autocantigen homolog)			
DE	SSB.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; Bovidae; Bovinae; Bos.			
OX	NCBI_Taxid=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISUB=Pituitary; PubMed=2468131.			
RX	MEDLINE=69202037; Chan E.K.L., Sullivan K.F., Tan E.M.;			
RA	"Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences for RNA-binding."			
RT	Nucleic Acids Res. 17:2233-2244(1989).			
RL	-1- FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' terminus of virtually all nascent polymerase III transcripts. It is associated with precursor forms of RNA polymerase III transcripts including rRNA and 4.5S, 5S, 7S, and 7-2 rRNAs.			
CC	-1- SUBUNIT: Interacts with DDX15 (by similarity).			
CC	-1- SUBCELLULAR LOCATION: Nuclear (Probable).			
CC	-1- PTM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES ARE AT THE C-TERMINAL PART OF THE PROTEIN.			
CC	-1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.			
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CC	EMBL; X13698; CAA31986.1; -.			
DR	PIR; S03849; S03849.			
DR	InterPro; IPR002344; Lapus_La.			
DR	InterPro; IPR006630; Lapus_La_dom.			
DR	InterPro; IPR005054; RNA_rec_mot.			
DR	Pfam; PF05383; La; 1.			
DR	Pfam; PF00076; rrm; 1.			
DR	PRINTS; PR00302; LUPUSLA.			
DR	SMART; SM00715; LA; 1.			
DR	SMART; SM00360; RRM; 1.			
DR	PROSITE; PS0102; RRM; 1.			
DR	PROSITE; PS00030; RRM_NRP_1; 1.			
KW	RNA-binding; Nuclear protein; Phosphorylation.			

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A/Molecule type: DNA
 A/Residues: 1-166 <DAV>
 A/Cross-references: EMBL:AF039051; PIDN:AB94258.1; GSPDB:GN00023; CESP:CI4C6.12
 A/Experimental source: strain Bristol N2; clone CI4C6
 C/Genetics:
 A/Gene: CESP:CI4C6.12
 A/Map position: 5
 A/Introns: 42/1; 156/3

Query Match 44.8%; Score 43; DB 2; Length 166;
 Best Local Similarity 61.5%; Pred. No. 7.8;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 QICQIEYFGDF 18
 :|||
 Db 81 KICNVIEYMTGDF 93

RESULT 15

T00677
 hypothetical protein At2g43970 [imported] - Arabidopsis thaliana

N/Alternate names: hypothetical protein F6E13.10
 C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 23-Mar-2001

C/Accession: T00677; G84872

R/Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, June 1998

A/Description: Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence.

A/Reference number: Z14180

A/Accession: T00677

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-529 <ROU>
 A/Cross-references: EMBL:AC004005; NID:G3212846; PID:G3212854

A/Experimental source: cultivar Columbia

R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Xoo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.

euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J

Nature 402, 761-768, 1999

A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A/Reference number: A84420; MUID:20083487; PMID:10617197

A/Accession: G84872

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-529 <STO>

A/Cross-references: GB:AE002093; NID:G3212854; PID:ACC23405.1; GSPDB:GN00139

C/Genetics:

A/Gene: F6E13.10; At2g43970

A/Map position: 2

A/Introns: 200/3; 228/1; 259/3; 283/3; 310/2; 344/3; 367/3; 421/3

Query Match 44.8%; Score 43; DB 2; Length 529;

Best Local Similarity 58.3%; Pred. No. 27;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 QICQIEYFGDF 17
 :|||
 Db 196 KIVNQVEYFSD 207

Search completed: September 10, 2004, 18:02:25
 Job time : 17.0782 secs

RESULT 10

T43542
 RNA-binding protein La1 homolog - fission yeast (Schizosaccharomyces pombe)
 N:Alternate names: La autoantigen; ribonucleoprotein La homolog
 C:Species: Schizosaccharomyces pombe
 C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
 C:Accession: T43542; T43325
 R:Van Horn, D.J.; 100, C.D.; Xue, D.; Shi, H.; Wolin, S.L.
 RNA 3, 1434-1443, 1997
 A:Title: The La protein in Schizosaccharomyces pombe: a conserved yet dispensable phosph
 A:Reference number: Z22560; PMID:98067398; PMID:9404894
 A:Accession: T43542
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-298 <VAN>
 A:Cross-references: EMBL:AF022949; PIDN:AAB82145.1
 R:Utsumi, R.
 submitted to the EMBL Data Library, February 1998
 A:Description: Screening of S. pombe cDNA library using E. coli defective in signal tran
 A:Reference number: Z22428
 A:Accession: T43325
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-298 <UTS>
 A:Cross-references: EMBL:AB011371; PIDN:BAA24981.1
 C:Genetics:
 A:Gene: bla1
 C:Function:
 A:Description: the binding of the La protein to rRNA precursors is required for the end
 C:Keyword: phosphoprotein, RNA binding

Query Match 51.0%; Score 49; DB 2; Length 298;
 Best Local Similarity 50.0%; Pred. No. 1.4;
 Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 4 EAQICQIERYFGD 17
 ||:|||||
 Db 64 EAEVLKQERYFSD 77

RESULT 11

T14907
 trans-cinnamate 4-monooxygenase (EC 1.14.13.11) - parsley
 C:Species: Petroselinum crispum (parsley)
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
 C:Accession: T14907
 R:Logemann, E.; Parlske, M.; Hahlbrock, K.
 Proc. Natl. Acad. Sci. U.S.A. 92, 5905-5909, 1995
 A:Title: Modes of expression and common structural features of the complete phenylalanin
 A:Reference number: Z18260; PMID:95320184; PMID:7597051
 A:Accession: T14907
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1506 <LOG>
 A:Cross-references: EMBL:L38896; NID:G903871; PIDN:AAC41660.1; PID:G903872
 A:Genetics:
 A:Gene: CAH
 C:Function:
 A:Description: catalyzes the formation of p-coumaric acid from trans-cinnamic acid
 C:Superfamily: phenylpropanoid biosynthesis
 C:Superfamily: human cytochrome P450; CYP2D6; cytochrome P450 homology
 C:Keywords: heme; iron; metalloprotein; oxidoreductase
 F:304-470/Domain: cytochrome P450 homology <P45>
 F:448/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 49.0%; Score 47; DB 2; Length 506;
 Best Local Similarity 50.0%; Pred. No. 5.4;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 5 AQICQIERYFGD 18
 ||:|||||
 Db 215 SRLAQSEYHFGDF 228

RESULT 12

T30953
 hypothetical protein C44E4.4 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
 C:Accession: T30953
 R:Sammons, L.; Wohldmann, P.; Gillam, B.
 submitted to the EMBL Data Library, August 1999
 A:Description: The sequence of C. elegans cosmid C44E4.
 A:Reference number: Z20945
 A:Accession: T30953
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-396 <SAM>
 A:Cross-references: EMBL:AF003140; PIDN:AAB54169.1
 A:Experimental source: strain Bristol N2; clone C44E4
 C:Genetics:
 A:Map position: 1
 A:Introns: 45/1; 114/3
 A>Note: C44E4.4
 C:Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology

Query Match 46.9%; Score 45; DB 2; Length 396;
 Best Local Similarity 50.0%; Pred. No. 9;
 Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 4 EAQICQIERYFGD 17
 ||:|||||
 Db 13 DQKITQIERYFGN 26

RESULT 13

F85016
 probable RING zinc finger protein [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
 C:Accession: F85016
 R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
 Nature 402, 769-777, 1999
 A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
 A:Reference number: AB5001; PMID:20083488; PMID:10617198
 A:Accession: F85016
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-506 <STO>
 A:Cross-references: GB:NC_001268; NID:G7267624; PIDN:CAE80936.1; GSPDB:GN00140
 C:Genetics:
 A:Gene: AT4G01270
 A:Map position: 4
 C:Superfamily: Arabidopsis thaliana hypothetical protein A_IG002N01.19

Query Match 45.8%; Score 44; DB 2; Length 506;
 Best Local Similarity 66.7%; Pred. No. 17;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 5 AQICQIERYFG 16
 ||:|||||
 Db 491 SQGCIQIERYFG 502

RESULT 14

T32701
 hypothetical protein C14C6.12 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T32701
 R:David, M.; Wohldmann, P.; Bauer, C.; Antoniou, B.
 submitted to the EMBL Data Library, December 1997
 A:Description: The sequence of C. elegans cosmid C14C6.
 A:Reference number: Z21210
 A:Accession: T32701
 A:Status: preliminary; translated from GB/EMBL/DBJ

A:Reference number: S03848; MUID:89202037; PMID:2468131
 A:Accession: S03848
 A:Molecule type: mRNA
 A:Residues: 1-408 <CH2>
 A:Cross-references: EMBL:X13697; NID:g36414; PID:CAA31985.1; PID:g36415
 R:Chambers, J.C.; Keene, J.D.
 Proc. Natl. Acad. Sci. U.S.A. 82, 2115-2119, 1985
 A:Title: Isolation and analysis of cDNA clones expressing human lupus La antigen.
 A:Reference number: A22956; MUID:85166283; PMID:3856888
 A:Accession: A22956
 A:Molecule type: mRNA
 A:Residues: 45-97, 'LK' <CH3>
 A:Cross-references: GB:J04205
 A:Note: This sequence has been revised in reference A31888
 R:Nyman, U.; Ringertz, N.R.; Petersen, I.
 Immunol. Lett. 22, 65-72, 1989
 A:Title: Demonstration of an amino terminal La epitope recognized by human anti-La sera.
 A:Reference number: A61051; MUID:89379261; PMID:2476379
 A:Accession: A61051
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-19, 'E', '21-47' <NTM>
 R:Sturges, A.D.; Peterson, M.G.; McNeillage, L.J.; Whittingham, S.; Coppel, R.L.
 J. Immunol. 140, 3212-3218, 1988
 A:Title: Characteristics and epitope mapping of a cloned human autoantigen La.
 A:Reference number: S11013; MUID:8819081; PMID:2452201
 A:Accession: S11013
 A:Molecule type: mRNA
 A:Residues: 'E', '55-287', 'V', '289-408' <STU>
 A:Cross-references: EMBL:M0328; NID:g337456; PID:AAA36577.1; PID:g337457
 R:Kohaka, H.; Yamamoto, K.; Fujii, H.; Miura, H.; Miyasaka, N.; Nishiooka, K.; Miyamoto, J.
 Clin. Invest. 85, 1566-1574, 1990
 A:Title: Fine epitope mapping the human SS-B/La protein: Identification of a distinct La
 A:Reference number: I55553; MUID:90237237; PMID:1692037
 A:Accession: I55553
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 81-107 <RES>
 A:Cross-references: GB:M35261; NID:g338491; PID:AAA3652.1; PID:g338495
 A:Accession: I70205
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 174-224 <RE2>
 A:Cross-references: GB:M35263; NID:g338492; PID:AAA3653.1; PID:g338496
 A:Accession: I70206
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 279-342 <RE3>
 A:Cross-references: GB:M35262; NID:g338493; PID:AAA3654.1; PID:g338497
 C:Comment: This protein associates with a variety of small RNA molecules, most of which
 act as a transcription termination factor.
 C:Keywords: C:Genetics:
 A:Gene: GDB:SSB
 A:Cross-references: GDB:I25359; OMIM:109090
 A:Map position: 2
 A:Intons: 22/3, 57/2, 115/3, 151/3, 185/2, 209/2, 223/3, 264/3, 380/2
 C:Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology
 C:Keywords: phosphoprotein; RNA binding
 F:112-178/Domain: ribonucleoprotein repeat homology <RRM>
 F:113-118/Region: RNA-binding RNP2 motif
 F:151-158/Region: RNA-binding RNP1 motif
 F:228-408/Domain: phosphorylated #status experimental <PHY>

Query Match 90.6%; Score 87; DB 1; Length 408;
 Best Local Similarity 88.9%; Pred. No. 6.8e-07;
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LALEAQCQIIEYFGDF 18
 |||||:|||||
 Db 11 LALEAKICQIIEYFGDF 28

RESULT 3

JCI494
 ribonucleoprotein La - rat
 N:Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 24-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
 C:Accession: JCI494; S25145
 R:Semsei, I.; Troester, H.; Bartsch, H.; Schwemme, M.; Igloi, G.L.; Bachmann, M.
 Gene 126, 265-268, 1993
 A:Title: Isolation of rat cDNA clones coding for the autoantigen SS-B/La: Detection of
 A:Reference number: JCI494; MUID:93246255; PMID:7916708
 A:Accession: JCI494
 A:Molecule type: mRNA
 A:Residues: 1-415 <SEM>
 A:Cross-references: GB:X67859; NID:g55778; PID:CAA48043.1; PID:g55779
 A:Experimental source: liver
 C:Comment: This protein associates with a variety of small RNA molecules, most of which
 act as a transcription termination factor.
 C:Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology
 C:Keywords: phosphoprotein; RNA binding
 F:112-178/Domain: ribonucleoprotein repeat homology <RRM>
 F:113-118/Region: RNA-binding RNP2 motif
 F:151-158/Region: RNA-binding RNP1 motif
 F:227-415/Domain: phosphorylated #status predicted <PHY>

Query Match 90.6%; Score 87; DB 1; Length 415;
 Best Local Similarity 88.9%; Pred. No. 6.9e-07;
 Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LALEAQCQIIEYFGDF 18
 |||||:|||||
 Db 11 LALEAKICQIIEYFGDF 28

RESULT 4
 S33817
 ribonucleoprotein La.B - African clawed frog
 N:Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
 C:Accession: S33817; S28544
 R:Schery, D.; Stutz, F.; Lin-Marg, N.; Clarkson, S.G.
 J. Mol. Biol. 231, 196-204, 1993
 A:Title: La proteins from Xenopus laevis. cDNA cloning and developmental expression.
 A:Reference number: S33817; MUID:93287095; PMID:8510143
 A:Accession: S33817
 A:Molecule type: mRNA
 A:Residues: 1-427 <SCH>
 A:Cross-references: EMBL:X68818; NID:g64875; PID:CAA48716.1; PID:g64876
 C:Comment: This protein associates with a variety of small RNA molecules, most of which
 act as a transcription termination factor.
 C:Superfamily: ribonucleoprotein la; ribonucleoprotein repeat homology
 C:Keywords: phosphoprotein; RNA binding
 F:111-177/Domain: ribonucleoprotein repeat homology <RRM>
 F:112-117/Region: RNA-binding RNP2 motif
 F:150-157/Region: RNA-binding RNP1 motif
 F:227-427/Domain: phosphorylated #status predicted <PHY>

Query Match 70.8%; Score 68; DB 1; Length 427;
 Best Local Similarity 73.3%; Pred. No. 0.0012;
 Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 LALEAQCQIIEYFGDF 17
 |||||:|||||
 Db 12 LDTKICEQIIEYFGDF 26

RESULT 5
 S33818
 ribonucleoprotein La.A - African clawed frog
 N:Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 03-Feb-1994 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
 C:Accession: S33818; S28545

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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:33:11 ; Search time 14.0782 seconds
(without alignments)
122.988 Million cell updates/sec

Title: US-09-836-073-2

Perfect score: 96
Sequence: 1 AALEAQICQIEYFGDF 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR 78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	90.6	404	1 S03849	ribonucleoprotein
2	87	90.6	408	1 A31888	ribonucleoprotein
3	87	90.6	415	1 JCI494	ribonucleoprotein
4	68	70.8	427	1 S33817	ribonucleoprotein
5	64	66.7	428	1 S33818	ribonucleoprotein
6	52	54.2	390	2 A53773	La/SS-B homolog D-
7	52	54.2	390	2 A53781	ribonucleoprotein
8	50	52.1	391	2 H89777	capsular polysacch
9	49	51.0	298	2 T38937	rna binding protei
10	49	51.0	298	2 T35442	RNA-binding protei
11	47	49.0	506	2 T14907	trans-cinnamate 4-
12	47	46.9	396	2 T30953	hypothetical prote
13	44	45.8	506	2 P85016	probable RING zinc
14	43	44.8	166	2 T32701	hypothetical prote
15	43	44.8	529	2 T52056	vacuolar protein s
16	43	44.8	569	2 T52056	vacuolar protein s
17	43	44.8	569	2 T00445	lactoylglytation 1
18	42	43.8	159	2 C96967	ATP-dependent RNA
19	42	43.8	482	2 A83381	hypothetical prote
20	41	42.7	466	2 S19365	hypothetical prote
21	41	42.7	469	2 C70357	hypothetical prote
22	41	42.7	837	2 B82932	preproteins translo
23	41	42.7	2160	2 T30241	hypothetical prote
24	40	41.7	51	2 G81188	hypothetical prote
25	40	41.7	176	2 G64049	inorganic pyrophos
26	40	41.7	220	2 T08628	hypothetical prote
27	40	41.7	262	2 E75516	conserved hypotet
28	40	41.7	292	1 B65040	yfjB protein - Bsc
29	40	41.7	292	2 A85908	MND kinase (EC 2.7

30	40	41.7	292	2 AF0834	conserved hypotet
31	40	41.7	292	2 E91063	NMD kinase (EC 2.7
32	40	41.7	346	2 AB0942	hypothetical prote
33	40	41.7	389	2 S36638	glycoprotein Epi -
34	40	41.7	467	2 T24889	hypothetical prote
35	40	41.7	503	2 T06522	trans-cinnamate 4-
36	40	41.7	505	2 T09525	trans-cinnamate 4-
37	40	41.7	505	2 JCI458	trans-cinnamate 4-
38	40	41.7	505	2 A47454	trans-cinnamate 4-
39	40	41.7	505	2 A84709	cinnamate-4-hydrox
40	40	41.7	505	2 B90181	Na+/H+ antiporter
41	40	41.7	506	1 S36878	cytochrome P450 -
42	40	41.7	517	2 T10857	trans-cinnamate 4-
43	40	41.7	646	2 T38022	probable GRP-bindi
44	40	41.7	658	2 D96656	hypothetical prote
45	40	41.7	788	2 A71076	hypothetical prote

ALIGNMENTS

RESULT 1
S03849
ribonucleoprotein La - bovine
N/Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B
C/Species: Bos primigenius taurus (cattle)
C/Date: 31-Dec-1990 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C/Accession: S03849
R/Chan, E.K.L.; Sullivan, K.F.; Tan, E.M.
Nucleic Acids Res. 17, 2233-2244, 1989
A/Title: Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences
A/Reference number: S03848; MUID:89202037; PMID:2468131
A/Accession: S03849
A/Molecule type: mRNA
A/Residues: 1-404 <CHA>
A/Cross-references: EMBL:X13698; NID:g756; PIDD:CAA3186.1; PIDD:g756
A/Note: Part of this sequence was confirmed by protein sequencing
C/Comment: This protein associates with a variety of small RNA molecules, most of which
ay act as a transcription termination factor.
C/Superfamily: ribonucleoprotein La; ribonucleoprotein repeat homology
C/Keywords: blocked amino end; phosphoprotein; RNA binding
F/112-178/Domain: ribonucleoprotein repeat homology <RNM>
F/113-118/Region: RNA-binding RNP2 motif
F/151-158/Region: RNA-binding RNP1 motif
F/228-404/Domain: phosphorylated #status predicted <PHX>

Query Match 90.6%; Score 87; DB 1; Length 404;
Best Local Similarity 88.9%; Pred. No. 6.7e-07;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 1 AALEAQICQIEYFGDF 18
Db 11 AALEAQICQIEYFGDF 28

RESULT 2
A31888
ribonucleoprotein La - human
N/Alternate names: autoantigen SS-B/La; ribonucleoprotein SS-B; Sjogren syndrome antige
C/Species: Homo sapiens (man)
C/Date: 21-May-1990 #sequence_revision 26-May-1994 #text_change 22-Jun-1999
C/Accession: A31888; S03848; A22956; A61051; S11013; I55553; I70205; I70206; A31273
R/Chan, E.K.L.; Sullivan, K.F.; Tan, E.M.
Nucleic Acids Res. 17, 2233-2244, 1989
A/Title: Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences

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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:01:41; Search time 7.24022 Seconds
(without alignments)
129.452 Million cell updates/sec

Title: US-09-836-073-14

Perfect score: 99
Sequence: 1 AALEAKICHQIEHYFGDF 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	99	100.0	404	LA_BOVIN	P10881 bos taurus
2	99	100.0	408	LA_HUMAN	P05455 homo sapien
3	99	100.0	415	LA_RAT	P38656 rattus norv
4	95	96.0	415	LA_MOUSE	P23067 mus musculu
5	70	70.7	427	LAB_XENLA	P28049 xenopus lae
6	66	66.7	428	LA_XENLA	P28048 xenopus lae
7	55	55.6	383	LA_AEDAL	P26457 aedes albop
8	51	51.5	380	LA_DROME	P40786 drosophila
9	46	46.5	298	LAH1_SCHPO	P87058 schizosacch
10	43	43.4	487	GATB_CHLVC	P82306 chlamydomon
11	43	43.4	506	TCMO_PETCR	P43033 petroselinu
12	42	42.4	242	GLNO_BACST	P27675 bacillus st
13	42	42.4	482	LBP_RABIT	P17454 coryctolagus
14	41	41.4	251	FOL2_MOUSE	P05665 mus musculu
15	41	41.4	490	IFP4_HUMAN	P14879 homo sapien
16	41	41.4	573	CATT_YEAST	P06115 saccharomyc
17	41	41.4	1164	RPO2_COMPX	P17474 compox viru
18	41	41.4	1164	RPO2_VACCV	P19798 vaccinia vi
19	41	41.4	1164	RPO2_VARV	P13811 variola vir
20	41	41.4	1220	DPOL_HSVB	P28858 equine heip
21	41	41.4	1221	V143_NPVAC	P24307 autographa
22	40	40.4	264	GRAX_HUMAN	P49863 homo sapien
23	40	40.4	433	THIC_FUSNN	P49160 fusobacteri
24	40	40.4	466	SRO9_YEAST	P25567 saccharomyc
25	40	40.4	602	EXSA_BUCAI	P57550 buchnera ap
26	40	40.4	868	PD61_HUMAN	P05455 homo sapien
27	40	40.4	868	PD61_MOUSE	P05455 mus musculu
28	40	40.4	1107	MY1B_MOUSE	P46735 mus musculu
29	40	40.4	1136	MY1B_RAT	P05066 rattus norv
30	39	39.4	482	IFP5_HUMAN	P13355 homo sapien
31	39	39.4	488	RBL_OITIU	P14959 olisthodisc
32	39	39.4	755	SEC6_RAT	P02885 rattus norv
33	39	39.4	756	SEC6_HUMAN	P06645 homo sapien

34	39	39.4	812	1	PLMN_MOUSE	P20918 mus musculu
35	39	39.4	1048	1	ACQ1_ARATH	O04379 arabidopsis
36	38	38.4	176	1	IPR1_HABIN	P44529 haemophilus
37	38	38.4	281	1	Y818_PYRAS	O82921 pyrobaculum
38	38	38.4	354	1	ALKB_ARATH	O98898 arabidopsis
39	38	38.4	391	1	CYB_PASTE	P15585 paramedius
40	38	38.4	436	1	THIC_CLOPE	O84839 clostridium
41	38	38.4	488	1	RBL_ECTSI	P24313 ectocarpus
42	38	38.4	488	1	RBL_PYULI	P23651 pyralisella
43	38	38.4	591	1	Y875_CHLTR	O84883 chlamydia t
44	38	38.4	902	1	ATMA_SALTY	P36640 salmoneila
45	38	38.4	926	1	ME19_DROME	O24087 drosophila

ALIGNMENTS

RESULT 1
LA_BOVIN
ID LA_BOVIN STANDARD; PRT; 404 AA.
AC P10881;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lupus La protein homolog (La ribonucleoprotein) (La autoantigen homolog).
DE SSB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Plutitary;
RX MEDLINE=89202037; PubMed=2468131;
RA Chan E.K.L., Sullivan K.F., Tan E.M.;
RT "Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences for RNA-binding".
RL Nucleic Acids Res. 17:2233-2244(1989).
CC -1- FUNCTION: La protein plays a role in the transcription of RNA polymerase III transcripts. It is most probably of virtually all nascent factor. Binds to the 3' terminus of virtually all nascent polymerase III transcripts including tRNA and 4.5S, 5S, 7S, and 7-2 RNAs.
CC -1- SUBUNIT: Interacts with DDX15 (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- PTM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES ARE AT THE C-TERMINAL PART OF THE PROTEIN.
CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).
CC
CC EMBL, X13698; CAA1986.1; -.
CC PIR, S03849; S03849.
CC InterPro: IPR002344; Lupus_La.
CC InterPro: IPR006630; Lupus_La_dom.
CC InterPro: IPR000504; RNA_rec_mot.
CC Pfam, PF05383; La; 1.
CC Pfam, PF00076; rrm; 1.
CC PRINTS, PR00302; LUPUSLA.
CC SMART, SM00715; LA; 1.
CC SMART, SM00360; RRM; 1.
CC PROSITE, PSS0102; RRM; 1.
CC PROSITE, PSS0030; RRM_RNP_1; 1.
CC RNA-binding; Nuclear protein; Phosphorylation.

FT DOMAIN 111 187 RNA-BINDING (RRM).
 SQ SEQUENCE 404 AA; 46534 MW; 4EE30B5C262AD6A1 CRC64;
 Query Match 100.0%; Score 99; DB 1; Length 404;
 Best Local Similarity 100.0%; Pred. No. 3,1e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 AALEAKICHQIEYYRGDF 18
 11 AALEAKICHQIEYYRGDF 28
 Db 11 AALEAKICHQIEYYRGDF 28
 RESULT 2
 LA HUMAN STANDARD; PRT; 408 AA.
 AC P05455;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Lupus La protein (Sjogren syndrome type B antigen) (SS-B) (La ribonucleoprotein) (La autoantigen).
 GN SSB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=892020377; PubMed=2468131;
 RX Chan E.K.L., Sullivan K.F., Tan E.M.;
 RT "Ribonucleoprotein SS-B/La belongs to a protein family with consensus sequences for RNA-binding".
 RN Nucleic Acids Res. 17:2233-2244 (1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=89053970; PubMed=3192525;
 RX Chambers J.C., Kenan D., Martin B.J., Keene J.D.;
 RT "Genomic structure and amino acid sequence domains of the human La autoantigen".
 RN J. Biol. Chem. 263:18043-18051 (1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta, and Skeletal muscle;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F., Diatchenko L., Marulanda K., Farmer A.A., Rubin G.M., Hong L., Stempleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uedlin T.B., Toshiyuki S., Carrinci P., Prange C., Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Muzny D.K., Hale S., Garcia A.M., Gay L.J., Hultyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Skalius D.E., Schercher A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences".
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [4]
 RP SEQUENCE OF 54-408 FROM N.A.
 RX MEDLINE=88199081; PubMed=2452201;
 RA Sturgess A.D., Peterson M.G., McNeillage L.J., Whittingham S., Coppel R.S.;
 RT "Characteristics and epitope mapping of a cloned human autoantigen La".
 RN J. Immunol. 140:3212-3218 (1988).
 RN [5]

RP SEQUENCE OF 54-97 FROM N.A.
 RX MEDLINE=85166283; PubMed=3856888;
 RA Chambers J.C., Keene J.D.;
 RT "Isolation and analysis of cDNA clones expressing human Lupus La antigen".
 RN Proc. Natl. Acad. Sci. U.S.A. 82:2115-2119 (1985).
 RN [6]
 RP MEDLINE=89251617; PubMed=2470590;
 RX Gottlieb E., Steltz J.A.;
 RT "Function of the mammalian La protein: evidence for its action in transcription termination by RNA polymerase III".
 RN EMBO J. 8:851-861 (1989).
 RN [7]
 RP PHOSPHORYLATION.
 RX MEDLINE=97207017; PubMed=9054510;
 RA Fan H., Sakulich A.L., Goodier J.L., Zhang X., Qin J., Maraie R.J.;
 RT "Phosphorylation of the human La antigen on serine 366 can regulate recycling of RNA polymerase III transcription complexes".
 RN Cell 88:707-715 (1997).
 RN [8]
 RP INTERACTION WITH DDX15.
 RX MEDLINE=22346609; PubMed=12458796;
 RA Fouraux M.A., Kolman M.J.M., Van der Heijden A., De Jong A.S., Van Venrooij W.J., Pruijn G.J.M.;
 RT "The human La (SS-B) autoantigen interacts with DDX15/hPrp43, a putative DEAD-box RNA helicase".
 RN RNA 8:1428-1443 (2002).
 RN [9]
 RP FUNCTION: La protein plays a role in the transcription of RNA polymerase III. It is most probably a transcription termination factor. Binds to the 3' termini of virtually all nascent polymerase III transcripts. It is associated with precursor forms of RNA polymerase III transcripts including rRNA and 4.5S, 5S, 7S, and 7-2 RNAs.
 CC -1- SUBUNIT: Interacts with DDX15.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- PTM: PHOSPHORYLATED. THE PHOSPHORYLATION SITES ARE AT THE C-TERMINAL PART OF THE PROTEIN.
 CC -1- PTM: The N-terminus is blocked.
 CC -1- DISEASE: Sera from patients with systemic lupus erythematosus often contain antibodies that react with the normal cellular La protein as if this antigen was foreign.
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
 CC -----
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 CC -----
 CC EMBL: X13597; CAA31985.1; -;
 CC EMBL: J04205; AAAS1885.1; -;
 CC EMBL: BC001289; AAH01289.1; -;
 CC EMBL: BC020818; AAH02818.1; -;
 CC F01: A31888; A31888.
 CC Genew: HGNC:11316; SSB.
 CC MIM: 109090; -;
 CC GO: GO:0030529; C:ribonucleoprotein complex; TAS.
 CC GO: GO:0003729; F:mRNA binding; TAS.
 CC GO: GO:0000049; F:tRNA binding; TAS.
 CC GO: GO:0008334; F:histone mRNA metabolism; TAS.
 CC GO: GO:0006400; P:tRNA modification; TAS.
 CC InterPro: IPR002344; Lupus_La.
 CC InterPro: IPR006630; Lupus_La_dom.
 CC InterPro: IPR000504; RNA_rec_mot.
 CC Pfam: PF05383; La; 1.
 CC Pfam: PF00076; rtm; 1.
 CC PRINTS: PR00302; LUPUSLA.
 CC SMART: SM00715; La; 1.
 CC SMART: SM00360; RRM; 1.
 CC PROSITE: PS50102; RRM; 1.

DR PROSITE: PS00030; RRM_RNP_1.1.
 KW Systemic lupus erythematosus; RNA-binding; Phosphorylation;
 KM Nuclear protein.
 FT DOMAIN 111 187 RNA-BINDING (RRM).
 FT MOD RES 366 366 PHOSPHORYLATION (BY CK2).
 SQ SEQUENCE 408 AA; 46837 MW; EC153C15F9187FC4 CRC64;

Query Match 100.0%; Score 99; DB 1; Length 408;
 Best Local Similarity 100.0%; Pred. No. 3.1e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALEAKICHQIEFYFGDF 18
 Db 11 ALEAKICHQIEFYFGDF 28

RESULT 3

LA_RAT STANDARD; PRT; 415 AA.

ID LA_RAT
 AC P38656;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lupus La protein homolog (La ribonucleoprotein) (La autoantigen homolog).
 GN SSB OR SS-B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCB1_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93246255; PubMed=7916708;
 RA Semsei I., Troester H., Bartsch H., Schwemle M., Igloi G.L., Bachmann M.;

"Isolation of rat cDNA clones coding for the autoantigen SS-B/La: detection of species-specific variations.";

RT Gene 126:265-268(1993).

CC -1- FUNCTION: La protein plays a role in the transcription termination

CC factor. Binds to the 3' termin of virtually all nascent

CC polymerase III transcripts. It is associated with precursor forms

CC of RNA polymerase III transcripts including crRNA and 4.5S, 5S, 7S,

CC and 7-2 RNAs.

CC -1- SUBUNIT: Interacts with DDX15 (By similarity).

CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).

CC -1- PTM: Phosphorylated (By similarity).

CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.

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 CC or send an email to license@isb-sib.ch).

CC EMBL: X67859; CAA48043.1; -

DR PIR: JCI494; JCI494.

DR InterPro: IPR002344; Lupus_La.

DR InterPro: IPR006630; Lupus_La_dom.

DR InterPro: IPR000504; RNA_rec_mot.

DR Pfam: PF00383; La; 1.

DR Pfam: PF00076; rrm; 1.

DR PRINTS: PR00302; LUPUSLA.

DR SMART: SM00715; La; 1.

DR SMART: SM00360; RRM; 1.

DR PROSITE: PS0102; RRM; 1.

DR PROSITE: PS00030; RRM_RNP_1; 1.

KM RNA-binding; Nuclear protein; Phosphorylation.

FT DOMAIN 111 187 RNA-BINDING (RRM).
 SQ SEQUENCE 415 AA; 47777 MW; 033FD9CCE475F98 CRC64;

Query Match 100.0%; Score 99; DB 1; Length 415;
 Best Local Similarity 100.0%; Pred. No. 3.2e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ALEAKICHQIEFYFGDF 18
 Db 11 ALEAKICHQIEFYFGDF 28

RESULT 4

LA_MOUSE STANDARD; PRT; 415 AA.

ID LA_MOUSE
 AC P32067;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Lupus La protein homolog (La ribonucleoprotein) (La autoantigen homolog).
 GN SSB OR SS-B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93203630; PubMed=8454877;
 RA Topfner F., Gordon T., McCluskey J.;
 RT "Characterization of the mouse autoantigen La (SS-B). Identification
 RT of conserved RNA-binding motifs, a putative ATP binding site and
 RT reactivity of recombinant protein with poly(U) and human
 RT autoantibodies.";
 RL J. Immunol. 150:3091-3100(1993).

RN (2)
 RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Mammary gland;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Shapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mlinsky S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guntartne P.H.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,

RA Botterfield V.S.N., Krzywinski M.I., Skalska U., Smaluk D.E.,

RA Schnerker A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN (3)
 RP SEQUENCE OF 1-11 FROM N.A.

RA Grodz D., Bachmann M.;

RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: La protein plays a role in the transcription of RNA

CC polymerase III. It is most probably a transcription termination

CC factor. Binds to the 3' termin of virtually all nascent

CC polymerase III transcripts. It is associated with precursor forms

CC of RNA polymerase III transcripts including crRNA and 4.5S, 5S, 7S,

CC and 7-2 RNAs.

CC -1- SUBUNIT: Interacts with DDX15 (By similarity).

CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).

CC -1- PTM: Phosphorylated (By similarity).

CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; L00993; AAA9415.1; -
DR EMBL; BC003820; AAA03820.1; -
DR EMBL; X07951; CAA69249.1; -
DR MCD; MGI:98423; Sdb.
DR GO; GO:0005634; C:nucleus; IDA.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; rtm; 1.
DR PRINTS; PR0302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
DR RNA-binding; Nuclear protein; Phosphorylation.
KM DOMAIN; 111 187 RNA-BINDING (RRM).
SQ SEQUENCE 415 AA; 47756 MW; 2D75197692FDC933 CRC64;

Query Match 96.0%; Score 95; DB 1; Length 415;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ALEAKICHOIEYFGDF 18
Db 12 ALEAKICHOIEYFGDF 28

RESULT 5
LAB_XENLA STANDARD; PRT; 427 AA.
ID LAB_XENLA
AC P28049;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Lupus La protein homolog B (La ribonucleoprotein B) (La autoantigen
DE homolog B).
GN LAB1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocyte;
RX MEDLINE=93287095; PubMed=8510143;
RA Scherly D., Stutz F., Lin-Marg N., Clarkson S.G.;
RT "La proteins from Xenopus laevis. cDNA cloning and developmental
RT expression.";
RL J. Mol. Biol. 231:196-204(1993).
CC -1- FUNCTION: La protein plays a role in the transcription of RNA
CC polymerase III. It is most probably a transcription termination
CC factor. Binds to the 3' termini of virtually all nascent
CC polymerase III transcripts (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- DEVELOPMENTAL STAGE: Barely detectable in stage I/II oocytes,
CC accumulate in stage III/IV oocytes, then exhibit a roughly
CC constant steady state level in mature oocytes, eggs, and early
CC embryos.
CC -1- PTM: Phosphorylated (Probable).
CC -1- MISCELLANEOUS: There are two forms of La, Laa and Lab, in xenopus.
CC -1- SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN.
CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
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DR EMBL; X68818; CAA48716.1; -
DR PIR; S33817; S33817.
DR InterPro; IPR002344; Lupus_La.
DR InterPro; IPR006630; Lupus_La_dom.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF05383; La; 1.
DR Pfam; PF00076; rtm; 1.
DR PRINTS; PR0302; LUPUSLA.
DR SMART; SM00715; LA; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS50102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; FALSE NEG.
KM RNA-binding; Nuclear protein; Phosphorylation.
FT DOMAIN; 110 202 RNA-BINDING (RRM).
FT DOMAIN; 315 331 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
SQ SEQUENCE 427 AA; 48995 MW; 45F3146F934A355 CRC64;

Query Match 70.7%; Score 70; DB 1; Length 427;
Best Local Similarity 80.0%; Pred. No. 0.00027;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LEAKICHOIEYFGD 17
Db 12 LDTKICHOIEYFGD 26

RESULT 6
LAA_XENLA STANDARD; PRT; 428 AA.
ID LAA_XENLA
AC P28048;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Lupus La protein homolog A (La ribonucleoprotein A) (La autoantigen
DE homolog A).
GN LAA1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocyte;
RX MEDLINE=93287095; PubMed=8510143;
RA Scherly D., Stutz F., Lin-Marg N., Clarkson S.G.;
RT "La proteins from Xenopus laevis. cDNA cloning and developmental
RT expression.";
RL J. Mol. Biol. 231:196-204(1993).
CC -1- FUNCTION: La protein plays a role in the transcription of RNA
CC polymerase III. It is most probably a transcription termination
CC factor. Binds to the 3' termini of virtually all nascent
CC polymerase III transcripts (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- DEVELOPMENTAL STAGE: Barely detectable in stage I/II oocytes,
CC accumulate in stage III/IV oocytes, then exhibit a roughly
CC constant steady state level in mature oocytes, eggs, and early
CC embryos.
CC -1- PTM: Phosphorylated (Probable).
CC -1- MISCELLANEOUS: There are two forms of La, Laa and Lab, in xenopus.
CC -1- SIMILARITY: HIGH, TO MAMMALIAN LA PROTEIN.
CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
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DR EMBL: X68817; CAA48715.1; -

DR PIR: S33818; S33818

DR InterPro: IPR002344; Lupus_La

DR InterPro: IPR006350; Lupus_La_dom

DR InterPro: IPR00504; RNA_rec_mot

DR Pfam: PF05383; La; 1

DR Pfam: PF00076; rrm; 1

DR PRINTS: PR00302; LUPUSLA

DR SMART: SM00715; LA; 1

DR SMART: SM00360; RRM; 1

DR PROSITE: PS50102; RRM; 1

DR PROSITE: PS00030; RRM_RNP_1; 1

DR RNA-binding; Nuclear protein; Phosphorylation.

FT DOMAIN 111 203 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)

FT DOMAIN 316 332 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)

FT DOMAIN 428 AA; 48864 MW; AEB3A38B7D2E3EC3 CRC64;

SEQUENCE

Query Match 66.7%; Score 66; DB 1; Length 428;
Best Local Similarity 78.6%; Pred. No. 0.0013; Mismatches 2; Indels 0; Gaps 0;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 EAKICHOIEYFGD 17
14 DTKICEIYEYFGD 27

Db

RESULT 7

LA AEDAL STANDARD; PRT; 383 AA.

AC Q26457;

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE La protein homolog (La ribonucleoprotein) (La autoantigen homolog).

OS Aedes albopictus (Forest day mosquito).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Aedes; Neoptera; Endopterygota; Diptera; Nematocera; Culicidae; Aedes.

NCBI_TaxID=7160;

RN NCBI_TaxID=7160;

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RX MEDLINE=96135233; PubMed=8551578;

RA Parignon N., Straus J.H.;

RT "Mosquito homolog of the La autoantigen binds to Sindbis virus RNA.";

RL J. Virol. 70:1173-1181(1996).

CC -1- FUNCTION: May be involved in transcription termination by RNA polymerase II. Binds RNA and DNA. Binds to the 3' end of the minus strand of Sindbis virus RNA. This may be significant for Sindbis virus RNA replication.

CC -1- SUBCELLULAR LOCATION: Nuclear. Primarily nuclear, but significant amounts are present in the cytoplasm.

CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.

CC -1- SIMILARITY: TO VERTEBRATE PROTEIN LA.

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CC -----

DR EMBL: S80954; AAB35931.1; -

DR InterPro: IPR002344; Lupus_La

DR InterPro: IPR006350; Lupus_La_dom

DR InterPro: IPR00504; RNA_rec_mot

DR Pfam: PF05383; La; 1

DR Pfam: PF00076; rrm; 1

DR PRINTS: PR00302; LUPUSLA

DR SMART: SM00715; LA; 1.

DR SMART: SM00360; RRM; 1.

DR PROSITE: PS50102; RRM; 1

DR PROSITE: PS00030; RRM_RNP_1; FALSE NEG.

KW RNA-binding; Nuclear protein; DNA-binding (RM).

FT DOMAIN 141 228 RNA-BINDING (RM).

FT DOMAIN 383 AA; 44430 MW; 4E5CC8F21C40F452 CRC64;

SEQUENCE

Query Match 55.6%; Score 55; DB 1; Length 383;
Best Local Similarity 66.7%; Pred. No. 0.085;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 LEAKICHOIEYFGD 17
43 LEASTIRQLEIYFGD 57

Db

RESULT 8

LA DROME STANDARD; PRT; 390 AA.

AC P40796; Q24375; Q9VIN2;

DT 01-FEB-1995 (Rel. 31, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE La protein homolog (La ribonucleoprotein) (La autoantigen homolog).

GN LA OR CG10922.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Aedes; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;

RN NCBI_TaxID=7227;

RP SEQUENCE FROM N.A.

RX STRAIN=Canton-S; TISSUE=Ovary;

RX MEDLINE=94309632; PubMed=8035794;

RA Bai C., Li Z., Tollas P.P.;

RT "Developmental characterization of a Drosophila RNA-binding protein homologous to the human systemic lupus erythematosus-associated La/SS-B autoantigen.";

RL Mol. Cell. Biol. 14:5123-5129(1994).

RN NCBI_TaxID=7227;

RP SEQUENCE FROM N.A.

RX MEDLINE=94309661; PubMed=8035818;

RA Yoo C.J., Wolin S.L.;

RT "La proteins from Drosophila melanogaster and Saccharomyces cerevisiae: a yeast homolog of the La autoantigen is dispensable for growth.";

RL Mol. Cell. Biol. 14:5412-5424(1994).

RN NCBI_TaxID=7227;

RP SEQUENCE FROM N.A.

RX STRAIN=Berkeley;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Ananthanides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA April J.F., Abpayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,

RA Ballow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolhakov S.,

RA Borokva D., Botchan M.R., Bouck J., Brokstein P., Bottier P.,

RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Caswell S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablo K.B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodet A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kemison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Laeko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paele U.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., She B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier B., Spradling A.C., Stapleton M., Strong R., Sun E., Svrtkars R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weissbach G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of *Drosophila melanogaster*.";
 Science 287:2185-2195(2000).
 -1- FUNCTION: May be involved in transcription termination by RNA polymerase III. Binds RNA and DNA. Binds to precursors of RNA polymerase III transcripts. May play a specialized role during fly development.
 CC SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- DEVELOPMENTAL STAGE: Expressed throughout embryonic, larval, pupal, and adult development. Expression throughout the embryo is followed by a restricted pattern of mesodermal expression that is later confined to the visceral mesoderm, gonade, gut, and salivary glands.
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
 CC -1- SIMILARITY: TO VERTEBRATE PROTEIN LA.
 CC -----
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 CC -----
 DR EMBL; U07652; AAA20518.1; -;
 DR EMBL; L32988; AAA21776.1; -;
 DR EMBL; AE003666; AAF53885.1; -;
 DR PIR; A53773; A53773.
 DR PIR; A53781; A53781.
 DR FLYBase; FBgn00116381; LA.
 DR GO; GO:0008099; F:5S rRNA primary transcript binding; IDA.
 DR GO; GO:0003723; F:RNA binding; NAS.
 DR InterPro; IPR002344; Lupus_La.
 DR InterPro; IPR006530; Lupus_La_dom.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF00383; La; 1.
 DR Pfam; PF00076; rrm; 1.
 DR PRINTS; PR00302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PS50102; RRM; 1.
 DR PROSITE; PS00030; RRM_RNP_1; 1.
 KW RNA-binding; Nuclear protein; DNA-binding.
 FT DOMAIN 149 234
 FT CONFLICT 169 169 A -> T (IN REF. 1).
 FT CONFLICT 182 183 KH -> NS (IN REF. 1).
 FT CONFLICT 283 283 A -> R (IN REF. 1).
 FT CONFLICT 329 329 K -> N (IN REF. 1).
 SQ SEQUENCE 390 AA; 44884 MW; A809288B90446A5 CRC64;

Query Match 51.5%; Score 51; DB 1; Length 390;
 Best Local Similarity 64.3%; Pred. No. 0.41;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 EAKICHOLEYFGD 17
 DB 51 ERAIRIVQYIFGD 64

RESULT 9
 LAH1 SCHPO STANDARD: PRT; 298 AA.
 ID LAH1 SCHPO Q10458;
 AC P87058; Q13352; Q10458;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE La protein homolog (La ribonucleoprotein) (La autoantigen homolog).
 GN SLAI OR SPAC57A10.10C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98067398; PubMed=9404894;
 RA van Horn D.J., Yoo C.U., Xue D., Shi H., Wolin S.L.;
 RT "The La protein in Schizosaccharomyces pombe: a conserved yet dispensable phosphoprotein that functions in rRNA maturation.";
 RL RNA 3:1434-1443(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Utsunmi R.R.U.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21849401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajadream M.A., Lyne M., Lyne R., Stewart A., Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Fellwell J., Fraser A., Gentles M., Goble A., Hamlin N., Harris P., Hidalgo J., Hodson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jørgensen K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., Woodward J., Volkart G., Aert R., Robben J., Grymonprez B., Walteijens I., Vanstreels E., Rieger M., Schefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Egert P., Zimmermann W., Wedler H., Mambutt R., Punnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Motier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado J., Jimenez J., Sanchez M., del Rey F., Benito J., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovskii G.V., Ussery D., Barrett B.G., Nurse P.;
 RT "The genome sequence of *Schizosaccharomyces pombe*.";
 RL Nature 415:871-880(2002).
 CC -1- FUNCTION: Binds to the precursors of polymerase III RNAs. Functions in rRNA maturation.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- SIMILARITY: Contains 1 RNA recognition motif (RRM) domain.
 CC -1- SIMILARITY: TO VERTEBRATE PROTEIN LA.
 CC -----
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 CC -----
 DR EMBL; AF022949; AAB82145.1; -;
 DR EMBL; AB011371; BAA24981.1; -;
 DR EMBL; Z94864; CAB08173.1; -;
 DR PIR; T38937; T38937.

DR PIR: T43542; T43542.
 DR GenBank_Spomb; SPAC57A10.10c; -.
 DR InterPro; IPR002344; Lupus_La.
 DR InterPro; IPR006630; Lupus_La.dom.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF05383; La; 1.
 DR Pfam; PF00076; rtm; 1.
 DR SMART; PR00302; LUPUSLA.
 DR SMART; SM00715; LA; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PSS0102; RRM; 1.
 DR PROSITE; PSS00030; RRM_RN1; FALSE_NEG.
 DR RNA-binding; Nuclear protein.
 DR DOMAIN 154 236 RNA-BINDING (RRM).
 FT CONFLICT 188 188 M -> I (IN REF. 1 AND 2).
 SQ SEQUENCE 298 AA; 34616 MW; 64E6AB9940B87F4 CRC64;
 Query Match 46.5%; Score 46; DB 1; Length 298;
 Best Local Similarity 50.0%; Pred. No. 2.2;
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Oy 4 EAKICHOIEYFGD 17
 Db 64 EAEVLKQVEYFSD 77
 RESULT 10
 GATB_CHLGV STANDARD; PRT; 487 AA.
 AC 0823W6;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Aspartyl-glutamyl-tRNA(Asn/Gln) amidotransferase subunit B
 DE (EC 6.3.5.-) (Asp/Glu-ADT subunit B).
 GN GATB OR CCA00289.
 OS Chlamydomonas caviae.
 OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=83557;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GPIC.
 RX MEDLINE=22369155; PubMed=12682364;
 RA Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
 Heidelberg J., Holtapple E., Khouri H., Federova N.B., Carty H.A.,
 Umayam L.A., Haft D.H., Peterson J., Beaman M.J., White O.,
 Salzberg S.L., Hsiao R.-C., McClarty G., Rank R.G., Bavoil P.M.,
 Fraser C.M.,
 RA "Genome sequence of Chlamydomonas caviae (Chlamydia psittaci GPIC):
 examining the role of niche-specific genes in the evolution of the
 Chlamydiaceae.";
 RT Nucleic Acids Res. 31(21):2134-2147(2003).
 RL Nucleic Acids Res. 31(21):2134-2147(2003).
 CC -1- FUNCTION: Allows the formation of correctly charged Asn-tRNA(Asn)
 or Gln-tRNA(Gln) through the transamidation of misacylated Asp-
 tRNA(Asn) or Glu-tRNA(Gln) in organisms which lack either or both
 of aspartyl-tRNA or glutamyl-tRNA synthetases. The reaction
 takes place in the presence of glutamine and ATP through an
 activated phospho-Asp-tRNA(Asn) or phospho-Glu-tRNA(Gln) (By
 similarity)
 CC -1- CATALYTIC ACTIVITY: ATP + L-glutamyl-tRNA(Gln) + L-glutamine = ADP
 + phosphate + L-glutamyl-tRNA(Gln) + L-glutamate.
 CC -1- CATALYTIC ACTIVITY: ATP + L-aspartyl-tRNA(Asn) + L-glutamine = ADP
 + phosphate + L-aspartyl-tRNA(Asn) + L-glutamate.
 CC -1- SUBUNIT: Heterotrimer of A, B and C subunits (By similarity).
 CC -1- SIMILARITY: Belongs to the gatB/gatC family. GatB subfamily.
 CC -----
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 or send an email to license@isb-sib.ch).

CC EMBL: AE016995; AAP05038.1; -.
 DR TIGR; CCA00289; -; 1.
 DR HAMAP; MF_00121; -; 1.
 DR InterPro; IPR004413; GatB.
 DR InterPro; IPR006107; GatB_cent.
 DR InterPro; IPR006075; GatB_N.
 DR InterPro; IPR003789; GatB_Ygey.
 DR Pfam; PF01162; GatB; 1.
 DR Pfam; PF02934; GatB_N; 1.
 DR Pfam; PF02637; GatB_Ygey; 1.
 DR TIGRNAME; TIGR00133; GatB; 1.
 DR PROSITE; PSS0124; GATB; 1.
 DR Protein biosynthesis; Ligase; Complete proteome.
 KW SEQUENCE 487 AA; 54571 MW; 7DAB0EE7760A0AF7 CRC64;
 Query Match 43.4%; Score 43; DB 1; Length 487;
 Best Local Similarity 69.2%; Pred. No. 12;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Oy 2 ALEAKICHOIEY 14
 Db 228 ALEAERCIOIEAY 240
 RESULT 11
 TCMO_PETCR STANDARD; PRT; 506 AA.
 AC 043033;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Trans-cinnamate 4-monooxygenase (EC 1.14.13.11) (Cinnamic acid
 4-hydroxylase) (CAH) (P450CAH) (Cytochrome P450 73).
 GN CYP73A10 OR CYP73.
 OS Petroselinum crispum (Parsley) (Petroselinum hortense).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Campanulids; Apiales; Apiaceae; Apioidae; apioid superclade;
 OC Apium clade; Petroselinum.
 OX NCBI_TaxID=4043;
 [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=95320184; PubMed=7597051;
 RX Logemann E., Parniske M., Hahlbrock K.;
 RA "Modes of expression and common structural features of the complete
 RT phenylalanine ammonia-lyase gene family in parsley.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:5905-5909(1995).
 CC -1- FUNCTION: Controls carbon flux to pigments essential for
 CC pollination or UV protection, to numerous phytoalexins synthesized
 CC by plants when challenged by pathogens, and to lignins.
 CC -1- CATALYTIC ACTIVITY: Trans-cinnamate + NADPH + O(2) = 4-
 CC hydroxycinnamate + NADP(+) + H(2)O.
 CC -1- PATHWAY: Lignin biosynthesis.
 CC -1- SIMILARITY: Belongs to the cytochrome P450 family.
 CC -----
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SQ SEQUENCE 506 AA; 58047 MW; 32F00EE959D69CCF CRC64;
 Query Match 43.4%; Score 43; DB 1; Length 506;
 Best Local Similarity 42.9%; Pred. No. 12;
 Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 QY 5 AKICQIEYFGDF 18
 Db 215 SRLAQSFYHFGDF 228
 RESULT 12
 GLNQ_BACST STANDARD; PRT; 242 AA.
 ID GLNQ_BACST
 AC P27675;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Glutamine transport ATP-binding protein glnQ.
 GN GLNQ.
 OS Bacillus stearothermophilus.
 CC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
 CX NCBI_TaxID=1422;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NUB36;
 RX MEDLINE=91310597; PubMed=1856180;
 RA Wu L., Welker N.E.,
 RT "Cloning and characterization of a glutamine transport operon of
 RT Bacillus stearothermophilus NUB36: effect of temperature on
 RT regulation of transcription."
 RL J. Bacteriol. 173:4877-4888 (1991).
 CC -1- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM
 CC FOR GLUTAMINE. PROBABLY RESPONSIBLE FOR ENERGY COUPLING TO THE
 CC TRANSPORT SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Membrane-associated (Potential).
 CC -1- INDUCTION: By lack of glutamine.
 CC -1- SIMILARITY: Belongs to the ABC transporter family.
 CC
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 CC
 CC EMBL; M61017; AAA22483.1; -.
 DR PIR; A42478; A42478.
 DR InterPro; IPR003593; AAA ATPase.
 DR InterPro; IPR003439; ABC transporter.
 DR Pfam; PF00005; ABC_tran.1.
 DR ProDom; PD000006; ABC_transporter.1.
 DR SMART; SM00382; AAA.1.
 DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE; PS00893; ABC_TRANSPORTER_2; 1.
 KW Amino-acid transport; Transport; Membrane; ATP-binding.
 FT NP BIND 34
 FT SEQUENCE 242 AA; 27436 MW; 102B1C5E332F31C8 CRC64;
 Query Match 42.4%; Score 42; DB 1; Length 242;
 Best Local Similarity 60.0%; Pred. No. 8.4;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 9 HOIEYFGDF 18
 Db 5 HOVNKYGDF 14
 RESULT 13
 LBP_RABIT STANDARD; PRT; 482 AA.
 ID LBP_RABIT
 AC P17454;

DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lipopolysaccharide-binding protein precursor (LBP).
 GN LBP.
 OS Oryctolagus cuniculus (Rabbit).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 CX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=90385281; PubMed=2402637;
 RA Schumann R.R., Leong S.R., Flaegge G.W., Gray P.W., Wright S.D.,
 RA Mathison J.C., Tobias P.S., Ulevitch R.J.;
 RT "Structure and function of lipopolysaccharide binding protein.";
 RL Science 249:1429-1431 (1990).
 RN [2]
 RP SEQUENCE OF 27-66.
 RC TISSUE=Serum;
 RX MEDLINE=86306528; PubMed=2427635;
 RA Tobias P.S., Soldau K., Ulevitch R.J.;
 RT "Isolation of a lipopolysaccharide-binding acute phase reactant from
 RT rabbit serum."
 RL J. Exp. Med. 164:777-793 (1986).
 CC -1- FUNCTION: Binds to the lipid moiety of bacterial
 CC lipopolysaccharides (LPS), a glycolipid present in the outer
 CC membrane of all Gram-negative bacteria. The LBP/LPS complex seems
 CC to interact with the CD14 receptor.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the BPI/LBP/Plunc superfamily. BPI/LBP
 CC family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M35534; AAA99235.1; -.
 DR PIR; B35843; B35843.
 DR HSBP; P17213; BPI1.
 DR InterPro; IPR001124; LBP_BPI_CETP.
 DR Pfam; PF01273; LBP_BPI_CETP.1.
 DR Pfam; PF02886; LBP_BPI_CETP_C.1.
 DR SMART; SM00328; BPI.1.
 DR SMART; SM00329; BPI2.1.
 DR PROSITE; PS00400; LBP_BPI_CETP.1.
 DR PROSITE; PS00400; Antibiotic; Transmembrane; Glycoprotein; Signal.
 KW Lipid transport; Antibiotic; Transmembrane; Glycoprotein; Signal.
 FT SIGNAL 1
 FT CHAIN 27
 FT CARBOHYD 301
 FT CARBOHYD 351
 FT CARBOHYD 387
 FT CARBOHYD 387
 FT CONFLICT 57
 FT CONFLICT 63
 FT SEQUENCE 482 AA; 54001 MW; 628A6E0A47200C2 CRC64;
 Query Match 42.4%; Score 42; DB 1; Length 482;
 Best Local Similarity 80.0%; Pred. No. 17;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 LEAKICQIE 12
 Db 194 LESKICQIE 203
 RESULT 14
 FOL2_MOUSE STANDARD; PRT; 251 AA.
 ID FOL2_MOUSE
 AC Q05685;
 DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Folate receptor beta precursor (FR-beta) (Folate receptor 2) (Folate-binding protein 2).
 GN FOLR2 OR FOLBP2 OR FRP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX MEDLINE=91373339; PubMed=1894617;
 RA Brigle K.E., Westin E.H., Houghton M.T., Goldman I.D.;
 RT "Characterization of two cDNAs encoding folate-binding proteins from RL 11210 murine leukemia cells. Increased expression associated with a genomic rearrangement.";
 RL J. Biol. Chem. 266:17243-17249(1991).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94140851; PubMed=8307991;
 RA Brigle K.E., Seltzer R.L., Westin E.H., Goldman I.D.;
 RT "Increased expression and genomic organization of a folate-binding protein homologous to the human placental isoform in 11210 murine leukemia cell lines with a defective reduced folate carrier.";
 RL J. Biol. Chem. 269:4267-4272(1994).
 CC -1- FUNCTION: Binds to folate and reduced folic acid derivatives and mediates delivery of 5-methyltetrahydrofolate to the interior of cells.
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By similarity).
 CC -1- PTM: Eight disulfide bonds are present (Probable).
 CC -1- SIMILARITY: Belongs to the folate receptor family.
 CC -----
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 CC -----
 CC EMBL: M64817; AAA37599.1; -;
 CC EMBL: L25338; AAA37594.1; -;
 CC PIR: B40969; B40969.
 CC MGI: 95569; Folr2.
 CC InterPro: IPR004269; Folt_chemrecept.
 CC Pfam: PR03024; Folate_rec1.
 CC Receptor; Glycoprotein; Signal; Placenta; Folate-binding; Membrane; GPI-anchor; Multigene family; Lipoprotein.
 CC KW SIGNAL 1 20
 CC FT CHAIN 21 227 FOLATE RECEPTOR BETA.
 CC FT PROPEP 228 251 REMOVED IN MATURE FORM (POTENTIAL).
 CC FT LIPID 227 227 GPI-anchor amidated serine (POTENTIAL).
 CC FT CARBOHYD 62 62 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CARBOHYD 193 193 N-LINKED (GLCNAC...) (POTENTIAL).
 CC SQ SEQUENCE 251 AA; 28821 MW; 8404EACB1BFEC7 CRC64;
 CC
 CC Query Match 41.4%; Score 41; DB 1; Length 251;
 CC Best Local Similarity 75.0%; Pred. No. 13;
 CC Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 CC
 CC QY 8 CHQIEYYP 15
 CC Db 167 CHTFEYYP 174
 CC
 CC RESULT 15
 CC ID IFT4 HUMAN STANDARD; PRT; 490 AA.
 CC AC 014879; 099634; 09BSK7;
 CC DT 30-MAY-2000 (Rel. 39, Created)
 CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Interferon-induced protein with tetratricopeptide repeats 4 (IFIT-4)
 DE (Interferon-induced 60 kDa protein) (IFI-60K) (ISG-60) (CIG49)
 DE (Relic acid-induced gene G protein) (RIG-G).
 GN IFIT4 OR IFI60.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RX MEDLINE=9391139; PubMed=9391139;
 RA Zhu H., Cong J.P., Shenk T.;
 RT "Use of differential display analysis to assess the effect of human RT indomethacin infection on the accumulation of cellular RNAs: Proc. Natl. Acad. Sci. U.S.A. 94:13985-13990(1997).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99047533; PubMed=9828129;
 RA de Veer M.J., Sim H., Whistock J.C., Devenish R.J., Ralph S.J.;
 RT "IFI60/ISG60/IFI4, a new member of the human IFI54/IFI72 family of interferon-stimulated genes.";
 RL Genomics 54:267-277(1998).
 [3]
 RP SEQUENCE FROM N.A.
 RA Yu M., Tong J., Mao M., Chen S., Chen Z.;
 RT "RIG-G, a novel gene induced by ATRA in acute promyelocytic leukemia cells, is a new member of the ISG family.";
 RT Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant P., Prange C., Brownstein M.J., Ussid T.B., Toshiyuki S., Carninci P., Mallory S.J., Raha S.S., Loughellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Alakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E., Jones S.J.M., Maiti M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- SIMILARITY: Belongs to the IFIT family.
 CC -1- SIMILARITY: Contains 8 TPR repeats.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AF026939; AAB95160.1; -;
 CC EMBL: AF083470; AAC63524.1; -;
 CC EMBL: U52513; AAB40606.1; -;
 CC EMBL: BC001383; AAB01383.1; -;
 CC EMBL: BC004977; AAH04977.1; -;
 CC Genew; HGNC:5411; IFIT4.
 CC MIM: 604650; -;
 CC InterPro: IPR008941; TPR-like.

DR InterPro; IPR001440; TPR.
 DR Pfam; PF00515; TPR; 5.
 DR SMART; SM00028; TPR; 4.
 KW Repeat; TPR repeat; Interferon induction.
 FT REPEAT 51 84 TPR 1.
 FT REPEAT 94 127 TPR 2.
 FT REPEAT 136 169 TPR 3.
 FT REPEAT 172 206 TPR 4.
 FT REPEAT 207 240 TPR 5.
 FT REPEAT 241 274 TPR 6.
 FT REPEAT 415 448 TPR 7.
 FT REPEAT 450 481 TPR 8.
 FT CONFLICT 44 44 F -> S (IN REF. 4; AAH04977).
 FT CONFLICT 359 359 Q -> QQ (IN REF. 2).
 FT CONFLICT 435 435 MISSING (IN REF. 2).
 SQ SEQUENCE 490 AA: 55984 MW; B9F042D4DF7151D2 CRC64;

Query Match 41.4%; Score 41; DB 1; Length 490;
 Best local Similarity 43.8%; Pred. No. 26;
 Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 3 LEAKICHOIEYFQDF 18
 ||:::||||:|
 Db 34 LEDRVCNQIEFLNTEF 49

Search completed: September 10, 2004, 17:53:06
 Job time : 8.24022 secs

RESULT 14
US-10-054-611-26
Sequence 26, Application US/10054611
Publication No. US20030059787A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. US20030059787A1e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,611
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: No. US20030059787A1 Relevant
TOPOLOGY: No. US20030059787A1 Relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-054-611-26
Query Match 67.9%; Score 57; DB 14; Length 39;
Best Local Similarity 90.9%; Pred. No. 0.021;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 5 IIRQVEYFGD 15
DB 1 IIRQVEYFGD 11
RESULT 15
US-10-170-385-477
Sequence 477, Application US/10170385
Publication No. US20030203372A1
GENERAL INFORMATION:
APPLICANT: Ward, Neil Raymond
APPLICANT: Mundy, Christopher Robert

APPLICANT: Kan, On
APPLICANT: Harris, Robert Alan
APPLICANT: White, Jonathan
APPLICANT: Binley, Katie Mary
APPLICANT: Rayner, William Nigel
APPLICANT: Naylor, Stuart
APPLICANT: Kingsman, Susan Mary
APPLICANT: Krige, David
TITLE OF INVENTION: ANALYSIS METHOD
FILE REFERENCE: 53268200100
CURRENT APPLICATION NUMBER: US/10/170,385
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: PCT/GB02/01662
PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: PCT/GB01/05458
PRIOR FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 549
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 477
LENGTH: 408
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-170-385-477
Query Match 67.9%; Score 57; DB 12; Length 408;
Best Local Similarity 66.7%; Pred. No. 0.25;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 2 ERAIRQVEYFGDF 16
DB 14 EAKICQIEYFGDF 28

Search completed: September 10, 2004, 18:11:58
Job time : 36.9436 secs

STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 216:
US-10-325-810-216

Query Match 67.9%; Score 57; DB 12; Length 39;
Best Local Similarity 90.9%; Pred. No. 0.021;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IIRQVEYFGD 15
|:|||||
Db 1 IIRQVEYFGD 11

RESULT 12
US-10-053-758-26
; Sequence 26, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
TITLE OF INVENTION: No. US20030032075A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/053,758
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: No. US20030032075A1 Relevant
TOPOLOGY: No. US20030032075A1 Relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-053-758-26

Query Match 67.9%; Score 57; DB 14; Length 39;
Best Local Similarity 90.9%; Pred. No. 0.021;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IIRQVEYFGD 15
|:|||||
Db 1 IIRQVEYFGD 11

RESULT 13
US-10-054-295-26
; Sequence 26, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
TITLE OF INVENTION: No. US20030044953A1el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/054,295
FILING DATE: 18-Jan-2002
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/854,050
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: No. US20030044953A1 Relevant
TOPOLOGY: No. US20030044953A1 Relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-054-295-26

Query Match 67.9%; Score 57; DB 14; Length 39;
Best Local Similarity 90.9%; Pred. No. 0.021;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IIRQVEYFGD 15
|:|||||
Db 1 IIRQVEYFGD 11

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-766-253-26

Query Match 67.9%; Score 57; DB 9; Length 39;
Best Local Similarity 90.9%; Pred. No. 0.021;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IIRQVEYIFGD 15
Db 1 IIRQVEYIFGD 11

RESULT 10
US-09-438-486-26
Sequence 26, Application US/09438486
Publication No. US2003009019A1
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. US2003009019A1el Telomerase
NUMBER OF SEQUENCES: 223
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/438,486
FILING DATE: 12-NOV-1999
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002931US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide

US-09-438-486-26

Query Match 67.9%; Score 57; DB 10; Length 39;
Best Local Similarity 90.9%; Pred. No. 0.021;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IIRQVEYIFGD 15
Db 1 IIRQVEYIFGD 11

RESULT 11
US-10-325-810-216
Sequence 216, Application US/10325810
Publication No. US20030204069A1
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausehus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 216:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid

RESULT 7
US-09-836-073-14
Sequence 14, Application US/09836073
Patent No. US20020173475A1
GENERAL INFORMATION:
APPLICANT: Daegupta, Asim
APPLICANT: Das, S.
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 18
TYPE: PRT
ORGANISM: Bovine
US-09-836-073-14

Query Match 67.9%; Score 57; DB 9; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0095;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 ERAIIRQVEYFGDF 16
|:|||||
Db 4 EAKICHQIEYFGDF 18

RESULT 8
US-09-843-676-26
Sequence 26, Application US/09843676
Patent No. US20020164786A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. US20020164786A1e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/843,676
FILING DATE: 26-Apr-2001
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: NO. US20020164786A1 Relevant
MOLECULE TYPE: peptide
TOPOLOGY: NO. US20020164786A1 Relevant
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-843-676-26

Query Match 67.9%; Score 57; DB 9; Length 39;
Best Local Similarity 90.9%; Pred. No. 0.021;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IIRQVEYFGD 15
|:|||||
Db 1 IIRQVEYFGD 11

RESULT 9
US-09-766-253-26
Sequence 26, Application US/09766253
Publication No. US20020187471A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. US20020187471A1e1 Telomerase
NUMBER OF SEQUENCES: 171
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/766,253
FILING DATE: 19-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,017
FILING DATE: 1997-04-25
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002920US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant

```

; APPLICANT: Balidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRF
; ORGANISM: Homo Sapiens
US-09-836-073-4

Query Match      73.8%; Score 62; DB 9; Length 18;
Best Local Similarity 68.8%; Pred. No. 0.0013;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 ERATIRQVEYFGRDF 16
        |||:|||||
Db      3 QEAKICHQIEYFGRDF 18

RESULT 3
US-09-836-073-2
; Sequence 2, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Balidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRF
; ORGANISM: Homo Sapiens
US-09-836-073-2

Query Match      69.0%; Score 58; DB 9; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0064;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      2 ERATIRQVEYFGRDF 16
        |||:|||||
Db      4 EAQICQIEYFGRDF 18

RESULT 4
US-09-836-073-13
; Sequence 13, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Balidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 17
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; TYPE: PRF
; ORGANISM: Mouse
US-09-836-073-13

Query Match      67.9%; Score 57; DB 9; Length 17;
Best Local Similarity 66.7%; Pred. No. 0.0089;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2 ERATIRQVEYFGRDF 16
        |||:|||||
Db      3 EAKICHQIEYFGRDF 17

RESULT 5
US-09-836-073-1
; Sequence 1, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Balidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRF
; ORGANISM: Homo Sapiens
US-09-836-073-1

Query Match      67.9%; Score 57; DB 9; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.0095;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2 ERATIRQVEYFGRDF 16
        |||:|||||
Db      4 EAKICHQIEYFGRDF 18

RESULT 6
US-09-836-073-5
; Sequence 5, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Balidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRF
; ORGANISM: Homo Sapiens
US-09-836-073-5

Query Match      67.9%; Score 57; DB 9; Length 18;
Best Local Similarity 62.5%; Pred. No. 0.0095;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      1 ERATIRQVEYFGRDF 16
        |||:|||||
Db      3 QEAKICHQIEYFGRDF 18
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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:52:06 ; Search time 35.8436 Seconds
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143.151 Million cell updates/sec

Title: US-09-836-073-19

Sequence: 1 QERRAIRQVEYFGDF 16

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

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- 9: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	62	73.8	18	US-09-836-073-4	Sequence 4, Appl
3	58	69.0	18	US-09-836-073-2	Sequence 2, Appl
4	57	67.9	17	US-09-836-073-13	Sequence 13, Appl
5	57	67.9	18	US-09-836-073-1	Sequence 1, Appl
6	57	67.9	18	US-09-836-073-5	Sequence 5, Appl
7	57	67.9	18	US-09-836-073-14	Sequence 14, Appl
8	57	67.9	39	US-09-843-676-26	Sequence 26, Appl
9	57	67.9	39	US-09-766-253-26	Sequence 26, Appl
10	57	67.9	39	US-09-438-486-26	Sequence 26, Appl
11	57	67.9	39	US-10-325-810-216	Sequence 216, Appl
12	57	67.9	39	US-10-053-758-26	Sequence 26, Appl
13	57	67.9	39	US-10-054-295-26	Sequence 26, Appl
14	57	67.9	39	US-10-054-611-26	Sequence 26, Appl
15	57	67.9	408	US-10-170-385-477	Sequence 477, Appl

16	57	67.9	460	12	US-09-925-298-695	Sequence 695, Appl
17	57	67.9	460	14	US-10-102-806-695	Sequence 695, Appl
18	57	67.9	460	15	US-10-264-049-2643	Sequence 2643, Appl
19	55	65.5	488	12	US-10-424-559-272690	Sequence 272690, Appl
20	54	64.3	18	9	US-09-836-073-15	Sequence 15, Appl
21	54	64.3	21	15	US-10-376-121A-20	Sequence 20, Appl
22	53	63.1	411	14	US-10-177-478-8	Sequence 8, Appl
23	51	60.7	18	9	US-09-836-073-9	Sequence 9, Appl
24	50	59.5	18	9	US-09-836-073-17	Sequence 17, Appl
25	50	59.5	38	12	US-10-325-810-214	Sequence 214, Appl
26	50	59.5	143	12	US-10-424-559-254661	Sequence 254661, Appl
27	50	59.5	395	12	US-10-424-559-254664	Sequence 254664, Appl
28	49	58.3	18	9	US-09-836-073-11	Sequence 11, Appl
29	49	58.3	18	9	US-09-836-073-12	Sequence 12, Appl
30	49	58.3	376	16	US-10-767-701-45524	Sequence 45524, Appl
31	49	58.3	405	16	US-10-437-963-134637	Sequence 134637, Appl
32	49	58.3	467	16	US-10-437-963-15751	Sequence 15751, Appl
33	48	57.1	18	9	US-09-836-073-10	Sequence 10, Appl
34	48	57.1	38	9	US-09-843-676-25	Sequence 25, Appl
35	48	57.1	38	9	US-09-766-253-25	Sequence 25, Appl
36	48	57.1	38	10	US-09-438-486-25	Sequence 25, Appl
37	48	57.1	38	12	US-10-325-810-215	Sequence 215, Appl
38	48	57.1	38	14	US-10-053-758-25	Sequence 25, Appl
39	48	57.1	38	14	US-10-054-295-25	Sequence 25, Appl
40	48	57.1	38	14	US-10-054-611-25	Sequence 25, Appl
41	48	57.1	148	16	US-10-767-701-53447	Sequence 53447, Appl
42	48	57.1	420	16	US-10-437-963-128072	Sequence 128072, Appl
43	48	57.1	433	16	US-10-437-963-179489	Sequence 179489, Appl
44	47	56.0	48	12	US-10-424-559-269667	Sequence 269667, Appl
45	47	56.0	192	16	US-10-767-701-40959	Sequence 40959, Appl

ALIGNMENTS

RESULT 1
US-09-836-073-19
Sequence 19, Application US/09836073
Patent No. US20020173475A1
GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 22002054822
CURRENT APPLICATION NUMBER: US/09/836,073
PRIOR FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 19
LENGTH: 16
TYPE: PRT
ORGANISM: Drosophila
US-09-836-073-19

Query Match 100.0%; Score 84; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 2.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QERRAIRQVEYFGDF 16
DB 1 QERRAIRQVEYFGDF 16

RESULT 2
US-09-836-073-4
Sequence 4, Application US/09836073
Patent No. US20020173475A1
GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.

FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-215

Query Match 57.1%; Score 48; DB 3; Length 38;
Best Local Similarity 72.7%; Pred. No. 0.082;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 IIRQVEYYFGD 15
| : |||||
Db 1 ICEQIEYYFGD 11

RESULT 15
US-08-854-050-25
Sequence 25, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin H.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-854-050-25

Query Match 57.1%; Score 48; DB 3; Length 38;
Best Local Similarity 72.7%; Pred. No. 0.082;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 IIRQVEYYFGD 15
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Db 1 ICEQIEYYFGD 11

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FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-721-456-214

Query Match 59.5%; Score 50; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 0.036;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 IIRQVEYFGDF 16
DB 1 ICHQXEYFGDF 12

RESULT 13
US-08-851-843A-25
Sequence 25, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
MOLECULE TYPE: peptide
US-08-851-843A-25

Query Match 57.1%; Score 48; DB 3; Length 38;
Best Local Similarity 72.7%; Pred. No. 0.082;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 IIRQVEYFGDF 15
DB 1 ICHQXEYFGDF 11

RESULT 14
US-08-974-549A-215
Sequence 215, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017

APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION DATA:
PRIOR APPLICATION NUMBER: WO PCT/US97/117618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/117885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-214

Query Match 59.5%; Score 50; DB 3; Length 38;
Best Local Similarity 75.0%; Pred. No. 0.036;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 IIRQVEYYFGDF 16
DB 1 ICHQXEVYFGDF 12

RESULT 11
US-09-402-181B-214
Sequence 214, Application US/09402181B
Patent No. 6610839
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/117885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenius, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-402-181B-214

Query Match 59.5%; Score 50; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 0.036;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 IIRQVEYYFGDF 16
DB 1 ICHQXEVYFGDF 12

RESULT 12
US-09-721-456-214
Sequence 214, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-NOV-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017

FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 216:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 216:
US-09-721-456-216

Query Match 67.9%; Score 57; DB 4; Length 39;
Best Local Similarity 90.9%; Pred. No. 0.0021;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IIRQVEYFGD 15
|:|||||
Db 1 ILRQVEYFGD 11

RESULT 9
US-08-475-955-20
Sequence 20, Application US/08475955
Patent No. 6641813
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,955
FILING DATE: June 7, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/667,819
FILING DATE: April 13, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF114CIP(2) DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Binding-site
LOCATION: 8..15
US-08-475-955-20

Query Match 64.3%; Score 54; DB 4; Length 21;
Best Local Similarity 75.0%; Pred. No. 0.0035;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 IIRQVEYFGDF 16
|:|||||
Db 1 ICHQIEYFGDF 12

RESULT 10
US-08-974-549A-214
Sequence 214, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:

REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-430-323-26

Query Match 67.9%; Score 57; DB 4; Length 39;
Best Local Similarity 90.9%; Pred. No. 0.0021;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IIRQVEYYPGD 15
DB 1 IIRQVEYYPGD 11

RESULT 7
US-09-402-181B-216
Sequence 216, Application US/09402181B
Patent No. 6610839
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:

NAME: Ausehus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 216:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 216:
US-09-402-181B-216

Query Match 67.9%; Score 57; DB 4; Length 39;
Best Local Similarity 90.9%; Pred. No. 0.0021;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IIRQVEYYPGD 15
DB 1 IIRQVEYYPGD 11

RESULT 8
US-09-721-456-216
Sequence 216, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 216:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-216

Query Match 67.9%; Score 57; DB 3; Length 39;
Best Local Similarity 90.9%; Pred. No. 0.0021;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IIRQVEYFGD 15
|:|||||||
Db 1 IIRQVEYFGD 11

RESULT 5
US-08-854-050-26
Sequence 26, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-854-050-26

Query Match 67.9%; Score 57; DB 3; Length 39;
Best Local Similarity 90.9%; Pred. No. 0.0021;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IIRQVEYFGD 15
|:|||||||
Db 1 IIRQVEYFGD 11

RESULT 6
US-09-430-323-26
Sequence 26, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-OCT-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429

PRIOR FILING DATE: 1997-10-06
PRIOR APPLICATION NUMBER: 08/321,427
PRIOR FILING DATE: 1994-10-11
PRIOR APPLICATION NUMBER: 60/086,527
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patent Ver. 2.1
SEQ ID NO: 4
LENGTH: 18
TYPE: PR1
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: B-LAP
US-09-316-630-4

Query Match 67.9%; Score 57; DB 3; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.00085;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 ERAIRQVEYFGDF 16
DB 4 EAKICHQIRYFGDF 18

RESULT 3
US-08-851-843A-26
Sequence 26, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-851-843A-26

Query Match 67.9%; Score 57; DB 3; Length 39;
Best Local Similarity 90.9%; Pred. No. 0.0021;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 IIRQVEYFGDF 15
DB 1 IIRQVEYFGDF 11

RESULT 4
US-08-974-549A-216
Sequence 216, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997

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OM protein - protein search, using SW model

Run on: September 10, 2004, 17:43:01 ; Search time 14.1229 Seconds
(without alignments)
58,488 Million cell updates/sec

Title: US-09-836-073-19

Perfect score: 84
Sequence: 1,GERAIIRROYEYFGDF 16

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/2/1aa/5H_COMB.pep.*
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep.*
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6: /cgn2_6/prodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	67.9	18	3	US-09-316-630-3
2	57	67.9	18	3	US-09-316-630-4
3	57	67.9	39	3	US-08-851-843A-26
4	57	67.9	39	3	US-08-974-549A-216
5	57	67.9	39	3	US-08-854-050-26
6	57	67.9	39	4	US-09-430-323-26
7	57	67.9	39	4	US-09-402-181B-216
8	57	67.9	39	4	US-09-721-456-216
9	54	64.3	21	4	US-08-475-955-20
10	50	59.5	38	3	US-08-974-549A-214
11	50	59.5	38	4	US-09-402-181B-214
12	50	59.5	38	4	US-09-721-456-214
13	48	57.1	38	4	US-08-851-843A-25
14	48	57.1	38	3	US-08-974-549A-215
15	48	57.1	38	3	US-08-854-050-25
16	48	57.1	38	4	US-09-430-323-25
17	48	57.1	38	4	US-09-402-181B-215
18	48	57.1	38	4	US-09-721-456-215
19	43	51.2	37	3	US-08-851-843A-24
20	43	51.2	37	3	US-08-854-050-24
21	43	51.2	37	4	US-09-430-323-24
22	42	50.0	38	3	US-08-851-843A-27
23	42	50.0	38	3	US-08-974-549A-217
24	42	50.0	38	3	US-08-854-050-27
25	42	50.0	38	4	US-09-430-323-27
26	42	50.0	38	4	US-09-402-181B-217
27	42	50.0	38	4	US-09-721-456-217

28	42	50.0	167	4	US-09-134-000C-3435	Sequence 3435, Ap
29	41	48.8	74	4	US-09-439-554-6	Sequence 6, Appl1
30	41	48.8	141	4	US-09-540-236-2332	Sequence 2332, Ap
31	41	48.8	292	4	US-09-439-554-24	Sequence 24, Appl1
32	40.5	48.2	2710	2	US-08-568-459A-12	Sequence 12, Appl1
33	40.5	48.2	2710	2	US-08-487-826B-12	Sequence 12, Appl1
34	40.5	48.2	2710	4	US-09-210-288-12	Sequence 12, Appl1
35	40.5	48.2	3060	2	US-08-487-826B-14	Sequence 14, Appl1
36	40	47.6	376	4	US-09-489-039A-11743	Sequence 11743, A
37	40	47.6	506	4	US-09-672-785-2	Sequence 2, Appl1
38	40	47.6	506	4	US-09-672-785-8	Sequence 8, Appl1
39	40	47.6	512	4	US-09-672-785-4	Sequence 4, Appl1
40	40	47.6	1076	4	US-09-470-443-6	Sequence 6, Appl1
41	40	47.6	1145	4	US-09-470-443-2	Sequence 2, Appl1
42	40	47.6	1145	4	US-09-470-443-4	Sequence 4, Appl1
43	40	47.6	3571	4	US-09-911-842A-2	Sequence 2, Appl1
44	39	46.4	69	4	US-09-621-976-7385	Sequence 7385, Ap
45	39	46.4	319	4	US-09-252-991A-29238	Sequence 29238, A

ALIGNMENTS

```

RESULT 1
; Sequence 3, Application US/09316630
; Patent No. 6291637
; GENERAL INFORMATION:
; APPLICANT: Das, Saumitra
; TITLE OF INVENTION: INTERFERENCE WITH VIRAL IRES-MEDIATED TRANSLATION BY A
; FILE REFERENCE: 22000-20548.21
; CURRENT APPLICATION NUMBER: US/09/316,630
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 08/817,953
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 08/321,427
; PRIOR FILING DATE: 1994-10-11
; PRIOR APPLICATION NUMBER: 60/086,527
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: IAP
US-09-316-630-3
Query Match      67.9%; Score 57; DB 3; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.00085;
Mat.:es 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Cy      2 ERAIIRROYEYFGDF 16
Db      4 ERAIIRROYEYFGDF 18

RESULT 2
US-09-316-630-4
; Sequence 4, Application US/09316630
; Patent No. 6291637
; GENERAL INFORMATION:
; APPLICANT: Das, Saumitra
; TITLE OF INVENTION: INTERFERENCE WITH VIRAL IRES-MEDIATED TRANSLATION BY A
; FILE REFERENCE: 22000-20548.21
; CURRENT APPLICATION NUMBER: US/09/316,630
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 08/817,953

```


modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 408 AA:

Query Match 67.9%; Score 57; DB 7; Length 408;
Best Local Similarity 66.7%; Pred. No. 0.18;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 ERAIRQVEYFGDF 16
| | | | | | | | | | | | | | | | | | | | | |
Db 14 EAKICHQIEYFGDF 28

RESULT 14
ADD46272
ID ADD46272 standard; protein; 408 AA.

AC ADD46272;

DT 29-JAN-2004 (first entry)

DE Human Protein P05455, SEQ ID NO 11947.

XX Human; pain; neuronal tissue; gene therapy;

KM spinal segmental nerve injury; chronic constriction injury; CCI;

KW spared nerve injury; SNI; Chung.

OS Homo sapiens.

XX WO2003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-033347P.

PA (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

DR GENBANK; P05455.

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XX

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XX

XX

XX

method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 408 AA:

Query Match 67.9%; Score 57; DB 7; Length 408;
Best Local Similarity 66.7%; Pred. No. 0.18;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 ERAIRQVEYFGDF 16
| | | | | | | | | | | | | | | | | | | | | |
Db 14 EAKICHQIEYFGDF 28

RESULT 15
ADE63995
ID ADE63995 standard; protein; 408 AA.

AC ADE63995;

DT 29-JAN-2004 (first entry)

DE Human Protein P05455, SEQ ID NO 9941.

XX Human; pain; neuronal tissue; gene therapy;

KM spinal segmental nerve injury; chronic constriction injury; CCI;

KW spared nerve injury; SNI; Chung.

OS Homo sapiens.

XX WO2003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-033347P.

PA (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

DR GENBANK; P05455.

XX

XX

XX

XX

XX

XX

XX

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal

CC autoimmune patients. Ia and Ro antigens sometimes reside on the same
 CC cellular ribonucleoprotein particle; most Ia patients contain some Ro
 CC antibodies and vice versa. Ia cDNA has been isolated from a human liver
 CC library. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 XX
 SQ Sequence 408 AA;

Query Match 67.9%; Score 57; DB 2; Length 408;
 Best Local Similarity 66.7%; Pred. No. 0.18;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 ERATIRQVEYFYRGDF 16
 | | : |||||
 Db 14 EAKICHQIEYFYRGDF 28

RESULT 12

ABP65252
 ID ABP65252 standard; protein; 408 AA.

AC ABP65252;

DT 12-NOV-2002 (first entry)

DE Hypoxia-regulated protein #126.

KM Cytostatic; vasotropic; tranquilizer; antiatherosclerotic; gene therapy;
 KM antiinflammatory; vulnery; gynecological; ophthalmological; vaccine;
 KM hypoxia; tumorigenesis; angiogenesis; apoptosis; cancer;
 KM ischaemic condition; reperfusion injury; retinopathy; neonatal stress;
 KM preclapmsia; atherosclerosis; inflammatory condition; wound healing;
 KM inflammation; erythropoiesis; hair loss; human.

XX Homo sapiens.

OS WO200246465-A2.

PN 13-JUN-2002.

PD 10-DEC-2001; 2001WO-GB005458.

PF 08-DEC-2000; 2000GB-00030076.

PR 08-FEB-2001; 2001GB-00003156.

PR 25-OCT-2001; 2001GB-00025666.

PA (OXFO-) OXFORD BIOMEDICA UK LTD.

PI White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;

PI Rayner WN;

PT WPI; 2002-627238/67.

PT Identifying a gene involved in disease for treating hypoxia-regulated
 PT conditions, comprises comparing the transcriptome/proteome of two cell
 PT type under different conditions and identifying a differentially
 PT regulated gene.

XX Claim 35; Page 425; 538pp; English.

CC The present invention relates to methods for identifying genes and
 CC proteins that are implicated in a specific disease or physiological
 CC condition. The method comprises comparing the transcriptome/proteome of a
 CC specialised cell type implicated in a disease or condition with that of a
 CC second specialised cell type, under two experimental conditions, and
 CC identifying a gene that is differentially regulated in the two
 CC specialised cell types under experimental conditions. ABV77873-ABV78116
 CC and ABP65061-ABP65257 were identified using the methods of the invention.
 CC The coding sequences and proteins are useful for treating a disease in a
 CC patient, for manufacture of a medicament for treating hypoxia-regulated
 CC conditions, and for regulating tumorigenesis, angiogenesis, apoptosis,
 CC biological response to hypoxia conditions, or hypoxic-associated
 CC pathology in a patient. The coding sequences and proteins are also useful
 CC for monitoring the therapeutic treatment of a disease or physiological

CC condition, such as cancer, ischaemic conditions, reperfusion injury,
 CC retinopathy, neonatal stress, preclapmsia, atherosclerosis, inflammatory
 CC conditions, wound healing, inflammation, erythropoiesis or hair loss
 XX
 XX
 SQ Sequence 408 AA;

Query Match 67.9%; Score 57; DB 5; Length 408;
 Best Local Similarity 66.7%; Pred. No. 0.18;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 ERATIRQVEYFYRGDF 16
 | | : |||||
 Db 14 EAKICHQIEYFYRGDF 28

RESULT 13

ADE63991
 ID ADE63991 standard; protein; 408 AA.

AC ADE63991;

DT 29-JAN-2004 (first entry)

DE Human Protein P05455; SEQ ID NO 9937.

KM Human; pain; neuronal tissue; gene therapy;
 KM spinal segmental nerve injury; chronic constriction injury; CCI;
 KM spared nerve injury; SN1; Chung.

OS Homo sapiens.

PN WO2003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

PA (GENO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;

PI GENBANK; P05455.

PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that

KW	vital life cycle; antiviral therapy; pharmaceutical; veterinary;
KM	agricultural; horticultural; virucide; bovine.
XX	
OS	Bovinae.
PN	WO200283858-A2.
XX	
PD	24-OCT-2002.
XX	
PE	12-APR-2002; 2002MO-US011589.
XX	
PR	16-APR-2001; 2001US-00836073.
XX	
PA	(UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.
PI	Dasgupta A, Das S, Baidya N;
XX	
DR	WPI; 2003-058634/05.
XX	
PT	New compound containing acidic and aromatic amino acids, useful as
PT	antiviral therapy in pharmaceutical, veterinary or
PT	agricultural/horticultural applications.
PS	
CC	Disclosure; Page 6; 19pp; English.
XX	
CC	The present invention relates to peptides and methods of inhibiting the
CC	replication of viruses that utilize internal ribosome entry site (IRES)
CC	initiated translation, and/or inhibiting viruses that utilise the Ia
CC	antigen protein (IAP) in any phase of their life cycle. The peptides of
CC	the invention compete with IAP and inhibit the utilisation of various
CC	biochemical and physiological functions of IAP required for a productive
CC	life cycle. The methods and compositions are useful as antiviral therapy
CC	in pharmaceutical, veterinary or agricultural/horticultural applications.
CC	ABG72101-ABG72119 represent peptides useful as antiviral agents
XX	
SQ	Sequence 18 AA:
Query Match	67.9%; Score 57; DB 6; Length 18;
Best Local Similarity	66.7%; Pred. No. 0.0048;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;	
QY	2 ERAIIROVEYFYFGDF 16 : 4 EAKICHQIRVYFGDF 18
DB	
RESULT 10	
AAG01351	
ID	AAG01351 standard; protein; 92 AA.
XX	
AC	AAG01351;
XX	
DT	06-OCT-2000 (first entry)
XX	
DE	Human secreted protein, SEQ ID NO: 5432.
XX	
KW	Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KM	gene therapy; chromosome mapping.
XX	
OS	Homo sapiens.
XX	
PN	EP1033401-A2.
XX	
PD	06-SEP-2000.
XX	
PF	21-FEB-2000; 2000EP-00200610.
XX	
PR	26-FEB-1999; 99US-0122487P.
XX	
PA	(GEST) GENSET.
PI	Dumas Milne Edwards J, Duclert A, Giordano J;
XX	

DR WPI: 2000-500381/45.
DR N-PSDB: AAC01357..

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
PS Claim 13; SEQ ID NO 5432; 71pp + Sequence Listing; English.

XX The present sequence is a polypeptide encoded by one of a large number of
CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
CC tissues. EST sequences usually correspond mainly to the 3' untranslated
CC region (UTR) of the mRNA because they are often obtained from oligo-dT
CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
CC sequences derived from the 5' ends of mRNAs and even in those cases where
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
CC are also used in diagnostic, forensic, gene therapy and chromosome
CC mapping procedures. They are used to obtain upstream regulatory sequences
CC and to design expression and secretion vectors

XX Sequence 92 AA:

QY Query Match 67.9%; Score 57; DB 3; Length 92;
Best Local Similarity 66.7%; Pred. No. 0.032;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0

OY 2 ERAIRIQVEYYFGDF 16
| | | | | | | | | |
14 EAKICHQIEYYFGDF 28

Db

RESULT 11
AAW03716
ID AAW03716 standard; protein; 408 AA.

XX AAW03716;
XX
XX 25-MAR-2003 (revised)
DT 12-MAR-1997 (first entry)
XX
XX Human autoantigen La(SS-B).
DE
XX Autoimmune disease; La autoantigen; Sjogren's syndrome;
KW systemic lupus erythematosus; diagnosis.
XX
XX Homo sapiens.
OS
XX USS541291-A.
PN
XX 30-JUL-1996.
PD
XX 27-MAY-1987; 87US-00054871.
PF
XX 31-DEC-1984; 84US-00687908.
PR
XX (UYDU-) UNIV DUKE.
PA
XX
XX Keene JD;
PI
XX
XX WPI; 1996-362015/36.
DR
XX Auto-antigen U2-RNP, associated with severe polymyositis-scleroderma
PT overlap syndrome - useful for diagnosis and treatment of autoimmune
PT diseases.
XX
XX Disclosure; Col 15-16; 21pp; English.
PS
XX The human lupus antigen (la) is diagnostic for Sjogren's syndrome, as
CC well as occurring in systemic lupus erythematosus patients. The La protein
CC is clinically related to the Ro protein that is highly common among

CC coxsackie virus, encephalomyocarditis virus, foot-and-mouth disease
 CC virus, echo virus, hepatitis C virus, infectious bronchitis virus, duck
 CC and human hepatitis B virus, and vesicular stomatitis virus. The peptide
 CC also inhibits replication of the above viruses. The LAP peptide
 CC selectively inhibits viral protein translation, and is therefore not
 CC toxic to the host cell
 XX

SQ Sequence 18 AA;

Query Match 67.9%; Score 57; DB 3; Length 18;
 Best Local Similarity 66.7%; Pred. No. 0.0048;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 ERAIRIQVEYFGDF 16
 DB 4 EAKICHQIEYFGDF 18

RESULT 7

ID ABG72101 standard; peptide; 18 AA.

AC ABG72101;

DT 28-JAN-2003 (first entry)

DE Viral replication inhibiting peptide, LAP.

KM Viral replication inhibitor; IRES initiated translation; LAP;

KM internal ribosome entry site initiated translation; La antigen protein;

KM viral life cycle; antiviral therapy; pharmaceutical; veterinary;

KM agricultural; horticultural; virucide.

OS Unidentified.

PN WO200283858-A2.

PD 24-OCT-2002.

PF 12-APR-2002; 2002WO-US011589.

PR 16-APR-2001; 2001US-00836073.

RA (UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.

PI Dasgupta A, Das S, Baidya N;

DR WPI; 2003-058634/05.

PT New compound containing acidic and aromatic amino acids, useful as
 PT antiviral therapy in pharmaceutical, veterinary or
 PT agricultural/horticultural applications.

PS Claim 1; Page 15; 19pp; English.

CC The present invention relates to peptides and methods of inhibiting the
 CC replication of viruses that utilise internal ribosome entry site (IRES)
 CC initiated translation, and/or inhibiting viruses that utilise the La
 CC antigen protein (LAP) in any phase of their life cycle. The peptides of
 CC the invention compete with LAP and inhibit the utilisation of various
 CC biochemical and physiological functions of LAP required for a productive
 CC life cycle. The methods and compositions are useful as antiviral therapy
 CC in pharmaceutical, veterinary or agricultural/horticultural applications.
 CC ABG72101-ABG72119 represent peptides useful as antiviral agents
 XX

SQ Sequence 18 AA;

Query Match 67.9%; Score 57; DB 6; Length 18;
 Best Local Similarity 66.7%; Pred. No. 0.0048;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 ERAIRIQVEYFGDF 16
 DB 4 EAKICHQIEYFGDF 18

DB 4 EAKICHQIEYFGDF 18

RESULT 8
 ABG72105
 ID ABG72105 standard; peptide; 18 AA.

AC ABG72105;

DT 28-JAN-2003 (first entry)

DE Viral replication inhibiting peptide, 762.

KM Viral replication inhibitor; IRES initiated translation; LAP;

KM internal ribosome entry site initiated translation; La antigen protein;

KM viral life cycle; antiviral therapy; pharmaceutical; veterinary;

KM agricultural; horticultural; virucide.

OS Unidentified.

PN WO200283858-A2.

PD 24-OCT-2002.

PF 12-APR-2002; 2002WO-US011589.

PR 16-APR-2001; 2001US-00836073.

RA (UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.

PI Dasgupta A, Das S, Baidya N;

DR WPI; 2003-058634/05.

PT New compound containing acidic and aromatic amino acids, useful as
 PT antiviral therapy in pharmaceutical, veterinary or
 PT agricultural/horticultural applications.

PS Example 3; Page 14; 19pp; English.

CC The present invention relates to peptides and methods of inhibiting the
 CC replication of viruses that utilise internal ribosome entry site (IRES)
 CC initiated translation, and/or inhibiting viruses that utilise the La
 CC antigen protein (LAP) in any phase of their life cycle. The peptides of
 CC the invention compete with LAP and inhibit the utilisation of various
 CC biochemical and physiological functions of LAP required for a productive
 CC life cycle. The methods and compositions are useful as antiviral therapy
 CC in pharmaceutical, veterinary or agricultural/horticultural applications.
 CC ABG72101-ABG72119 represent peptides useful as antiviral agents
 XX

SQ Sequence 18 AA;

Query Match 67.9%; Score 57; DB 6; Length 18;
 Best Local Similarity 62.5%; Pred. No. 0.0048;
 Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 QERAIRIQVEYFGDF 16
 DB 3 QEOXCHQIEYFGDF 18

RESULT 9

ABG72114
 ID ABG72114 standard; peptide; 18 AA.

AC ABG72114;

DT 28-JAN-2003 (first entry)

DE Viral replication inhibiting peptide, BOVINE.

KM Viral replication inhibitor; IRES initiated translation; LAP;

KM internal ribosome entry site initiated translation; La antigen protein;

PD 24-OCT-2002.
 XX
 PS 12-APR-2002; 2002WO-US011589.
 CC 16-APR-2001; 2001US-00836073.
 PR (UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.
 PA Dasgupta A, Das S, Baidya N;
 XX WPI; 2003-058634/05.
 DR
 XX
 PT New compound containing acidic and aromatic amino acids, useful as
 PT antiviral therapy in pharmaceutical, veterinary or
 PT agricultural/horticultural applications.
 PS Claim 10; Page 16; 19pp; English.
 CC The present invention relates to peptides and methods of inhibiting the
 CC replication of viruses that utilise internal ribosome entry site (IRES)
 CC initiated translation, and/or inhibiting viruses that utilise the la
 CC antigen protein (LAP) in any phase of their life cycle. The peptides of
 CC the invention compete with LAP and inhibit the utilisation of various
 CC biochemical and physiological functions of LAP required for a productive
 CC life cycle. The methods and compositions are useful as antiviral therapy
 CC in pharmaceutical, veterinary or agricultural/horticultural applications.
 CC ABG72101-ABG72119 represent peptides useful as antiviral agents
 XX
 SQ Sequence 18 AA;
 XX
 Query Match 69.0%; Score 58; DB 6; Length 18;
 Best Local Similarity 66.7%; Pred. No. 0.0032;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 2 ERAIIIRQVEYYFGDF 16
 Db 4 EAQICQIQEYFYFGDF 18
 XX
 RESULT 5
 ABG72113
 ID ABG72113 standard; peptide; 17 AA.
 XX
 AC ABG72113;
 XX
 DT 28-JAN-2003 (first entry)
 XX
 DE Viral replication inhibiting peptide, MOUSE.
 XX
 KW Viral replication inhibitor; IRES initiated translation; LAP;
 KW internal ribosome entry site initiated translation; la antigen protein;
 KW viral life cycle; antiviral therapy; pharmaceutical; veterinary;
 KW agricultural, horticultural; virucide; mouse.
 XX
 OS Mus sp.
 XX
 PN WO200283858-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 12-APR-2002; 2002WO-US011589.
 XX
 PR 16-APR-2001; 2001US-00836073.
 XX
 PA (UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.
 XX
 PI Dasgupta A, Das S, Baidya N;
 XX WPI; 2003-058634/05.
 DR
 XX
 PT New compound containing acidic and aromatic amino acids, useful as
 PT antiviral therapy in pharmaceutical, veterinary or
 PT agricultural/horticultural applications.

XX
 PS Claim 1; Page 15; 19pp; English.
 CC The present invention relates to peptides and methods of inhibiting the
 CC replication of viruses that utilise internal ribosome entry site (IRES)
 CC initiated translation, and/or inhibiting viruses that utilise the la
 CC antigen protein (LAP) in any phase of their life cycle. The peptides of
 CC the invention compete with LAP and inhibit the utilisation of various
 CC biochemical and physiological functions of LAP required for a productive
 CC life cycle. The methods and compositions are useful as antiviral therapy
 CC in pharmaceutical, veterinary or agricultural/horticultural applications.
 CC ABG72101-ABG72119 represent peptides useful as antiviral agents
 XX
 SQ Sequence 17 AA;
 XX
 Query Match 67.9%; Score 57; DB 6; Length 17;
 Best Local Similarity 66.7%; Pred. No. 0.0045;
 Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 2 ERAIIIRQVEYYFGDF 16
 Db 3 EAKICQIQEYFYFGDF 17
 XX
 RESULT 6
 AAY52200
 ID AAY52200 standard; peptide; 18 AA.
 XX
 AC AAY52200;
 XX
 DT 14-MAR-2000 (first entry)
 XX
 DE Human la autoantigen peptide (LAP).
 XX
 KW La autoantigen; LAP; internal ribosome entry site; IRES; translation;
 KW viral replication; IRNA; antiviral agent; picornavirus; flavivirus;
 KW coronavirus; hepatitis virus; rhinovirus; coxsackie virus;
 KW parainfluenza virus; poliovirus; encephalomyocarditis virus;
 KW foot-and-mouth disease virus; echo virus; infectious bronchitis virus;
 KW vesicular stomatitis virus.
 XX
 OS Homo sapiens.
 XX
 PN WO9961613-A2.
 XX
 PD 02-DEC-1999.
 XX
 PF 21-MAY-1999; 99WO-US011281.
 XX
 PR 22-MAY-1998; 98US-0086527P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Das S, Dasgupta A;
 XX WPI; 2000-062712/05.
 DR
 XX
 PT New yeast inhibitory peptide useful for inhibiting viral protein
 PT translation and replication.
 XX
 PS Claim 5; Page 57; 81pp; English.
 CC This sequence is the la autoantigen binding domain (LAP). LAP is a
 CC cellular protein which binds to an internal ribosome entry site (IRES).
 CC The peptide is used to inhibit mRNA translation, viral protein
 CC translation or viral replication. Viral mRNA translation is initiated at
 CC the IRES and the LAP peptide prevents translation initiation factors from
 CC binding at the site. The peptide can be used alone or in combination with
 CC an inhibitor RNA (RNA see A4245200). The LAP peptide is useful as an
 CC antiviral agent, which works through the inhibition of mRNA translation,
 CC especially viral mRNA. Examples of viruses which can be inhibited are
 CC picornavirus, flavivirus, coronavirus, hepatitis A B or C viruses,
 CC rhinovirus, adenovirus, and parainfluenza virus, poliovirus, rhinovirus,

Query Match 100.0%; Score 84; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7.1e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QERAIRROYEYFGDP 16
 |||||
 DB 1 QERAIRROYEYFGDP 16

RESULT 2

ABG72104
 ID ABG72104 standard; protein; 390 AA.

XX ABB65316;
 XX ABB65316;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 22740.

KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.

OS Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US009231.

PR 23-MAR-2000; 2000US-0191637P.

PT 11-JUL-2000; 2000US-00614150.

PA (PEKS) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EM;

DR WPI; 2001-656860/75.

XX N-PSDB; ABL09419.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.

PS Disclosure; SEQ ID NO 22740; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 390 AA;

Query Match 92.9%; Score 78; DB 4; Length 390;
 Best Local Similarity 100.0%; Pred. No. 3.3e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QERAIRROYEYFGD 15
 |||||
 DB 50 QERAIRROYEYFGD 64

RESULT 3

ABG72104
 ID ABG72104 standard; peptide; 18 AA.

AC ABG72104;

DT 28-JAN-2003 (first entry)

DE Viral replication inhibiting peptide, 761.

KW Viral replication inhibitor; IRES initiated translation; LAP;
 KW internal ribosome entry site initiated translation; La antigen protein;
 KW viral life cycle; antiviral therapy; pharmaceutical; veterinary;
 KW agricultural; horticultural; virucide.

OS Unidentified.

PN WO200283858-A2.

PD 24-OCT-2002.

PF 12-APR-2002; 2002WO-US011589.

PR 16-APR-2001; 2001US-00836073.

PA (UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.

PI Dasgupta A, Das S, Baidya N;

DR WPI; 2003-058634/05.

PT New compound containing acidic and aromatic amino acids, useful as
 PT antiviral therapy in pharmaceutical, veterinary or
 PT agricultural/horticultural applications.

PS Claim 10; Page 16; 19pp; English.

CC The present invention relates to peptides and methods of inhibiting the
 CC replication of viruses that utilize internal ribosome entry site (IRES)
 CC initiated translation, and/or inhibiting viruses that utilise the La
 CC antigen protein (LAP) in any phase of their life cycle. The peptides of
 CC the invention compete with LAP and inhibit the utilisation of various
 CC biochemical and physiological functions of LAP required for a productive
 CC life cycle. The methods and compositions are useful as antiviral therapy
 CC in pharmaceutical, veterinary or agricultural/horticultural applications.
 CC ABG72101-ABG72119 represent peptides useful as antiviral agents

XX SQ Sequence 18 AA;

Query Match 73.8%; Score 62; DB 6; Length 18;
 Best Local Similarity 68.8%; Pred. No. 0.00063;
 Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 QERAIRROYEYFGDP 16
 |||||
 DB 3 QERAIRROYEYFGDP 18

RESULT 4

ABG72102
 ID ABG72102 standard; peptide; 18 AA.

XX ABG72102;

DT 28-JAN-2003 (first entry)

DE Viral replication inhibiting peptide, 702.

KW Viral replication inhibitor; IRES initiated translation; LAP;
 KW internal ribosome entry site initiated translation; La antigen protein;
 KW viral life cycle; antiviral therapy; pharmaceutical; veterinary;
 KW agricultural; horticultural; virucide.

OS Unidentified.

PN WO200283858-A2.

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Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 SKLEASTIROEYFGDA 18
|||||:|:|

Db 589 SKLEASTTKYADVFGNA 605

RESULT 15

US-10-651-183-20

; Sequence 20, Application US/10651183

; Publication No. US20040096929A1

; GENERAL INFORMATION:

; APPLICANT: KAWASAKI, GLENN

; APPLICANT: WEBB, HEATHER K.

; APPLICANT: OWENS, JEFFREY

; APPLICANT: LIEDTKE, RAYMOND

; APPLICANT: FOREST, DOREEN

; APPLICANT: LEGAZ, MARK

; APPLICANT: LAWSON, SOBOMABO

; TITLE OF INVENTION: ENZYMATIC CYCLING ASSAYS FOR HOMOCYSTEINE AND CYSTATIONINE

; FILE REFERENCE: 30865

; CURRENT APPLICATION NUMBER: US/10/651,183

; CURRENT FILING DATE: 2003-08-28

; PRIOR APPLICATION NUMBER: US/10/012,762

; PRIOR FILING DATE: 2002-09-26

; PRIOR APPLICATION NUMBER: 60/163,126

; PRIOR FILING DATE: 1999-11-02

; PRIOR APPLICATION NUMBER: 09/704,036

; PRIOR FILING DATE: 2000-11-01

; PRIOR APPLICATION NUMBER: 60/203,349

; PRIOR FILING DATE: 2000-05-10

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 20

; LENGTH: 1252

; TYPE: PRT

; ORGANISM: Saccharomyces cerevisiae

; US-10-651-183-20

Query Match 47.8%; Score 43; DB 16; Length 1252;

Best Local Similarity 58.8%; Pred. No. 2.3e+02;

Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 SKLEASTIROEYFGDA 18
|||||:|:|

Db 589 SKLEASTTKYADVFGNA 605

Search completed: September 10, 2004, 18:11:57
Job time : 40.424 secs

Qy 1 VSKLEASTIRQRYFGD 16
Db 61 ISKGNIGRIKREYFG 76

RESULT 11

US-09-734-017A-32
; Sequence 32, Application US/09734017A
; Patent No. US2002014222A1
; GENERAL INFORMATION:
; APPLICANT: Lerchl, Jens
; APPLICANT: Benz, Andreas
; APPLICANT: Ehrhardt, Thomas
; APPLICANT: Reindl, Andreas
; APPLICANT: Clippus, Petra
; APPLICANT: Bischoff, Friedrich
; APPLICANT: Frank, Markus
; APPLICANT: Freund, Annette
; APPLICANT: Duwenig, Elke
; APPLICANT: Schmidt, Ralf-Michael
; TITLE OF INVENTION: Moss genes from *Physcomitrella patens* encoding proteins involved
; TITLE OF INVENTION: the
; TITLE OF INVENTION: synthesis of amino acids, vitamins, cofactors, nucleosides and
; FILE REFERENCE: BASF-NAE-1331-99-US
; CURRENT APPLICATION NUMBER: US/09/734,017A
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/171,100
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.1/WordPerfect
; SEQ ID NO 32
; LENGTH: 184
; TYPE: PRT
; ORGANISM: *Physcomitrella patens*
US-09-734-017A-32

Query Match 47.8%; Score 43; DB 9; Length 184;
Best Local Similarity 41.2%; Pred. No. 26;
Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 VSKLEASTIRQRYFGD 17
Db 35 IHSAAQTMBEYYIGD 51

RESULT 12

US-10-464-811-20
; Sequence 20, Application US/10464811
; Publication No. US2004003319A1
; GENERAL INFORMATION:
; APPLICANT: Kraus, Jan
; APPLICANT: Oliveriusova, Jana
; TITLE OF INVENTION: Human Cytacthionine B-Synthase Variants and Methods of Production
; FILE REFERENCE: 2848-49
; CURRENT APPLICATION NUMBER: US/10/464,811
; PRIOR FILING DATE: 2003-06-17
; PRIOR APPLICATION NUMBER: 60/389,541
; PRIOR FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 507
; TYPE: PRT
; ORGANISM: *Saccharomyces cerevisiae*
US-10-464-811-20

Query Match 47.8%; Score 43; DB 12; Length 507;
Best Local Similarity 58.8%; Pred. No. 82;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 SKLEASTIRQRYFGD 18

Db 351 SKLEASTIRQRYFGD 367

RESULT 13

US-10-451-467A-182
; Sequence 182, Application US/10451467A
; Publication No. US20040161840A1
; GENERAL INFORMATION:
; APPLICANT: CONTRERAS, ROLAND HENRI
; APPLICANT: EBERHARDT, INES
; APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
; APPLICANT: REEMANS, RIKKA JOSEPHINA
; TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
; TITLE OF INVENTION: YEAST AND FUNGI
; FILE REFERENCE: JAB-1667
; CURRENT APPLICATION NUMBER: US/10/451,467A
; PRIOR FILING DATE: 2003-06-19
; PRIOR APPLICATION NUMBER: EP 00870318.3
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: EP 01870002.1
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: EP 01870003.9
; PRIOR FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 732
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 182
; LENGTH: 507
; TYPE: PRT
; ORGANISM: *Saccharomyces cerevisiae*
US-10-451-467A-182

Query Match 47.8%; Score 43; DB 16; Length 507;
Best Local Similarity 58.8%; Pred. No. 82;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 SKLEASTIRQRYFGD 18
Db 351 SKLEASTIRQRYFGD 367

RESULT 14

US-10-012-762-20
; Sequence 20, Application US/10012762
; Publication No. US20030138872A1
; GENERAL INFORMATION:
; APPLICANT: KAWASAKI, GLENN
; APPLICANT: WEBB, JEFFREY K.
; APPLICANT: OWENS, JEFFREY
; APPLICANT: LIEDTKE, RAYMOND
; APPLICANT: FOREST, DOREEN
; APPLICANT: LEGAZ, MARK
; APPLICANT: LAWSON, SOBOUABO
; TITLE OF INVENTION: ENZYMATIC CYCLING ASSAYS FOR HOMOCYSTEINE AND CYSTATIONINE
; FILE REFERENCE: 30865
; CURRENT APPLICATION NUMBER: US/10/012,762
; PRIOR FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: 60/163,126
; PRIOR FILING DATE: 1999-11-02
; PRIOR APPLICATION NUMBER: 09/704,036
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/203,349
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 1252
; TYPE: PRT
; ORGANISM: *Saccharomyces cerevisiae*
US-10-012-762-20

Query Match 47.8%; Score 43; DB 14; Length 1252;
Best Local Similarity 58.8%; Pred. No. 2.3e+02;

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-102-806-695

Query Match
Best Local Similarity 48.3%; Score 43.5; DB 14; Length 460;
Matches 10; Conservative 55.6%; Pred. No. 60; Mismatches 2; Indels 5; Gaps 1;

QY 1 VSKLEASTIRQ-EYRFGD 17
DB 62 MALEAKICHQIEYRFGD 79

RESULT 7
US-10-264-049-2643
; Sequence 2643, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2643
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-2643

Query Match
Best Local Similarity 48.3%; Score 43.5; DB 15; Length 460;
Matches 10; Conservative 55.6%; Pred. No. 60; Mismatches 2; Indels 5; Gaps 1;

QY 1 VSKLEASTIRQ-EYRFGD 17
DB 62 MALEAKICHQIEYRFGD 79

RESULT 8
US-10-437-963-128214
; Sequence 128214, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbara, Brad
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 128214
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(169)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_3058C.1.pep
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US-10-437-963-128214

Query Match
Best Local Similarity 47.8%; Score 43; DB 16; Length 169;
Matches 8; Conservative 30.8%; Pred. No. 24; Mismatches 7; Indels 1; Gaps 1;

QY 3 KLEASTIROE-----YRFGDA 18
DB 95 KLDTTVKQDELDKTLVHTYYGGA 120

RESULT 9
US-10-425-114-37684
; Sequence 37684, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 37684
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700337382_FLI.pep
US-10-425-114-37684

Query Match
Best Local Similarity 47.8%; Score 43; DB 12; Length 172;
Matches 8; Conservative 50.0%; Pred. No. 24; Mismatches 3; Indels 5; Gaps 0;

QY 1 VSKLEASTIROEYRFG 16
DB 61 ISKGNLGRIRKEFYFG 76

RESULT 10
US-10-425-114-71728
; Sequence 71728, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 71728
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMRCWO17113D10_FLI.pep
US-10-425-114-71728

Query Match
Best Local Similarity 47.8%; Score 43; DB 12; Length 172;
Matches 8; Conservative 50.0%; Pred. No. 24; Mismatches 3; Indels 5; Gaps 0;
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; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 19
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Drosophila
US-09-836-073-19

Query Match
Best Local Similarity 49.4%; Score 44.5; DB 9; Length 16;
Matches 10; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 5 EASTIRQ-EYFQD 17
DB 2 ERAIRQVEYFQD 15

RESULT 3
US-09-836-073-2
; Sequence 2, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-2

Query Match
Best Local Similarity 48.3%; Score 43.5; DB 9; Length 18;
Matches 10; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 4 LEASTIRQ-EYFQD 17
DB 3 LEAQICQIEYFQD 17

RESULT 4
US-10-170-385-477
; Sequence 477, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
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; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 477
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-477

Query Match
Best Local Similarity 48.3%; Score 43.5; DB 12; Length 408;
Matches 10; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 1 VSKLEASTIRQ-EYFQD 17
DB 10 MALEAKICHOIEYFQD 27

RESULT 5
US-09-925-298-695
; Sequence 695, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103
; CURRENT APPLICATION NUMBER: US/09/925,298
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 695
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-298-695

Query Match
Best Local Similarity 48.3%; Score 43.5; DB 12; Length 460;
Matches 10; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 1 VSKLEASTIRQ-EYFQD 17
DB 62 MALEAKICHOIEYFQD 79

RESULT 6
US-10-102-806-695
; Sequence 695, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103PCT
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 695
; LENGTH: 460
```


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CORRESPONDENCE ADDRESS:

ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/430,323

FILING DATE: 29-Oct-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002930US

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 24:

US-09-430-323-24

Query Match 46.7%; Score 42; DB 4; Length 37;

Best Local Similarity 100.0%; Pred. No. 1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 QERYFGD 17

DB 4 QERYFGD 10

RESULT 15

US-09-328-352-8030

Sequence 8030, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 8030

LENGTH: 287

TYPE: PRT

ORGANISM: Acinetobacter baumannii

US-09-328-352-8030

Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 SKLEASTIROEYF 15

DB 170 SKQEBITIKDRYF 183

Search completed: September 10, 2004, 18:05:12

Job time: 16.8883 secs

Query Match 44.4%; Score 40; DB 4; Length 287;

Best Local Similarity 57.1%; Pred. No. 26;

APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-851-843A-24

Query Match 46.7%; Score 42; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 OEYFGD 17
|||||
Db 4 OEYFGD 10

RESULT 13
US-08-854-050-24
Sequence 24, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.

TITLE OF INVENTION: No. 6261836e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-854-050-24

Query Match 46.7%; Score 42; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 OEYFGD 17
|||||
Db 4 OEYFGD 10

RESULT 14
US-09-430-323-24
Sequence 24, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6309867e1 Telomerase
NUMBER OF SEQUENCES: 225

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausehus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 216:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 216:
US-09-402-181B-216

Query Match 47.2% Score 42.5; DB 4; Length 39;
Best Local Similarity 81.8% Pred. No. 0.91;
Matches 9; Conservative 1; Mismatches 0; Indels 1; Gaps 1

QY 9 IRQ-EYFGDA 18
: || || || || ||
Db 2 LROVEYFGDA 12

RESULT 11
US-09-721-456-216
; Sequence 216, Application US/09721456
; Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
;

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TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
City: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-NO. 6617110-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 216:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 216:
US-09-721-456-216

Query Match 47.2% Score 42.5; DB 4, Length 39,
Best Local Similarity 81.8%; Pred.No. 0.91;
Matches 9; Conservative 1; Mismatches 0; Indels 1; Gaps 14;

QY 9 IRQ-EYYFGDA 18
:|||||
Db 2 LROVEYYFGDA 12

RESULT 12
US-08-851-843A-24
; Sequence 24, Application US/08851843A
; Patent No. 6093809
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.

```



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APPLICANT: Linger, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261936el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-854-050-26

Query Match 47.2%; Score 42.5; DB 3; Length 39;
Best Local Similarity 81.8%; Pred. No. 0.91;
Matches 9; Conservative 1; Mismatches 0; Indels 1; Gaps 1

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:|||||
:|||||
Db 2 LROVEYFQDA 12

RESULT 9
US-09-430-323-26
; Sequence 26, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Linger, Joachim
; Nakamura, Toru

```

```

1      Chapman, Karen B.
2      Morin, Gregg B.
3      Harley, Calvin
4      Andrews, William H.
5      TITLE OF INVENTION: No. 6309867e1 Telomerase
6      NUMBER OF SEQUENCES: 225
7      CORRESPONDENCE ADDRESS:
8      ADDRESSEE: Townsend and Townsend and Crew LLP
9      STREET: Two Embarcadero Center, 8th Floor
10     CITY: San Francisco
11     STATE: California
12     COUNTRY: United States of America
13     ZIP: 94111
14
15     COMPUTER READABLE FORM:
16     MEDIUM TYPE: Floppy disk
17     COMPUTER: IBM PC compatible
18     OPERATING SYSTEM: PC-DOS/MS-DOS
19     SOFTWARE: Patent Release #1.0, Version #1.30
20     CURRENT APPLICATION DATA:
21     APPLICATION NUMBER: US/09/430,323
22     FILING DATE: 29-Oct-1999
23     CLASSIFICATION: <Unknown>
24     PRIOR APPLICATION DATA:
25     APPLICATION NUMBER: US 08/854,050
26     FILING DATE: 09-MAY-1997
27     APPLICATION NUMBER: US 08/851,843
28     FILING DATE: 06-MAY-1997
29     APPLICATION NUMBER: US 08/846,017
30     FILING DATE: 25-APR-1997
31     APPLICATION NUMBER: US 08/844,419
32     FILING DATE: 18-APR-1997
33     APPLICATION NUMBER: US 08/724,643
34     FILING DATE: 01-OCT-1996
35     ATTORNEY/AGENT INFORMATION:
36     NAME: Apple, Randolph T.
37     REGISTRATION NUMBER: 36,429
38     REFERENCE/DOCKET NUMBER: 015389-002930US
39     TELECOMMUNICATION INFORMATION:
40     TELEPHONE: (415) 576-0200
41     TELEFAX: (415) 576-0300
42     INFORMATION FOR SEQ ID NO: 26:
43     SEQUENCE CHARACTERISTICS:
44     LENGTH: 39 amino acids
45     TYPE: amino acid
46     STRANDEDNESS: not relevant
47     TOPOLOGY: not relevant
48     MOLECULE TYPE: peptide
49     SEQUENCE DESCRIPTION: SEQ ID NO: 26:
50
51     US-09-430-323-26
52
53     Query Match          47.2%; Score 42.5; DB 4; Length 39;
54     Best Local Similarity 81.8%; Pred.No. 0.91;
55     Matches          9; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
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57     QY      9 IRQ-EYFFGDA 18
58           :||| |||||
59           2 LRQVEYFFGDA 12
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61     RESULT 10
62     US-09-402-181B-216
63     ; Sequence 216, Application US/09402181B
64     ; Patent No. 6610839
65     ; GENERAL INFORMATION:
66     APPLICANT: Cecch, Thomas R.
67     ;
68     ; Lingner, Joachim
69     ; Nakamura, Toru
70     ; Chapman, Karen B.
71     ; Morin, Gregg B.
72     ; Harley, Calvin B.
73     ; Andrews, William H.
74     TITLE OF INVENTION: Human Telomerase Catalytic Subunit
75     NUMBER OF SEQUENCES: 633

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TITLE OF INVENTION: No. 609380961 Telomerase
 NUMBER OF SEQUENCES: 225
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: United States of America
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/851,843A
 FILING DATE: 06-MAY-1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 015389-002930US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 39 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 MOLECULE TYPE: peptide
 US-08-851-843A-26

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Query Match          47.2%   Score 42.5; DB 3; Length 39;
Best Local Similarity 81.8%   Pred No. 0.91;
Matches          9; Conservative      1; Mismatches      0; Indels      1; Gaps      1.
OY
          9 IRO-EYFEGDA 18
          :|| |||||
          2 LRQVEYFEGDA 12

RESULT 7
US-08-974-549A-216
: Sequence 216, Application US/08974549A
: Patent No. 6166178
: GENERAL INFORMATION:
: APPLICANT: Cech, Thomas R.
: APPLICANT: Lingner, Joachim
: APPLICANT: Nakamura, Toru
: APPLICANT: Chapman, Karen B.
: APPLICANT: Morin, Gregg B.
: APPLICANT: Harley, Calvin B.
: APPLICANT: Andrews, William H.
: TITLE OF INVENTION: Human Telomerase Catalytic Subunit
: NUMBER OF SEQUENCES: 727
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
:

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STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 216:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-216

Query Match 47.2%; Score 42.5; DB 3; Length 39;
Best Local Similarity 81.8%; Pred. No. 0.91;
Matches 9; Conservative 1; Mismatches 0; Indels 1; Gaps 1.

QY 9 IRQ-RIYFGDA 18
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DB 2 IROVEYFGDA 12

RESULT 8
US-08-854-050-26
; Sequence 26, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.

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; MOLECULE TYPE: peptide
US-08-974-549A-216

Query Match 47.2%; Score 42.5; DB 3; Length 39;
Best Local Similarity 81.8%; Pred No 0.91;
Matches 9; Conservative 1; Mismatches 0; Indels 1; Gaps 1.

QY 9 IRQ-EYFQDA 18
: || || || || ||
DB 2 LROVEYFQDA 12

RESULT 8
US-08-854-050-26
; Sequence 26, Application US/08854050
; Patent No. 6261896
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
;

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; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/203,349
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 1252
; TYPE: prt
; ORGANISM: Saccharomyces cerevisiae
; US-10-012-762-20

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Query Match	47.8%	Score 43	DB 4	Length 1252
Best Local Similarity	58.8%	Pred. No. 42		
Matches 10; Conservative	2	Mismatches 5	Indels 0	Gaps 0

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DB      589 SKLEASTTKYADVEFGNA 605
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RESULT 3
US-09-704-036B-20
; Sequence 20, Application US/09704036B

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: GENERAL INFORMATION:
: APPLICANT: KAWASAKI, GLENN
: APPLICANT: WEBB, HEATHER
: APPLICANT: OWENS, JEFFREY
: APPLICANT: LIEDTKE, RAYMOND
: APPLICANT: FOREST, DOREEN
: APPLICANT: LEGAZ, MARK
: APPLICANT: LAWSON, SOBOMABO
: TITLE OF INVENTION: ENZYMATIC CYCLING ASSAYS FOR HOMOCYSTEINE AND CYSTATHIONINE
: FILE REFERENCE: 30865
: CURRENT APPLICATION NUMBER: US/09/704,036B
: CURRENT FILING DATE: 2000-11-01
: PRIOR APPLICATION NUMBER: 60/163,126
: PRIOR FILING DATE: 1999-11-02
: PRIOR APPLICATION NUMBER: 09/704,036
: PRIOR FILING DATE: 2000-11-01
: PRIOR APPLICATION NUMBER: 60/203,349
: PRIOR FILING DATE: 2000-05-10
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 20
: LENGTH: 1252
: TYPE: prt
: ORGANISM: Saccharomyces cerevisiae
: US-09-704-036B-20

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RESULT 4
US-09-316-630-3
; Sequence 3, Application US/09316630
; Patent No. 6281637
; GENERAL INFORMATION:
; APPLICANT: Dae, Saumittra
; APPLICANT: Dasgupta, Asim
; TITLE OF INVENTION: INTERFERENCE WITH VIRAL IRES-MEDIATED TRANSLATION BY A
; TITLE OF INVENTION: SMALL YEAST RNA REVEALS CRITICAL RNA-PROTEIN INTERACTIONS
; FILE REFERENCE: 22000-20548 21
; CURRENT APPLICATION NUMBER: US/09/316,630
; CURRENT FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 08/817,953
; PRIOR FILING DATE: 1997-10-06

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1 PRIOR APPLICATION NUMBER: 08/321,427
2 PRIOR FILING DATE: 1994-10-11
3 PRIOR APPLICATION NUMBER: 60/086,527
4 PRIOR FILING DATE: 1998-05-22
5 NUMBER OF SEQ ID NOS: 4
6 SOFTWARE: PatentIn Ver. 2.1
7 SEQ ID NO 3
8
9 LENGTH: 18
10
11 TYPE: PRT
12 ORGANISM: Artificial Sequence
13 FEATURE:
14 OTHER INFORMATION: Description of Artificial Sequence: LAMP
15 US-09-316-630-3

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Query Match	47.2%	Score 42.5;	DB 3;	Length 18;
Best Local Similarity	66.7%	Pred. No. 0.37;		
Matches 10; Conservative	0;	Mismatches 4;	Indels 1;	Gaps 1;

QY 4 LEASTIRQ-EYFFGD 17
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Db 3 LEAKICHQIEYFFGD 17

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RESULT 5
US-09-316-630-4
Sequence 4, Application US/09316630
Patent No. 6291637
GENERAL INFORMATION:
APPLICANT: Dae, Saumitra
APPLICANT: Dae, Saumitra
TITLE OF INVENTION: INTERFERENCE WITH VIRAL IRES-MEDIATED TRANSLATION BY A
FILE OF INVENTION: SMALL YEAST RNA REVEALS CRITICAL RNA-PROTEIN INTERACTIONS
FILE REFERENCE: 22000-20548-21
CURRENT APPLICATION NUMBER: US/09/316,630
CURRENT FILING DATE: 1999-05-21
PRIORITY APPLICATION NUMBER: 08/817,953
PRIORITY FILING DATE: 1997-10-06
PRIORITY APPLICATION NUMBER: 08/321,427
PRIORITY FILING DATE: 1994-10-11
PRIORITY APPLICATION NUMBER: 60/086,527
PRIORITY FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
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LENGTH: 18
TYPE: PR
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: B-LAP
US-09-316-630-4

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		47.2%;	Score 42.5;	DB 3;	Length 18;
Query Match		66.7%;	Pred. No. 0.37;		
Best Local Similarity		0;	Mismatches	4;	Indels 1;
Matches	10;	Conservative			Gaps 1.
Oy	4 LEASTRO-EYFGD 17				
Db	3 LEAKICHOIEYFGD 17				

RESULT 6
US-08-851-843A-26
Sequence 26, Application US/08651843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Hartley, Calvin
APPLICANT: Andrews, William H.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:43:01; Search time 15.8883 Seconds
(without alignments)
58.488 Million cell updates/sec

Title: US-09-836-073-18

Perfect score: 90

Sequence: 1 VSKLEASTIRQRYFFGDA 18

Scoring table: BLOSUM62

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Searched: 389414 seqs, 51625971 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	42.5	47.2	18	3 US-09-316-630-3	Sequence 3, App1
5	42.5	47.2	18	3 US-09-316-630-4	Sequence 4, App1
6	42.5	47.2	39	3 US-08-851-843A-26	Sequence 26, App1
7	42.5	47.2	39	3 US-08-851-843A-26	Sequence 26, App1
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9	42.5	47.2	39	4 US-09-430-323-26	Sequence 26, App1
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14	42	46.7	37	4 US-09-430-323-24	Sequence 24, App1
15	40	44.4	287	4 US-09-328-352-8030	Sequence 8030, App
16	40	44.4	346	4 US-09-457-040B-24	Sequence 24, App1
17	40	44.4	876	1 US-08-785-071A-2	Sequence 2, App1
18	40	44.4	876	1 US-09-012-872-2	Sequence 2, App1
19	39.5	43.9	506	2 US-08-849-480A-5	Sequence 5, App1
20	39	43.3	418	4 US-09-328-352-5700	Sequence 5700, App
21	39	43.3	550	1 US-08-674-168-29	Sequence 29, App1
22	39	43.3	550	3 US-08-985-908-19	Sequence 19, App1
23	39	43.3	550	3 US-08-852-730-4	Sequence 4, App1
24	39	43.3	550	3 US-08-985-916-11	Sequence 11, App1
25	39	43.3	767	4 US-09-540-236-3346	Sequence 163, App
26	39	43.3	872	4 US-09-198-452A-163	Sequence 163, App
27	38.5	42.8	-128	6 5514582-33	Patent No. 5514582

28	38	42.2	147	4 US-09-621-976-4310	Sequence 4310, App
29	38	42.2	226	4 US-09-489-039A-7662	Sequence 7662, App
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31	38	42.2	423	3 US-09-009-433-7	Sequence 7, App1
32	38	42.2	477	1 US-08-136-922-2	Sequence 2, App1
33	38	42.2	655	4 US-08-556-422A-3	Sequence 3, App1
34	38	42.2	771	1 US-08-121-713D-54	Sequence 54, App1
35	38	42.2	771	1 US-08-835-268-54	Sequence 54, App1
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37	38	42.2	771	3 US-08-833-391-54	Sequence 54, App1
38	38	42.2	771	4 US-09-060-610-54	Sequence 54, App1
39	38	42.2	771	5 PCT-US84-10151A-54	Sequence 54, App1
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41	38	42.2	897	4 US-09-134-001C-3600	Sequence 3600, App
42	37.5	41.7	249	4 US-09-134-001C-3910	Sequence 3910, App
43	37	41.1	21	4 US-08-475-955-20	Sequence 20, App1
44	37	41.1	38	3 US-08-851-843A-25	Sequence 25, App1
45	37	41.1	38	3 US-08-974-549A-214	Sequence 214, App

ALIGNMENTS

```
RESULT 1
US-09-134-001C-4980
; Sequence 4980, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4980
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4980

Query Match      48.3%; Score 43.5; DB 4; Length 136;
Best Local Similarity 57.9%; Pred. No. 2.6;
Matches 11; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Cy      1 VSKLEASTIRQRYFFGDA 18
Db      98 ISKLESTIRQRYFFGDA 116

RESULT 2
US-10-012-762-20
; Sequence 20, Application US/10012762
; Patent No. 6635438
; GENERAL INFORMATION:
; APPLICANT: KAWASAKI, GLENN
; APPLICANT: WEBB, HEATHER K.
; APPLICANT: OWENS, JEFFREY
; APPLICANT: LLEDITE, RAYMOND
; APPLICANT: FOREST, DOREEN
; APPLICANT: LEGAZ, MARK
; APPLICANT: LAWSON, SOBOMABO
; TITLE OF INVENTION: ENZYMATIC CYCLING ASSAYS FOR HOMOCYSTEINE AND CYSTATHIONINE
; FILE REFERENCE: 30865
; CURRENT APPLICATION NUMBER: US/10/012,762
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: 60/163,126
; PRIOR FILING DATE: 1999-11-02
; PRIOR APPLICATION NUMBER: 09/704,036
```

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PD 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
PI MPI; 2003-268312/26.
DR GENBANK; P05455.
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page: 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more of the
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 408 AA;
SQ
Query Match 48.3%; Score 43.5; DB 7; Length 408;
Best Local Similarity 55.6%; Pred. No. 49;
Matches 10; Conservative 2; Mismatches 5; Indels 1; Gaps 1;
QY 1 VSKLEASTIRQ-EYFPGD 17
Db 10 MAALBAKICHOIEYFPGD 27
RESULT 14
ADE62859
ID ADE62859 standard; protein; 408 AA.
XX
XX ADE62859;
XX
XX 29-JAN-2004 (first entry)
DT
XX Human Protein P05455, SEQ ID NO 8793.
DE
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.

XX
XX Homo sapiens.
OS
XX WO2003016475-A2.
EN
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
PI MPI; 2003-268312/26.
DR GENBANK; P05455.
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page: 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 408 AA;
SQ
Query Match 48.3%; Score 43.5; DB 7; Length 408;
Best Local Similarity 55.6%; Pred. No. 49;
Matches 10; Conservative 2; Mismatches 5; Indels 1; Gaps 1;
QY 1 VSKLEASTIRQ-EYFPGD 17
Db 10 MAALBAKICHOIEYFPGD 27
RESULT 15
ADE63989
ID ADE63989 standard; protein; 415 AA.
XX
XX ADE63989;
XX
XX 29-JAN-2004 (first entry)
DT
XX

DE Human autoantigen Ia(SS-B).
XX
XX Autoimmune disease; La autoantigen; Sjogren's syndrome;
KW systemic lupus erythematosus; diagnosis.
XX
XX Homo sapiens.
XX
XX USS541291-A.
XX
XX 30-JUL-1996.
XX
XX 27-MAY-1987; 87US-00054871.
XX
XX 31-DEC-1984; 84US-00687908.
XX
XX (UYDU-) UNIV DUKE.
XX
XX Keene JD;
XX
XX WPI; 1996-362015/36.
XX
XX Auto-antigen U2-RNP, associated with severe polymyositis-scleroderma
PT overlap syndrome - useful for diagnosis and treatment of autoimmune
PT diseases.
XX
XX PS Disclosure: Col 15-16; 21pp; English.
XX
XX The human lupus antigen (La) is diagnostic for Sjogren's syndrome, as
CC well as occurring in systemic lupus erythematosus patients. The La protein
CC is clinically related to the Ro protein that is highly common among
CC autoimmune patients. La and Ro antigens sometimes reside on the same
CC cellular ribonucleoprotein particle; most La patients contain some Ro
CC antibodies and vice versa. La cDNA has been isolated from a human liver
CC library. (Updated on 25-MAR-2003 to correct PF field.)
XX
XX SQ Sequence 408 AA;

Query Match 48.3%; Score 43.5; DB 2; Length 408;
Best Local Similarity 55.6%; Pred. No. 49;
Matches 10; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 1 VSKLEASTIRQ-EYFGD 17
::||| |
DB 10 MALEAKICHQIEYFGD 27

RESULT 10
ID ABB65252 standard; protein; 408 AA.
XX
XX ABB65252;
AC
XX
DT 12-NOV-2002 (first entry)
XX
DE Hypoxia-regulated protein #126.
XX
XX Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy;
KW antiinflammatory; vulnery; gynecological; ophthalmological; vaccine;
KW hypoxia; tumorigenesis; angiogenesis; apoptosis; cancer;
KW ischaemic condition; reperfusion injury; retinopathy; neonatal stress;
KW preclapmsia; atherosclerosis; inflammatory condition; wound healing;
KW inflammation; erythropoiesis; hair loss; human.
XX
XX Homo sapiens.
XX
XX WO200246465-A2.
XX
XX 13-JUN-2002.
PD
XX 10-DEC-2001; 2001WO-GB005458.
PF
XX 08-DEC-2000; 2000GB-00030076.
PR
XX 08-FEB-2001; 2001GB-00003156.
PA

PR 25-OCT-2001; 2001GB-00025666.
XX
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
XX White J, Mundy CR, Ward NR, Krige D, Kingman SM, Harris RA;
PI Rayner WN;
XX
XX WPI; 2002-627238/67.
XX
XX Identifying a gene involved in disease for treating hypoxia-regulated
PT conditions, comprises comparing the transcriptome/proteome of two cell
PT types under different conditions and identifying a differentially
PT regulated gene.
XX
XX Claim 35; Page 425; 538pp; English.
XX
XX The present invention relates to methods for identifying genes and
CC proteins that are implicated in a specific disease or physiological
CC condition. The method comprises comparing the transcriptome/proteome of a
CC specialised cell type implicated in a disease or condition with that of a
CC second specialised cell type, under two experimental conditions, and
CC identifying a gene that is differentially regulated in the two
CC specialised cell types under experimental conditions. ABV77873-ABV78116
CC and ABB65061-ABB65257 were identified using the methods of the invention.
CC The coding sequences and proteins are useful for treating a disease in a
CC patient, for manufacture of a medicament for treating hypoxia-regulated
CC conditions, and for regulating tumorigenesis, angiogenesis, apoptosis,
CC biological response to hypoxia conditions, or hypoxic-associated
CC pathology in a patient. The coding sequences and proteins are also useful
CC for monitoring the therapeutic treatment of a disease or physiological
CC condition, such as cancer, ischaemic conditions, reperfusion injury,
CC retinopathy, neonatal stress, preclapmsia, atherosclerosis, inflammatory
CC conditions, wound healing, inflammation, erythropoiesis or hair loss
XX
XX SQ Sequence 408 AA;

Query Match 48.3%; Score 43.5; DB 5; Length 408;
Best Local Similarity 55.6%; Pred. No. 49;
Matches 10; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 1 VSKLEASTIRQ-EYFGD 17
::||| |
DB 10 MALEAKICHQIEYFGD 27

RESULT 11
ID ABB63991 standard; protein; 408 AA.
XX
XX ABB63991;
AC
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P05455, SEQ ID NO 9937.
XX
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
XX Homo sapiens.
XX
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
PD
XX 14-AUG-2002; 2002WO-US025765.
PF
XX 14-AUG-2001; 2001US-0312147P.
PR
XX 01-NOV-2001; 2001US-0346362P.
XX
XX 26-NOV-2001; 2001US-0333347P.
PA
XX (GENO) GEN HOSPITAL CORP.
XX
XX (FARB) BAYER AG.

CC antigen protein (IAP) in any phase of their life cycle. The peptides of
 CC the invention compete with IAP and inhibit the utilisation of various
 CC biochemical and physiological functions of IAP required for a productive
 CC life cycle. The methods and compositions are useful as antiviral therapy
 CC in pharmaceutical, veterinary or agricultural/horticultural applications.
 CC ABG72101-ABG72119 represent peptides useful as antiviral agents

XX SQ Sequence 18 AA;

Query Match 48.3%; Score 43.5; DB 6; Length 18;
 Best Local Similarity 66.7%; Pred. No. 1.1;
 Matches 10; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 4 LEASTIRQ-EYVFGD 17
 |||:|||||
 Db 3 LEAQICQQLRYVFGD 17

RESULT 7
 AAG01351

ID AAG01351 standard; protein; 92 AA.

XX AAG01351;

DT 06-OCT-2000 (first entry)

DE Human secreted protein, SEQ ID NO: 5432.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

XX gene therapy; chromosome mapping.

OS Homo sapiens.

XX EPI033401-A2.

PD 06-SEP-2000.

PF 21-FEB-2000; 2000EP-00200610.

XX 26-FEB-1999; 99US-0122487P.

PA (GEST) GENSET.

PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

DR N-PSDB; AAC01357.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX Claim 13; SEQ ID NO 5432; 71pp + Sequence Listing; English.

XX The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also useful in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors

XX SQ Sequence 92 AA;

Query Match 48.3%; Score 43.5; DB 3; Length 92;
 Best Local Similarity 55.6%; Pred. No. 8;
 Matches 10; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 1 VSKLEASTIRQ-EYVFGD 17
 ::|||:|||||
 Db 10 MALEAKICHQLEYYVFGD 27

RESULT 8
 ABP40135

ID ABP40135 standard; protein; 136 AA.

XX ABP40135;

DT 24-JUL-2002 (first entry)

DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:4980.

XX Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;

XX antibacterial; gene therapy.

OS Staphylococcus epidermidis.

XX US6380370-B1.

PD 30-APR-2002.

PF 13-AUG-1998; 98US-00134001.

PR 14-AUG-1997; 97US-0055779P.

XX 08-NOV-1997; 97US-0064964P.

PA (GENO-) GENOME THERAPEUTICS CORP.

XX Doucette-Stamm LA, Bush D;

XX WPI; 2002-381255/41.

DR N-PSDB; ABN92680.

XX Novel isolated nucleic acid encoding a Staphylococcus epidermis
 PT polypeptide, useful for diagnosing and treating bacterial infections.
 XX Disclosure; SEQ ID NO 4980; 267pp; English.

XX ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading
 CC frame (ORF) nucleic acid sequences which encode the amino acid sequences
 CC given in ABP35124 to ABP37960. The S. epidermidis sequences have
 CC antibacterial activity and can be used in gene therapy. The sequences can
 CC also be used in the diagnosis and treatment of bacterial infections,
 CC particularly S. epidermidis infections. The sequences can be used to
 CC screen for compounds able to interfere with the S. epidermidis life cycle
 CC or inhibit S. epidermidis infection. N.B. The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from the USPTO web site

XX SQ Sequence 136 AA;

Query Match 48.3%; Score 43.5; DB 5; Length 136;
 Best Local Similarity 57.9%; Pred. No. 13;
 Matches 11; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 1 VSKLEAST-IRQVYVFGD 18
 :|||:|||||
 Db 98 ISKLRSETDERQVYVFGD 116

RESULT 9
 AAM03716

ID AAM03716 standard; protein; 408 AA.

XX AAM03716;

DT 25-MAR-2003 (revised)

XX 12-MAR-1997 (first entry)

PR	24-SEP-1999;	99US-0155659P.
PR	28-SEP-1999;	99US-0156458P.
PR	29-SEP-1999;	99US-0156596P.
PR	04-OCT-1999;	99US-0157117P.
PR	05-OCT-1999;	99US-0157753P.
PR	06-OCT-1999;	99US-0157865P.
PR	07-OCT-1999;	99US-0158029P.
PR	08-OCT-1999;	99US-0158232P.
PR	12-OCT-1999;	99US-0158369P.
PR	13-OCT-1999;	99US-0159293P.
PR	13-OCT-1999;	99US-0159294P.
PR	13-OCT-1999;	99US-0159295P.
PR	14-OCT-1999;	99US-0159329P.
PR	14-OCT-1999;	99US-0159330P.
PR	14-OCT-1999;	99US-0159331P.
PR	14-OCT-1999;	99US-0159637P.
PR	14-OCT-1999;	99US-0159638P.
PR	18-OCT-1999;	99US-0159584P.
PR	21-OCT-1999;	99US-0160741P.
PR	21-OCT-1999;	99US-0160767P.
PR	21-OCT-1999;	99US-0160768P.
PR	21-OCT-1999;	99US-0160770P.
PR	21-OCT-1999;	99US-0160814P.
PR	21-OCT-1999;	99US-0160815P.
PR	22-OCT-1999;	99US-0160980P.
PR	22-OCT-1999;	99US-0160981P.
PR	22-OCT-1999;	99US-0160989P.
PR	25-OCT-1999;	99US-0161404P.
PR	25-OCT-1999;	99US-0161405P.
PR	25-OCT-1999;	99US-0161406P.
PR	26-OCT-1999;	99US-0161359P.
PR	26-OCT-1999;	99US-0161360P.
PR	26-OCT-1999;	99US-0161361P.
PR	28-OCT-1999;	99US-0161920P.
PR	28-OCT-1999;	99US-0161992P.
PR	29-OCT-1999;	99US-0162142P.

[illegible]

Pt	Venter JC, Adams M, Li FMD, Myers EW;
XX	
DR	WPI; 2001-656860/75.
DR	N-PSDB; ABL01944.
XX	
XX	New isolated nucleic acid detection reagent for detecting 1000 or more
Pt	genes from Drosophila and for elucidating cell signaling and cell-cell
Pt	interactions.
Pt	
XX	
PS	Disclosure; SEQ ID NO 315; 21pp + Sequence Listing; English.
XX	
CC	The invention relates to an isolated nucleic acid detection reagent
CC	capable of detecting 1000 or more genes from Drosophila. The invention is
CC	useful in developmental biology and in elucidating cell signalling and
CC	cell-cell interactions in higher eukaryotes for the development of
CC	insecticides, therapeutics and pharmaceutical drugs. The invention
CC	discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
CC	sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC	ABB572072). The sequence data for this patent did not form part of the
CC	printed specification, but was obtained in electronic format directly
CC	from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 512 AA;

	Query Match	48.9%	Score 44;	DB 4;	Length 512;	
	Best Local Similarity	57.1%	Pred. No. 53;			
	Matches	8;	Conservative	3;	Mismatches	3; Indels 0; Gaps 0.
QY	I VSKLEASTROEYY 14	:	: :			
Db	278 ISPLQAQIROSYV 291					
RESULT 6						
ABG72102						
ID	ABG72102 standard; peptide; 18 AA.					
XX						
AC	ABG72102;					
XX						
DT	28-JAN-2003 (first entry)					
XX						
DE	Viral replication inhibiting peptide, 702.					
XX						
KM	Viral replication inhibitor; IRES initiated translation; LBP;					
KM	internal ribosome entry site initiated translation; Va antigen protein;					
KW	viral life cycle; antiviral therapy; pharmaceutical; veterinary;					
XX	agricultural; horticultural; virucide.					
OS	Unidentified.					
XX						
PN	WO200283858-A2.					
PD						
24-OCT-2002.						
PF	12-APR-2002; 2002MO-US011589.					
XX						
PR	16-APR-2001; 2001US-00836073.					
XX						
PA	(UYCA-) UNITV CALIFORNIA OFFICE PRESIDENT.					
XX						
P1	Dasgupta A, Das S, Baidya N;					
DR	WPI; 2003-058634/05.					
PT	New compound containing acidic and aromatic amino acids, useful as					
PT	antiviral therapy in pharmaceutical, veterinary or					
PT	agricultural/horticultural applications.					
XX						
PS	Claim 10; Page 16; 19pp; English.					
CC	The present invention relates to peptides and methods of inhibiting the					
CC	replication of viruses that utilise internal ribosome entry site (IRES)					
CC	initiated translation, and/or inhibiting viruses that utilise the La					

```

XX 25-FEB-2000; 2000EP-00301439.
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130691P.
PR 30-APR-1999; 99US-0131449P.
PR 04-MAY-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0132863P.
PR 14-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-013470P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134841P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140655P.
PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-014091P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 07-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142350P.

PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145088P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145088P.
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PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
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PR 28-JUL-1999; 99US-0145591P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 05-AUG-1999; 99US-0147260P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147933P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
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PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 23-AUG-1999; 99US-0150566P.
PR 25-AUG-1999; 99US-0150884P.
PR 26-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151330P.
PR 01-SEP-1999; 99US-0151330P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153707P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.

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PD 06-SEP-2000.

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OM protein - protein search, using sw model

Run on: September 10, 2004, 16:58:20 ; Search time 56.3129 Seconds
(without alignments)
90.314 Million cell updates/sec

Title: US-09-836-073-18

Perfect score: 90

Sequence: 1 VSKLEASTIRQRYFGDA 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq.29Jan04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	90	100.0	18	6	ABG72118	Abg72118 Viral rep
2	52.5	58.3	390	4	ABB65316	Abb65316 Drosophila
3	44.5	49.4	16	6	ABG72119	Abg72119 Viral rep
4	44	48.9	413	3	AAG38952	Aag38952 Arabidops
5	44	48.9	512	4	ABBS7841	Abbs7841 Drosophila
6	43.5	48.3	18	6	ABG72102	Abg72102 Viral rep
7	43.5	48.3	92	3	AAO01351	Aao01351 Human sec
8	43.5	48.3	136	5	ABP40135	Abp40135 Stephyloc
9	43.5	48.3	408	2	AAW03716	Aaw03716 Human aut
10	43.5	48.3	408	5	ABP65252	Abp65252 Hypoxia-r
11	43.5	48.3	408	7	ADBE63991	Adbe63991 Human pro
12	43.5	48.3	408	7	ADDA6272	Adda6272 Human pro
13	43.5	48.3	408	7	ADBE63995	Adbe63995 Human pro
14	43.5	48.3	408	7	ADBE62859	Adbe62859 Human pro
15	43.5	48.3	415	7	ADBE63989	Adbe63989 Rat Prote
16	43.5	48.3	415	7	ADBE63993	Adbe63993 Rat Prote
17	43.5	48.3	439	4	ABG08417	Abg08417 Novel hum
18	43.5	48.3	460	3	ABBS6987	Abbs6987 Breast an
19	43.5	48.3	460	5	ABP41511	Abp41511 Human ova
20	43	47.8	129	4	AAW84747	Aaw84747 Human imm
21	43	47.8	184	6	ABU54886	Abu54886 Metabolic
22	43	47.8	448	2	AAAR41516	Aaar41516 Cystachio
23	43	47.8	448	2	AAAR40920	Aaar40920 NHS-5 Pro
24	43	47.8	507	2	AAAR42284	Aaar42284 Protein w
25	43	47.8	507	5	ABG93112	Abg93112 S. cerevi

26	43	47.8	507	6	ABR53760	AbR53760 Protein S
27	43	47.8	1252	4	AAE02008	Aae02008 Yeast cys
28	43	47.8	1252	4	AAO29518	Aao29518 Yeast cys
29	42.5	47.2	17	6	ABG72113	Abg72113 Viral rep
30	42.5	47.2	18	3	AAV52200	Aav52200 Human la
31	42.5	47.2	18	6	ABG72109	Abg72109 Viral rep
32	42.5	47.2	18	6	ABG72101	Abg72101 Viral rep
33	42.5	47.2	18	6	ABG72114	Abg72114 Viral rep
34	42.5	47.2	19	6	ABG72116	Abg72116 Viral rep
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36	41	45.6	980	3	AAO51323	Aao51323 Arabidops
37	41	45.6	1007	2	AAV19957	Aav19957 B. burgdo
38	41	45.6	1031	3	AAO51322	Aao51322 Arabidops
39	41	45.6	1036	2	AAV19956	Aav19956 B. burgdo
40	41	45.6	1036	6	ABU19108	Abu19108 Protein e
41	41	45.6	1277	3	AAO51321	Aao51321 Arabidops
42	40.5	45.0	411	6	ABP70556	Abp70556 Histone d
43	40	44.4	176	4	ABBS64852	Abbs64852 Drosophila
44	40	44.4	287	6	ADA36743	Ada36743 Actinobola
45	40	44.4	379	6	ABU01543	Abu01543 S. pneumo

ALIGNMENTS

RESULT 1	ABG72118	standard; peptide; 18 AA.
ID	ABG72118	standard; peptide; 18 AA.
AC	ABG72118	
DT	28-JAN-2003	(first entry)
XX		
DE	Viral replication inhibiting peptide, MOSQUITO.	
XX		
KW	Viral replication inhibitor; IRES initiated translation; LAP;	
KW	internal ribosome entry site initiated translation; La antigen protein;	
KW	viral life cycle; antiviral therapy; pharmaceutical; veterinary;	
KW	agricultural; horticultural; virucide; mosquito.	
XX		
OS	Culicoides.	
XX		
PN	MO200283858-A2.	
PD	24-OCT-2002.	
XX		
PF	12-APR-2002; 2002MO-US011589.	
XX		
PR	16-APR-2001; 2001US-00836073.	
XX		
PA	(UYCA-) UNIT CALIFORNIA OFFICE PRESIDENT.	
XX		
PI	Dasgupta A, Das S, Baidya N;	
XX		
DR	WPI; 2003-058634/05.	
PT	New compound containing acidic and aromatic amino acids, useful as	
PT	antiviral therapy in pharmaceutical, veterinary or	
PT	agricultural/horticultural applications.	
XX		
PS	Claim 1; Page 15; 19pp; English.	
XX		
CC	The present invention relates to peptides and methods of inhibiting the	
CC	replication of viruses that utilize internal ribosome entry site (IRES)	
CC	initiated translation, and/or inhibiting viruses that utilize the La	
CC	antigen protein (LAP) in any phase of their life cycle. The peptides of	
CC	the invention compete with LAP and inhibit the utilization of various	
CC	biochemical and physiological functions of LAP required for a productive	
CC	life cycle. The methods and compositions are useful as antiviral therapy	
CC	in pharmaceutical, veterinary or agricultural/horticultural applications.	
CC	ABG72101-ABG72119 represent peptides useful as antiviral agents	
XX		
SO	Sequence 18 AA;	

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 215:
US-09-402-181B-215

Query Match 46.6%; Score 48.5; DB 4; Length 38;
Best Local Similarity 83.3%; Pred. No. 0.38; 1; Indels 1; Gaps 1;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Oy 7 ICHOIEEYFGD 18
Db 1 ICEQI-EYFGD 11

RESULT 15
US-09-721-456-215
Sequence 215, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Langner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-Nov. 6617110-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-Nov-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-Oct-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-Oct-1997
APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-Oct-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 215:
US-09-721-456-215

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Best Local Similarity 83.3%; Pred. No. 0.38; 1; Indels 1; Gaps 1;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Oy 7 ICHOIEEYFGD 18
Db 1 ICEQI-EYFGD 11

Search completed: September 10, 2004, 18:05:10
Job time : 16.771 secs

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-854-050-25

Query Match 46.6%; Score 48.5; DB 3; Length 38;
Best Local Similarity 83.3%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 7 ICHOIEEYFGD 18
Db 1 ICEQI-EYFEGD 11

RESULT 13
US-09-430-323-25
Sequence 25, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin H.
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430.323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-430-323-25

Query Match 46.6%; Score 48.5; DB 4; Length 38;
Best Local Similarity 83.3%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 7 ICHOIEEYFGD 18
Db 1 ICEQI-EYFEGD 11

RESULT 14
US-09-402-181B-215
Sequence 215, Application US/09402181B
Patent No. 6610839
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin H.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402.181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhuis, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:

TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-851-843A-25

Query Match 46.6%; Score 48.5; DB 3; Length 38;
Best Local Similarity 83.3%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 7 ICHQIEEYFGD 18
Db 1 ICEQI-EYFGD 11

RESULT 11
US-08-974-549A-215
Sequence 215, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,212
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-215

Query Match 46.6%; Score 48.5; DB 3; Length 38;
Best Local Similarity 83.3%; Pred. No. 0.38;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 7 ICHQIEEYFGD 18
Db 1 ICEQI-EYFGD 11

RESULT 12
US-08-854-050-25
Sequence 25, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 536
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536

STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-402-181B-214

Query Match 55.3%; Score 57.5; DB 4; Length 38;
Best Local Similarity 84.6%; Pred. No. 0.013;
Matches 11; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 7 ICHQIEYYFGDF 19
Db 1 ICHQ-XEYFGDF 12

RESULT 9
US-09-721-456-214
Sequence 214, Application US/09721456
Patent No. 6617110

GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-NOV-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-721-456-214

Query Match 55.3%; Score 57.5; DB 4; Length 38;
Best Local Similarity 84.6%; Pred. No. 0.013;
Matches 11; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 7 ICHQIEYYFGDF 19
Db 1 ICHQ-XEYFGDF 12

RESULT 10
US-08-851-843A-25
Sequence 25, Application US/08851843A
Patent No. 6093809

GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 01-OCT-1996
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids

RESULT 7
US-08-974-549A-214
Sequence 214, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-214
Query Match 55.3%, Score 57.5, DB 3, Length 38;
Best Local Similarity 84.6%, Pred. No. 0.013;
Matches 11; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 7 ICHOIEYFGDF 19
||| |||||
Db 1 ICHOXEYFGDF 12
RESULT 8
US-09-402-181B-214
Sequence 214, Application US/09402181B
Patent No. 6610839
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-SEP-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Aussenhub, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid

Query Match 55.8%; Score 58; DB 3; Length 37;
Best Local Similarity 84.6%; Pred. No. 0.011; 0; Indels 2; Gaps 1;
Matches 11; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
QY 7 ICHQIEEYFGDF 19
1 ICHQ--EYFGDF 11
Db

RESULT 5
US-08-854-050-24
; Sequence 24, Application US/08854050
; Patent No. 6261836
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin H.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6261836el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-08-854-050-24
Query Match 55.8%; Score 58; DB 3; Length 37;
Best Local Similarity 84.6%; Pred. No. 0.011;

Matches 11; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
QY 7 ICHQIEEYFGDF 19
1 ICHQ--EYFGDF 11
Db

RESULT 6
US-09-430-323-24
; Sequence 24, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin H.
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
; FILING DATE: 29-OCT-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-430-323-24

Query Match 55.8%; Score 58; DB 4; Length 37;
Best Local Similarity 84.6%; Pred. No. 0.011;
Matches 11; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
QY 7 ICHQIEEYFGDF 19
1 ICHQ--EYFGDF 11
Db

PRIOR FILING DATE: 1997-10-06
PRIOR APPLICATION NUMBER: 08/321,427
PRIOR FILING DATE: 1994-10-11
PRIOR APPLICATION NUMBER: 60/086,527
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 4
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: B-LAP
OTHER INFORMATION: this peptide is biotinylated
US-09-316-630-4

Query Match 85.1%; Score 88.5; DB 3; Length 18;
Best Local Similarity 94.7%; Pred. No. 5.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 AALEKICHQIEYYFGDF 19
Db 1 AALEKICHQI-EYYFGDF 18

RESULT 3
US-08-475-955-20
Sequence 20, Application US/08475955
Patent No. 6641813
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,955
FILING DATE: June 7, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/667,819
FILING DATE: April 13, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMF114CIP(2) DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Binding-site
LOCATION: 8..15
US-08-475-955-20

Query Match 60.1%; Score 62.5; DB 4; Length 21;
Best Local Similarity 92.3%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 7 ICHQIEYYFGDF 19
Db 1 ICHQI-EYYFGDF 12

RESULT 4
US-08-851-843A-24
Sequence 24, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-851-843A-24

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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:43:01; Search time 16.771 Seconds
(without alignments)
58.488 Million cell updates/sec

Title: US-09-836-073-16

Perfect score: 104

Sequence: 1 AALEAKICHOIEHYRGDP 19

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued Patents AA:
1: /cgn2_6/prodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/2/iaa/5H_COMB.pep.*
3: /cgn2_6/prodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	88.5	85.1	18	US-09-316-630-3	Sequence 3, Appl
2	88.5	85.1	18	US-09-316-630-4	Sequence 4, Appl
3	62.5	60.1	21	US-08-475-955-20	Sequence 20, Appl
4	58	55.8	37	US-08-851-843A-24	Sequence 24, Appl
5	58	55.8	37	US-08-854-050-24	Sequence 24, Appl
6	58	55.8	37	US-09-430-323-24	Sequence 24, Appl
7	57.5	55.3	38	US-08-974-549A-214	Sequence 214, App
8	57.5	55.3	38	US-09-402-181B-214	Sequence 214, App
9	57.5	55.3	38	US-09-721-456-214	Sequence 214, App
10	48.5	46.6	38	US-08-851-843A-25	Sequence 25, Appl
11	48.5	46.6	38	US-08-974-549A-215	Sequence 215, Appl
12	48.5	46.6	38	US-08-854-050-25	Sequence 25, Appl
13	48.5	46.6	38	US-09-430-323-25	Sequence 25, Appl
14	48.5	46.6	38	US-09-402-181B-215	Sequence 215, App
15	48.5	46.6	38	US-09-721-456-215	Sequence 215, App
16	47	45.2	45	US-08-205-719-4	Sequence 4, Appl
17	47	45.2	45	US-08-431-517F-6	Sequence 6, Appl
18	47	45.2	45	US-08-431-517F-5	Sequence 6, Appl
19	47	45.2	45	US-08-431-517F-5	Sequence 6, Appl
20	44	42.3	324	US-09-107-532A-4729	Sequence 4729, Ap
21	44	41.3	281	US-09-543-681A-4336	Sequence 4336, Ap
22	43	41.3	510	US-08-097-829-2	Sequence 2, Appl
23	43	41.3	510	US-08-577-403-2	Sequence 2, Appl
24	42.5	40.9	740	US-09-323-872A-23	Sequence 23, Appl
25	42.5	40.9	740	US-09-072-433-15	Sequence 15, Appl
26	42.5	40.9	864	US-09-323-872A-28	Sequence 28, Appl
27	42.5	40.9	864	US-09-072-433-16	Sequence 16, Appl

28	42	40.4	611	4	US-09-543-681A-5447	Sequence 5447, Ap
29	42	40.4	699	4	US-09-543-681A-5118	Sequence 5118, Ap
30	41.5	39.9	463	4	US-09-543-681A-6745	Sequence 6745, Ap
31	41	39.4	289	4	US-09-543-681A-8235	Sequence 8235, Ap
32	41	39.4	307	4	US-09-328-352-5689	Sequence 5689, Ap
33	41	39.4	410	4	US-09-543-681A-5407	Sequence 5407, Ap
34	41	39.4	497	4	US-09-489-039A-8926	Sequence 8926, Ap
35	40	38.5	41	4	US-09-205-258-970	Sequence 970, App
36	40	38.5	102	4	US-09-198-452A-56	Sequence 56, Appl
37	40	38.5	203	4	US-09-328-352-7692	Sequence 7692, Ap
38	40	38.5	214	4	US-09-205-258-965	Sequence 965, App
39	40	38.5	255	4	US-09-107-532A-6662	Sequence 6662, App
40	40	38.5	263	2	US-08-864-799-1	Sequence 1, Appl
41	40	38.5	1253	4	US-07-920-281C-3	Sequence 3, Appl
42	40	38.5	1253	3	US-08-466-277-3	Sequence 3, Appl
43	39	37.5	86	4	US-09-300-008B-55	Sequence 55, Appl
44	39	37.5	99	4	US-09-543-681A-6663	Sequence 6663, Ap
45	39	37.5	122	4	US-09-732-210-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
US-09-316-630-3
Sequence 3, Application US/09316630
Patent No. 6291637
GENERAL INFORMATION:
APPLICANT: Das, Saumitra
TITLE OF INVENTION: INTERFERENCE WITH VIRAL IRES-MEDIATED TRANSLATION BY A
FILE REFERENCE: 22000-20548.21
CURRENT APPLICATION NUMBER: US/09/316,630
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 08/817,953
PRIOR FILING DATE: 1997-10-06
PRIOR APPLICATION NUMBER: 08/321,427
PRIOR FILING DATE: 1994-10-11
PRIOR APPLICATION NUMBER: 60/086,527
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: LAP
US-09-316-630-3
Query Match 85.1%; Score 88.5; DB 3; Length 18;
Best Local Similarity 94.7%; Pred. No. 5.6e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
DB 1 AALEAKICHOIEHYRGDP 19
US-09-316-630-4
Sequence 4, Application US/09316630
Patent No. 6291637
GENERAL INFORMATION:
APPLICANT: Das, Saumitra
TITLE OF INVENTION: INTERFERENCE WITH VIRAL IRES-MEDIATED TRANSLATION BY A
FILE REFERENCE: 22000-20548.21
CURRENT APPLICATION NUMBER: US/09/316,630
PRIOR FILING DATE: 1999-05-21
CURRENT APPLICATION NUMBER: 08/817,953

DR N-PSDB; AAS72604.

XX New isolated polypeptide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity.

PS Claim 20; SEQ ID NO 38776; 103bp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)

CC sequences. (I) is useful as hybridisation probes, polymerase chain

CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,

CC and in recombinant production of (II). The polynucleotide is also used

CC in diagnostics as expressed sequence tags for identifying expressed

CC genes. (II) is useful in gene therapy techniques to restore normal

CC activity of (I) or to treat disease states involving (II). (II) is

CC useful for generating antibodies against it, detecting or quantitating a

CC polypeptide in tissue, as molecular weight markers and as a food

CC supplement. (II) and its binding partners are useful in medical imaging

CC of sites expressing (II). (I) and (II) are useful for treating disorders

CC involving aberrant protein expression or biological activity. The

CC polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. AAG00010-ABG30377 represent novel human diagnostic

CC amino acid sequences of the invention. Note: The sequence data for this

CC patent did not appear in the printed specification, but was obtained in

CC electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX

SO Sequence 439 AA:

Query Match 85.1%; Score 88.5; DB 4; Length 439;

Best Local Similarity 94.7%; Pred. No. 1.4e-05;

Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 AALEAKICHQIEYYFGDF 19

DB 41 AALEAKICHQI-EYYFGDF 58

RESULT 15

AAB58987 standard; protein; 460 AA.

AC AAB58987;

DT 27-MAR-2001 (first entry)

DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 695.

XX Human; breast cancer; ovarian cancer; cystic; immunosuppressive;

KW neoplastic; neuroprotective; antiviral; antiallergic; hepatotropic;

KW antidiabetic; antiinflammatory; antilicer; vulnerary; anticonvulsant;

KW antibacterial; antifungal; antiparasitic; cardiant; immune disorder;

KW Addison's disease; allergy; autoimmune haemolytic anaemia;

KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;

KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;

XX cardiovascular disorder; wound healing; neurological disease.

OS Homo sapiens.

PN WO200055173-A1.

PD 21-SEP-2000.

PF 08-MAR-2000; 2000WO-US005881.

PR 12-MAR-1999; 99US-0124270P.

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Rosen CA, Ruben SM;

XX WPI; 2000-611515/58.

DR N-PSDB; AAF21890.

XX

XX New human breast and ovarian cancer associated gene sequences and the

PT polypeptides encoded by these genes, useful in the prevention, treatment

PT and diagnosis of cancer, immune disorders, cardiovascular disorders and

PT neurological diseases.

XX

PS Claim 11; Page 1149-11150; 1299bp; English.

XX Sequences AAF21614 - AAF22031 represent DNA sequences encoding human

CC proteins AAB58711 - AAB59128. The DNA and protein sequences are

CC associated with breast and ovarian cancer. Included in the invention are

CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the

CC isolation and characterisation of the DNA and protein sequences of the

CC invention. The breast and ovarian cancer associated DNA, protein, agonist

CC or antagonist sequences exhibit cytostatic; immunosuppressive; neurotropic;

CC neuroprotective; antiviral; antiallergic; hepatotropic; antibacterial;

CC antiinflammatory; antilicer; vulnerary; anticonvulsant; antibacterial;

CC antifungal; antiparasitic and cardiant activity. The polynucleotide and

CC protein sequences are used in the diagnosis of cancer, particularly

CC breast and ovarian cancer. The nucleic acid sequences, proteins, agonists

CC and agonists may also be used in the diagnosis, prevention and treatment

CC of immune disorders e.g. Addison's disease, allergies, autoimmune

CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's

CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;

CC cardiovascular disorders such as myocardial ischaemias; wound healing;

CC neurological diseases such as cerebral anoxia and epilepsy; and

XX infectious diseases

SO Sequence 460 AA:

Query Match 85.1%; Score 88.5; DB 3; Length 460;

Best Local Similarity 94.7%; Pred. No. 1.4e-05;

Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 AALEAKICHQIEYYFGDF 19

DB 63 AALEAKICHQI-EYYFGDF 80

Search completed: September 10, 2004, 17:51:50

Job time : 60.5413 secs

CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 408 AA;

Query Match

85.1%; Score 88.5; DB 7; Length 408;

Best Local Similarity 94.7%; Pred. No. 1.3e-05;

Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 AALEAKICHQIEYYFGDF 19

Db 11 AALEAKICHQI-EYYFGDF 28

RESULT 11

ADE62859

ID ADE62859 standard; protein; 408 AA.

XX ADE62859;

DT 29-JAN-2004 (first entry)

DE Human Protein P05455, SEQ ID NO 8793.

XX Human; pain; neuronal tissue; gene therapy;

XX spinal segmental nerve injury; chronic constriction injury; CCI;

XX spared nerve injury; SNI; Chung.

XX Homo sapiens.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GHEO) GEN HOSPITAL CORP.

XX (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI, 2003-268312/26.

XX GENBANK; P05455.

XX New composition comprising two or more isolated polypeptides, useful for

XX preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat

XX or human polynucleotides or a polynucleotide which represents a fragment,

XX derivative or allelic variation of the nucleic acid sequence. Also

CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 408 AA;

Query Match

85.1%; Score 88.5; DB 7; Length 408;

Best Local Similarity 94.7%; Pred. No. 1.3e-05;

Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 AALEAKICHQIEYYFGDF 19

Db 11 AALEAKICHQI-EYYFGDF 28

RESULT 12

ADE63989

ID ADE63989 standard; protein; 415 AA.

XX ADE63989;

DT 29-JAN-2004 (first entry)

DE Rat Protein P38656, SEQ ID NO 9935.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;

XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GHEO) GEN HOSPITAL CORP.

XX (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI, 2003-268312/26.

XX GENBANK; P38656.

XX New composition comprising two or more isolated polypeptides, useful for

XX preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 408 AA;

XX Query Match 85.1%; Score 88.5; DB 7; Length 408;
XX Best Local Similarity 94.7%; Pred. No. 1.3e-05;
XX Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 AALEAKICHQIEYYFGDF 19
DB 11 AALEAKICHQI-EYYFGDF 28

RESULT 9
ADD46272
ID ADD46272 standard; protein; 408 AA.
XX
XX ADD46272;

XX 29-JAN-2004 (first entry)

XX Human Protein P05455, SEQ ID NO 11947.

XX Human; pain; neuronal tissue; gene therapy;
XX spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.

XX Homo sapiens.

XX MO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GENO) GEN HOSPITAL CORP.

XX (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

XX GENBANK; P05455.

XX Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the

CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 408 AA;

XX Query Match 85.1%; Score 88.5; DB 7; Length 408;
XX Best Local Similarity 94.7%; Pred. No. 1.3e-05;
XX Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 AALEAKICHQIEYYFGDF 19
DB 11 AALEAKICHQI-EYYFGDF 28

RESULT 10
ADE63995
ID ADE63995 standard; protein; 408 AA.
XX
XX ADE63995;

XX 29-JAN-2004 (first entry)

XX Human Protein P05455, SEQ ID NO 9941.

XX Human; pain; neuronal tissue; gene therapy;
XX spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.

XX Homo sapiens.

XX MO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GENO) GEN HOSPITAL CORP.

XX (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

XX GENBANK; P05455.

XX Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence

CC is clinically related to the Ro protein that is highly common among
CC autoimmune patients. La and Ro antigens sometimes reside on the same
CC cellular ribonucleoprotein particle; most La patients contain some Ro
CC antibodies and vice versa. La cDNA has been isolated from a human liver
CC library. (Updated on 25-MAR-2003 to correct PF field.)
CC
XX

SO Sequence 408 AA;

Query Match 85.1%; Score 88.5; DB 2; Length 408;
Best Local Similarity 94.7%; Pred. No. 1.3e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 AALEAKICHQIEEYFGDF 19
|||
DB 11 AALEAKICHQI-EYFGDF 28

RESULT 7
ABP65252

ID ABP65252 standard; protein; 408 AA.

AC ABP65252;

DT 12-NOV-2002 (first entry)

DE Hypoxia-regulated protein #126.

XX Cytostatic; vasotropic; tiranquilliser; antiatherosclerotic; gene therapy;
XX antiinflammatory; vulnery; gynecological; ophthalmological; vaccine;
XX hypoxia; tumorigenesis; angiogenesis; apoptosis; cancer;
XX ischaemic condition; reperfusion injury; retinopathy; neonatal stress;
XX preclapmia; atherosclerosis; inflammatory condition; wound healing;
XX inflammation; erythropoiesis; hair loss; human.

XX Homo sapiens.

OS WO200246465-A2.

PN 13-JUN-2002.

PF 10-DEC-2001; 2001WO-GB005458.

PR 08-DEC-2000; 2000GB-00030076.

PR 08-FEB-2001; 2001GB-00003156.

PR 25-OCT-2001; 2001GB-00025666.

PA (OXFORD) OXFORD BIOMEDICA UK LTD.

PI White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA,
PI Rayner WN;

DR WPI; 2002-627238/67.

XX Identifying a gene involved in disease for treating hypoxia-regulated
XX conditions, comprises comparing the transcriptome/proteome of two cell
XX types under different conditions and identifying a differentially
XX regulated gene.

PS Claim 35; Page 425; 538pp; English.

XX The present invention relates to methods for identifying genes and
XX proteins that are implicated in a specific disease or physiological
XX condition. The method comprises comparing the transcriptome/proteome of a
XX specialised cell type implicated in a disease or condition with that of a
XX second specialised cell type, under two experimental conditions, and
XX identifying a gene that is differentially regulated in the two
XX specialised cell types under experimental conditions. ABV7873-ABV78116
XX and ABP65061-ABP65257 were identified using the methods of the invention.
XX The coding sequences and proteins are useful for treating a disease in a
XX patient, for manufacture of a medicament for treating hypoxia-regulated
XX conditions, and for regulating tumorigenesis, angiogenesis, apoptosis,
XX biological response to hypoxia conditions, or hypoxia-associated
XX pathology in a patient. The coding sequences and proteins are also useful

CC for monitoring the therapeutic treatment of a disease or physiological
CC condition, such as cancer, ischaemic conditions, reperfusion injury,
CC retinopathy, neonatal stress, preclapmia, atherosclerosis, inflammatory
CC conditions, wound healing, inflammation, erythropoiesis or hair loss
XX

SO Sequence 408 AA;

Query Match 85.1%; Score 88.5; DB 5; Length 408;
Best Local Similarity 94.7%; Pred. No. 1.3e-05;
Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 AALEAKICHQIEEYFGDF 19
|||
DB 11 AALEAKICHQI-EYFGDF 28

RESULT 8
ADE63991

ID ADE63991 standard; protein; 408 AA.

AC ADE63991;

DT 29-JAN-2004 (first entry)

DE Human Protein P05455, SEQ ID NO 9937.

XX Human; pain; neuronal tissue; gene therapy;
XX spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.

XX Homo sapiens.

PN WO2003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

PA (GENO) GEN HOSPITAL CORP.

PI (PARB) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;

DR WPI; 2003-266312/26.

DR GENBANK; P05455.

XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity for identifying one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more

KW internal ribosome entry site initiated translation; La antigen protein;
 KW viral life cycle; antiviral therapy; pharmaceutical; veterinary;
 KM agricultural; horticultural; virucide; bovine.
 XX Bovinae.
 OS
 XX WO200283858-A2.
 PN
 XX 24-OCT-2002.
 PD
 XX 12-APR-2002; 2002WO-US011589.
 PF
 XX 16-APR-2001; 2001US-00836073.
 PR
 XX (UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.
 PA
 XX Dasgupta A, Das S, Balda N;
 PI
 XX WPI; 2003-058634/05.
 DR
 XX New compound containing acidic and aromatic amino acids, useful as
 PT antiviral therapy in pharmaceutical, veterinary or
 PT agricultural/horticultural applications.
 XX
 XX Disclosure; Page 6; 19pp; English.
 XX
 CC The present invention relates to peptides and methods of inhibiting the
 CC replication of viruses that utilize internal ribosome entry site (IRES)
 CC initiated translation, and/or inhibiting viruses that utilize the La
 CC antigen protein (IAP) in any phase of their life cycle. The peptides of
 CC the invention compete with IAP and inhibit the utilisation of various
 CC biochemical and physiological functions of IAP required for a productive
 CC life cycle. The methods and compositions are useful as antiviral therapy
 CC in pharmaceutical, veterinary or agricultural/horticultural applications.
 CC ABG72101-ABG72119 represent peptides useful as antiviral agents
 CC
 XX Sequence 18 AA:
 SQ
 Query Match 85.1%; Score 88.5; DB 6; Length 18;
 Best Local Similarity 94.7%; Pred. No. 4.3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 AALEAKICHOIEHYRGDF 19
 DB 1 AALEAKICHOI-EYRGDF 18
 RESULT 5
 AAG01351
 ID AAG01351 standard; protein; 92 AA.
 AC
 XX AAG01351;
 XX
 DT 06-OCT-2000 (first entry)
 DE Human secreted protein, SEQ ID NO: 5432.
 XX
 XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KM gene therapy; chromosome mapping.
 XX
 OS Homo sapiens.
 OS
 XX EP1033401-A2.
 PN
 XX 06-SEP-2000.
 PD
 XX 21-FEB-2000; 2000EP-00200610.
 PF
 XX 26-FEB-1999; 99US-0122487P.
 PR
 XX (GEST) GENSET.
 PA
 XX Dumas Malne Edwards J, Duclert A, Giordano J;
 PI

XX WPI; 2000-500381/45.
 DR N-PSDB; AAC01357.
 XX
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX
 PS Claim 13; SEQ ID NO 5432; 71pp + Sequence Listing; English.
 XX
 CC The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors
 CC
 XX Sequence 92 AA:
 SQ
 Query Match 85.1%; Score 88.5; DB 3; Length 92;
 Best Local Similarity 94.7%; Pred. No. 2.5e-06;
 Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 QY 1 AALEAKICHOIEHYRGDF 19
 DB 11 AALEAKICHOI-EYRGDF 28
 RESULT 6
 AAM03716
 ID AAM03716 standard; protein; 408 AA.
 AC
 XX AAM03716;
 XX
 DT 25-MAR-2003 (revised)
 DT 12-MAR-1997 (first entry)
 XX
 DE Human autoantigen Ia(SS-B).
 XX
 XX Autoimmune disease; Ia autoantigen; Sjogren's syndrome;
 KM systemic lupus erythematosus; diagnosis.
 XX
 OS Homo sapiens.
 OS
 XX US5541291-A.
 PN
 XX 30-JUL-1996.
 PD
 XX 27-MAY-1987; 87US-00054871.
 PF
 XX 31-DEC-1984; 84US-00687908.
 PR
 XX (UYDU-) UNIV DUKE.
 PA
 XX Keene JD;
 PI
 XX WPI; 1996-362015/36.
 DR
 XX Auto-antigen U2-RNP, associated with severe polymyositis-scleroderma
 PT overlap syndrome - useful for diagnosis and treatment of autoimmune
 PT diseases.
 XX
 PS Disclosure; Col 15-16; 21pp; English.
 XX
 CC The human lupus antigen (Ia) is diagnostic for Sjogren's syndrome, as
 CC well as occurring in systemic lupus erythematosus patients. The Ia protein

Query Match 100.0%; Score 104; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.5e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AALEAKICHQIEEYFGDF 19
 |||||
 1 AALEAKICHQIEEYFGDF 19

RESULT 2
 AAY52200
 ID AAY52200 standard; peptide; 18 AA.
 XX
 AC AAY52200;
 XX
 DT 14-MAR-2000 (first entry)
 XX
 DE Human Ia autoantigen peptide (LAP).
 XX

La autoantigen; LAP; internal ribosome entry site; IRES; translation;
 viral replication; IRNA; antiviral agent; picornavirus; flavivirus;
 coronavirus; hepatitis virus; rhadovirus; adenovirus; coxsackie virus;
 parainfluenza virus; poliovirus; rhinovirus; encephalomyocarditis virus;
 foot-and-mouth disease virus; echo virus; infectious bronchitis virus;
 vesicular stomatitis virus.

OS Homo sapiens.
 XX
 PN MO9961613-A2.
 XX
 PD 02-DEC-1999.
 XX
 PF 21-MAY-1999; 99WO-US011281.
 XX
 PR 22-MAY-1998; 98US-0086527P.
 XX
 PA (REGC). UNIV CALIFORNIA.
 XX

PI Das S, Dasgupta A;
 FI
 DX WPI; 2000-062712/05.
 DR

PT New yeast inhibitory peptide useful for inhibiting viral protein
 translation and replication.
 PT

XX Claim 5; Page 57; 81pp; English.
 PS

CC This sequence is the Ia autoantigen binding domain (LAP). LAP is a
 CC cellular protein which binds to an internal ribosome entry site (IRES).
 CC The peptide is used to inhibit mRNA translation, viral protein
 CC translation or viral replication. Viral mRNA translation is initiated at
 CC the IRES and the LAP peptide prevents translation initiation factors from
 CC binding at the site. The peptide can be used alone or in combination with
 CC an inhibitor RNA (IRNA see AAY5200). The LAP peptide is useful as an
 CC antiviral agent, which works through the inhibition of mRNA translation,
 CC especially viral RNA. Examples of viruses which can be inhibited are
 CC picornavirus, flavivirus, coronavirus, hepatitis A B or C viruses,
 CC rhadovirus, adenovirus, and parainfluenza virus, poliovirus, rhinovirus,
 CC coxsackie virus, encephalomyocarditis virus, foot-and-mouth disease
 CC virus, echo virus, hepatitis C virus, infectious bronchitis virus, duck
 CC and human hepatitis B virus, and vesicular stomatitis virus. The peptide
 CC also inhibits replication of the above viruses. The LAP peptide
 CC selectively inhibits viral protein translation, and is therefore not
 CC toxic to the host cell.
 CC
 SQ Sequence 18 AA;

Query Match 85.1%; Score 88.5; DB 3; Length 18;
 Best Local Similarity 94.7%; Pred. No. 4.3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 AALEAKICHQIEEYFGDF 19

DB 1 AALEAKICHQI-EYFGDF 18
 |||||

RESULT 3
 ABG72101
 ID ABG72101 standard; peptide; 18 AA.
 XX
 AC ABG72101;
 XX

DT 28-JAN-2003 (first entry)
 XX
 DE Viral replication inhibiting peptide, LAP.
 XX

Viral replication inhibitor; IRES initiated translation; LAP;
 internal ribosome entry site initiated translation; Ia antigen protein;
 viral life cycle; antiviral therapy; pharmaceutical; veterinary;
 agricultural; horticultural; virucide.

OS Unidentified.
 XX
 PN WO200283858-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 12-APR-2002; 2002WO-US011589.
 XX
 PR 16-APR-2001; 2001US-00836073.
 XX
 PA (UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.
 XX

PI Dasgupta A, Das S, Balady N;
 FI
 DX WPI; 2003-058634/05.
 DR

PT New compound containing acidic and aromatic amino acids, useful as
 PT antiviral therapy in pharmaceutical, veterinary or
 PT agricultural/horticultural applications.
 PT

PS Claim 1; Page 15; 19pp; English.
 FI

CC The present invention relates to peptides and methods of inhibiting the
 CC replication of viruses that utilise internal ribosome entry site (IRES)
 CC initiated translation, and/or inhibiting viruses that utilise the Ia
 CC antigen protein (LAP) in any phase of their life cycle. The peptides of
 CC the invention compete with LAP and inhibit the utilisation of various
 CC biochemical and physiological functions of LAP required for a productive
 CC life cycle. The methods and compositions are useful as antiviral therapy
 CC in pharmaceutical, veterinary or agricultural/horticultural applications.
 CC ABG72101-ABG72119 represent peptide useful as antiviral agents
 CC

SQ Sequence 18 AA;

Query Match 85.1%; Score 88.5; DB 6; Length 18;
 Best Local Similarity 94.7%; Pred. No. 4.3e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 AALEAKICHQIEEYFGDF 19
 |||||
 1 AALEAKICHQI-EYFGDF 18

DB 1 AALEAKICHQI-EYFGDF 18
 |||||
 1 AALEAKICHQI-EYFGDF 18

ABG72114
 ID ABG72114 standard; peptide; 18 AA.
 XX
 AC ABG72114;
 XX

DT 28-JAN-2003 (first entry)
 XX
 DE Viral replication inhibiting peptide, BOVINE.
 XX
 DE Viral replication inhibitor; IRES initiated translation; LAP;
 XX

XX Viral replication inhibitor; IRES initiated translation; LAP;
 XX

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OM protein - protein search, using sw model

Run on: September 10, 2004, 16:58:20 ; Search time 59.4413 Seconds
(without alignments)
90.314 Million cell updates/sec

Title: US-09-836-073-16

Perfect score: 104
Sequence: 1 AALEAKICHQIEEYFGDP 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20048:*
8: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	104	100.0	19	6	ABG72116
2	88.5	85.1	18	3	AAV52200 Human Ia
3	88.5	85.1	18	6	ABG72101
4	88.5	85.1	18	6	ABG72114
5	88.5	85.1	92	3	AAAG01351 Human sec
6	88.5	85.1	408	2	AAAG03716 Human aut
7	88.5	85.1	408	5	ABP65252 Hypoxia-r
8	88.5	85.1	408	5	ABP65252 Human pro
9	88.5	85.1	408	7	ADDA6272 Human pro
10	88.5	85.1	408	7	ADDE63995 Human pro
11	88.5	85.1	408	7	ADDE63995 Human pro
12	88.5	85.1	415	7	ADDE63989 Rat Prote
13	88.5	85.1	415	7	ADDE63993 Rat Prote
14	88.5	85.1	439	4	ABG08417 Novel hum
15	88.5	85.1	460	3	ABP45111 Human ova
16	88.5	85.1	460	5	ABP45111 Human ova
17	84.5	81.2	17	6	ABG72113
18	83.5	79.3	18	6	ABG72111
19	82.5	79.3	18	6	ABG72109
20	80.5	77.4	18	6	ABG72112
21	79.5	76.4	18	6	ABG72110
22	76.5	73.6	18	6	ABG72102
23	76.5	73.6	18	6	ABG72103
24	76.5	73.6	18	6	ABG72104
25	75.5	72.6	18	6	ABG72108

26	73.5	70.7	18	6	ABG72107	Abg72107 Viral rep
27	65.5	63.0	18	6	ABG72115	Abg72115 Viral rep
28	64.5	62.0	18	6	ABG72105	Abg72105 Viral rep
29	63	60.6	18	6	ABG72106	Abg72106 Viral rep
30	62.5	60.1	21	2	AAK43394	AAK43394 La/SSB ep
31	49	47.1	2169	4	AAAG91701	AAAG91701 C glutam
32	47	45.2	456	2	AAW41695	AAW41695 Rabbit LP
33	47	45.2	482	2	AAW41659	AAW41659 Lapine gr
34	47	45.2	482	2	AAW43461	AAW43461 Lapine po
35	47	45.2	482	2	AAW40813	AAW40813 Rabbit 11
36	47	45.2	482	2	AAW78355	AAW78355 Rabbit 11
37	46.5	44.7	16	6	ABG72119	ABG72119 Viral rep
38	46	44.2	352	3	ABR53809	ABR53809 Protein B
39	45.5	43.8	132	3	AAW51905	AAW51905 Human sec
40	45.5	43.8	425	4	AAW25631	AAW25631 Human pro
41	45.5	43.8	643	4	AAW99540	AAW99540 Prelimina
42	45.5	43.8	643	7	ADC21971	ADC21971 Human cad
43	45.5	43.8	675	6	ABR43633	ABR43633 Mouse CLA
44	45.5	43.8	863	7	ADC31112	ADC31112 Human nov
45	45.5	43.8	2047	4	AAW99541	AAW99541 Human CLA

ALIGNMENTS

RESULT 1
ID ABG72116 standard; peptide; 19 AA.
AC ABG72116;
XX
XX
XX 28-JUN-2003 (first entry)
XX
XX
XX Viral replication inhibiting peptide, RAT.
DE
XX Viral replication inhibitor; IRMS initiated translation; LAP;
KW internal ribosome entry site initiated translation; Ia antigen protein;
KW viral life cycle; antiviral therapy; pharmaceutical; veterinary;
KW agricultural; horticultural; virucide; rat.
XX
XX
XX Rattus sp.
OS
XX
XX WO200283858-A2.
PN
XX
XX 24-OCT-2002.
PD
XX
XX 12-APR-2002; 2002WO-US011589.
PF
XX
XX 16-APR-2001; 2001US-00836073.
PR
XX
XX (UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.
PA
XX
XX Dasgupta A, Das S, Balda N;
PI
XX
XX WPI; 2003-058634/05.
DR
XX
XX New compound containing acidic and aromatic amino acids, useful as
PT antiviral therapy in pharmaceutical, veterinary or
PT agricultural/horticultural applications.
PT
XX
XX Claim 1; Page 15; 19pp; English.
PS
XX
XX The present invention relates to peptides and methods of inhibiting the
CC replication of viruses that utilize internal ribosome entry site (IRES)
CC initiated translation, and/or inhibiting viruses that utilize the La
CC antigen protein (LAP) in any phase of their life cycle. The peptides of
CC the invention compete with LAP and inhibit the utilisation of various
CC biochemical and physiological functions of LAP required for a productive
CC life cycle. The methods and compositions are useful as antiviral therapy
CC in pharmaceutical, veterinary or agricultural/horticultural applications.
CC ABG72101-ABG72119 represent peptides useful as antiviral agents
SQ
XX Sequence 19 AA;

polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 408 AA;

Query Match 76.0%; Score 76; DB 7; Length 408;
Best Local Similarity 81.2%; Pred. No. 0.0022;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LDTKICEQIEYYFGDF 18
|:|||||
DB 13 LEAKICHQIEYYFGDF 28

RESULT 13
ADE63989
ID ADE63989 standard; protein; 415 AA.
XX
AC ADE63989;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein P38656, SEQ ID NO 9935.
XX
KM Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
XX
PR 01-NOV-2001; 2001US-0346382P.
XX
PR 26-NOV-2001; 2001US-033347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
PI MPI; 2003-268312/26.
XX
DR GENBANK; P38656.
XX
PT New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a

method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 415 AA;

Query Match 76.0%; Score 76; DB 7; Length 415;
Best Local Similarity 81.2%; Pred. No. 0.0022;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LDTKICEQIEYYFGDF 18
|:|||||
DB 13 LEAKICHQIEYYFGDF 28

RESULT 14
ADE63993
ID ADE63993 standard; protein; 415 AA.
XX
AC ADE63993;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein P38656, SEQ ID NO 9939.
XX
KM Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
XX
PR 01-NOV-2001; 2001US-0346382P.
XX
PR 26-NOV-2001; 2001US-033347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
XX
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
PI MPI; 2003-268312/26.
XX
DR GENBANK; P38656.
XX
PT New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates

SQL Sequence 408 AA; 76.0%; Score 76; DB 7; Length 408; Best Local Similarity 81.2%; Pred. No. 0.0022; Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LDTKICEQIEYFGDF 18
|:|||||
DB 13 LEAKICHQIEYFGDF 28

RESULT 11
ADE63995
ID ADE63995 standard; protein; 408 AA.
AC ADE63995;
DT 29-JAN-2004 (first entry)
XX Human Protein P05455, SEQ ID NO 9941.
DE
XX Human; pain; neuronal tissue; gene therapy;
KM spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR MPI; 2003-268312/26.
DR GENBANK; P05455.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page: 1017pp; English:

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of

CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX

SQL Sequence 408 AA; 76.0%; Score 76; DB 7; Length 408; Best Local Similarity 81.2%; Pred. No. 0.0022; Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 LDTKICEQIEYFGDF 18
|:|||||
DB 13 LEAKICHQIEYFGDF 28

RESULT 12
ADE62859
ID ADE62859 standard; protein; 408 AA.
AC ADE62859;
DT 29-JAN-2004 (first entry)
XX Human Protein P05455, SEQ ID NO 8793.
DE
XX Human; pain; neuronal tissue; gene therapy;
KM spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR MPI; 2003-268312/26.
DR GENBANK; P05455.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page: 1017pp; English:

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more

RESULT 9
 ADE63991
 ID ADE63991 standard; protein; 408 AA.
 AC ADE63991;
 XX
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein P05455, SEQ ID NO 9937.
 XX
 XX Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX
 OS Homo sapiens.
 XX
 XX WO2003016475-A2.
 PN
 PD 27-FEB-2003.
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GENO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 PI Woolf C, D'urso D, Befort K, Costigan M;
 DR WPI; 2003-268312/26.
 DR GENBANK; P05455.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX Sequence 408 AA;
 XX
 Query Match 76.0%; Score 76; DB 7; Length 408;
 Best Local Similarity 81.2%; Pred. NO. 0.0022;
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 IPTKICEQLEYFGDF 18
 DB 13 LEAKICHOLEYFGDF 28
 RESULT 10
 ADD46272
 ID ADD46272 standard; protein; 408 AA.
 AC ADD46272;
 XX
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein P05455, SEQ ID NO 11947.
 XX
 XX Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX
 OS Homo sapiens.
 XX
 XX WO2003016475-A2.
 PN
 PD 27-FEB-2003.
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GENO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 PI Woolf C, D'urso D, Befort K, Costigan M;
 DR WPI; 2003-268312/26.
 DR GENBANK; P05455.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX

CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
CC sequences derived from the 5' ends of mRNAs and even in those cases where
CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
CC are also used in diagnostic, forensic, gene therapy and chromosome
CC mapping procedures. They are used to obtain upstream regulatory sequences
CC and to design expression and secretion vectors

XX Sequence 92 AA;

Query Match 76.0%; Score 76; DB 3; Length 92;

Best Local Similarity 81.2%; Pred. No. 0.00042; Mismatches 2; Indels 0; Gaps 0;

Qy 3 LDTKICEQIEYFGDF 18
|:|||||
Db 13 LEAKICHQIEYFGDF 28

RESULT 7
AAM03716
ID AAM03716 standard; protein; 408 AA.

XX AAM03716;
XX
XX
XX 25-MAR-2003 (revised)
XX 12-MAR-1997 (first entry)
XX
XX Human autoantigen Ia (SS-B).

XX Autoimmune disease; Ia autoantigen; Sjogren's syndrome;
XX systemic lupus erythematosus; diagnosis.

XX Homo sapiens.

XX US5541291-A.

XX 30-JUL-1996.

XX 27-MAY-1987; 87US-00054871.

XX 31-DEC-1984; 84US-00687908.

XX (UYDU-) UNITV DUKE.

XX Keene JD;

XX WPI; 1996-362015/36.

XX Auto-antigen U2-RNP, associated with severe polymyositis-scleroderma
XX overlap syndrome - useful for diagnosis and treatment of autoimmune
XX diseases.

XX Disclosure; Col 15-16; 21pp; English.

XX The human lupus antigen (Ia) is diagnostic for Sjogren's syndrome, as
XX well as occurring in systemic lupus erythematosus patients. The Ia protein
XX is clinically related to the Ro protein that is highly common among
XX autoimmune patients. Ia and Ro antigens sometimes reside on the same
XX cellular ribonucleoprotein particle; most Ia patients contain some Ro
XX antibodies and vice versa. Ia cDNA has been isolated from a human liver
XX library. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 408 AA;

Query Match 76.0%; Score 76; DB 2; Length 408;

Best Local Similarity 81.2%; Pred. No. 0.0022; Mismatches 2; Indels 0; Gaps 0;

Qy 3 LDTKICEQIEYFGDF 18
|:|||||
Db 13 LEAKICHQIEYFGDF 28

RESULT 8
ABP65252
ID ABP65252 standard; protein; 408 AA.

XX ABP65252;

XX 12-NOV-2002 (first entry)

XX Hypoxia-regulated protein #126.

XX Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy;
XX antiinflammatory; vulnerrary; gynecological; ophthalmological; vaccine;
XX hypoxia; tumorigenesis; angiogenesis; apoptosis; cancer;
XX ischaemic condition; reperfusion injury; retinopathy; neonatal stress;
XX preclapmsia; atherosclerosis; inflammatory condition; wound healing;
XX inflammation; erythropoiesis; hair loss; human.

XX Homo sapiens.

XX WO200246465-A2.

XX 13-JUN-2002.

XX 10-DEC-2001; 2001WO-GB005458.

XX 08-DEC-2000; 2000GB-00030076.

XX 08-FEB-2001; 2001GB-00003156.

XX 25-OCT-2001; 2001GB-00025666.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

XX White J, Mundy CR, Ward NR, Krige D, Kingman SM, Harris RA;

XX Rayner WN;

XX WPI; 2002-627238/67.

XX Identifying a gene involved in disease for treating hypoxia-regulated

XX conditions, comprises comparing the transcriptome/proteome of two cell

XX PT types under different conditions and identifying a differentially

XX regulated gene.

XX Claim 35; Page 425; 538pp; English.

XX The present invention relates to methods for identifying genes and

XX proteins that are implicated in a specific disease or physiological

XX condition. The method comprises comparing the transcriptome/proteome of a

XX specialised cell type implicated in a disease or condition with that of a

XX second specialised cell type, under two experimental conditions, and

XX identifying a gene that is differentially regulated in the two

XX specialised cell types under experimental conditions. ABV7873-ABV78116

XX and ABP65061-ABP65257 were identified using the methods of the invention.

XX The coding sequences and proteins are useful for treating a disease in a

XX patient, for manufacture of a medicament for treating hypoxia-regulated

XX conditions, and for regulating tumourigenesis, angiogenesis, apoptosis,

XX biological response to hypoxia conditions, or hypoxic-associated

XX pathology in a patient. The coding sequences and proteins are also useful

XX for monitoring the therapeutic treatment of a disease or physiological

XX condition, such as cancer, ischaemic conditions, reperfusion injury,

XX retinopathy, neonatal stress, preclapmsia, atherosclerosis, inflammatory

XX conditions, wound healing, inflammation, erythropoiesis or hair loss

XX Sequence 408 AA;

Query Match 76.0%; Score 76; DB 5; Length 408;

Best Local Similarity 81.2%; Pred. No. 0.0022; Mismatches 2; Indels 0; Gaps 0;

Qy 3 LDTKICEQIEYFGDF 18
|:|||||
Db 13 LEAKICHQIEYFGDF 28

KW internal ribosome entry site initiated translation; La antigen protein;
KM viral life cycle; antiviral therapy; pharmaceutical; veterinary;
KM agricultural; horticultural; virucide.
XX Unidentified.
XX OS
XX PN WO200283858-A2.
XX PD 24-OCT-2002.
XX PF 12-APR-2002; 2002WO-US011589.
XX PR 16-APR-2001; 2001US-00836073.
XX PA (UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.
XX PI Dasgupta A, Das S, Baidya N;
XX DR WPI; 2003-058634/05.
XX PT New compound containing acidic and aromatic amino acids, useful as
XX PR antiviral therapy in pharmaceutical, veterinary or
XX PT agricultural/horticultural applications.
XX PS Claim 1; Page 15; 19pp; English.
XX CC The present invention relates to peptides and methods of inhibiting the
XX CC replication of viruses that utilize internal ribosome entry site (IRES)
XX CC initiated translation, and/or inhibiting viruses that utilize the La
XX CC antigen protein (LAP) in any phase of their life cycle. The peptides of
XX CC the invention compete with LAP and inhibit the utilisation of various
XX CC biochemical and physiological functions of LAP required for a productive
XX CC life cycle. The methods and compositions are useful as antiviral therapy
XX CC in pharmaceutical, veterinary or agricultural/horticultural applications.
XX CC ABG72101-ABG72119 represent peptides useful as antiviral agents
XX SO Sequence 18 AA;
XX
XX Query Match 76.0%; Score 76; DB 6; Length 18;
XX Best Local Similarity 81.2%; Pred. No. 7e-05;
XX Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 LDTKICEQIEYFGDF 18
DB 3 LEAKICHQIEYFGDF 18
RESULT 5
ABG72114
ID ABG72114 standard; peptide; 18 AA.
XX AC
XX ABG72114;
XX DT 28-JAN-2003 (first entry)
XX DE Viral replication inhibiting peptide, BOVINE.
XX KM Viral replication inhibitor; IRES initiated translation; LAP;
XX KM internal ribosome entry site initiated translation; La antigen protein;
XX KM viral life cycle; antiviral therapy; pharmaceutical; veterinary;
XX KM agricultural; horticultural; virucide; bovine.
XX OS Bovinae.
XX PN WO200283858-A2.
XX PD 24-OCT-2002.
XX PF 12-APR-2002; 2002WO-US011589.
XX PR 16-APR-2001; 2001US-00836073.
XX PA (UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.

XX Dasgupta A, Das S, Baidya N;
XX DR WPI; 2003-058634/05.
XX PT New compound containing acidic and aromatic amino acids, useful as
XX PR antiviral therapy in pharmaceutical, veterinary or
XX PT agricultural/horticultural applications.
XX PS Disclosure; Page 6; 19pp; English.
XX CC The present invention relates to peptides and methods of inhibiting the
XX CC replication of viruses that utilize internal ribosome entry site (IRES)
XX CC initiated translation, and/or inhibiting viruses that utilize the La
XX CC antigen protein (LAP) in any phase of their life cycle. The peptides of
XX CC the invention compete with LAP and inhibit the utilisation of various
XX CC biochemical and physiological functions of LAP required for a productive
XX CC life cycle. The methods and compositions are useful as antiviral therapy
XX CC in pharmaceutical, veterinary or agricultural/horticultural applications.
XX CC ABG72101-ABG72119 represent peptides useful as antiviral agents
XX SO Sequence 18 AA;
XX
XX Query Match 76.0%; Score 76; DB 6; Length 18;
XX Best Local Similarity 81.2%; Pred. No. 7e-05;
XX Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 LDTKICEQIEYFGDF 18
DB 3 LEAKICHQIEYFGDF 18
RESULT 6
AAG01351
ID AAG01351 standard; protein; 92 AA.
XX AC
XX AAG01351;
XX DT 06-OCT-2000 (first entry)
XX DE Human secreted protein, SEQ ID NO: 5432.
XX KM Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX KM gene therapy; chromosome mapping.
XX OS Homo sapiens.
XX PN EP1033401-A2.
XX PD 06-SEP-2000.
XX PF 21-FEB-2000; 2000EP-00200610.
XX PR 26-FEB-1999; 99US-0122487P.
XX PA (GEST) GENSET.
XX PI Dumas Malne Edwards J, Duclert A, Giordano J;
XX DR WPI; 2000-500381/45.
XX DR N-PDB; AAC01357.
XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX PS Claim 13; SEQ ID NO 5432; 71pp + Sequence Listing; English.
XX CC The present sequence is a polypeptide encoded by one of a large number of
XX CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
XX CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
XX CC tissues. EST sequences usually correspond mainly to the 3' untranslated
XX CC region (UTR) of the mRNA because they are often obtained from oligo-dT

Query Match 100.0%; Score 100; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.3e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDLPKICEQIEYFGDF 18
 |||||
 DB 1 LDLPKICEQIEYFGDF 18

RESULT 2
 ABG72113
 ID ABG72113 standard; peptide; 17 AA.
 XX
 AC ABG72113;
 XX
 DT 28-JAN-2003 (first entry)
 XX
 DE Viral replication inhibiting peptide, MOUSE.
 XX
 KM Viral replication inhibitor; IRES initiated translation; LAP;
 KM internal ribosome entry site initiated translation; La antigen protein;
 KM viral life cycle; antiviral therapy; pharmaceutical; veterinary;
 KM agricultural; horticultural; virucide; mouse.
 XX
 OS Mus sp.
 XX
 PN WO200283858-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 12-APR-2002; 2002MO-US011589.
 XX
 PR 16-APR-2001; 2001US-00836073.
 XX
 PA (UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.
 XX
 PI Dasgupta A, Das S, Baidya N;
 XX
 DR WPI; 2003-058634/05.
 XX
 PT New compound containing acidic and aromatic amino acids, useful as
 PT antiviral therapy in pharmaceutical, veterinary or
 PT agricultural/horticultural applications.
 XX
 PS Claim 1; Page 15; 19pp; English.
 XX
 CC The present invention relates to peptides and methods of inhibiting the
 CC replication of viruses that utilize internal ribosome entry site (IRES)
 CC initiated translation, and/or inhibiting viruses that utilize the La
 CC antigen protein (LAP) in any phase of their life cycle. The peptides of
 CC the invention compete with LAP and inhibit the utilisation of various
 CC biochemical and physiological functions of LAP required for a productive
 CC life cycle. The methods and compositions are useful as antiviral therapy
 CC in pharmaceutical, veterinary or agricultural/horticultural applications.
 CC ABG72101-ABG72113 represent peptides useful as antiviral agents
 CC
 XX
 SQ Sequence 17 AA;
 XX

Query Match 76.0%; Score 76; DB 6; Length 17;
 Best Local Similarity 81.2%; Pred. No. 6.5e-05;
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 LDLPKICEQIEYFGDF 18
 |||||
 DB 2 LEAKICHOIEYFGDF 17

RESULT 3
 AAY52200
 ID AAY52200 standard; peptide; 18 AA.
 XX
 AC AAY52200;

XX
 DT 14-MAR-2000 (first entry)
 XX
 DE Human La autoantigen peptide (LAP).
 XX
 KM La autoantigen; LAP; internal ribosome entry site; IRES; translation;
 KM viral replication; IRNA; antiviral agent; picornavirus; flavivirus;
 KM coronavirus; hepatitis virus; rhadovirus; adenovirus; coxsackie virus;
 KM parainfluenza virus; poliovirus; rhinovirus; encephalomyocarditis virus;
 KM foot-and-mouth disease virus; echo virus; infectious bronchitis virus;
 KM vesicular stomatitis virus.
 XX
 OS Homo sapiens.
 XX
 PN WO9961613-A2.
 XX
 PD 02-DEC-1999.
 XX
 PF 21-MAY-1999; 99WO-US011281.
 XX
 PR 22-MAY-1998; 98US-0086527P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Das S, Dasgupta A;
 XX
 DR WPI; 2000-062712/05.
 XX
 PT New yeast inhibitory peptide useful for inhibiting viral protein
 PT translation and replication.
 XX
 PS Claim 5; Page 57; 81pp; English.
 XX
 CC This sequence is the La autoantigen binding domain (LAP). LAP is a
 CC cellular protein which binds to an internal ribosome entry site (IRES).
 CC The peptide is used to inhibit mRNA translation, viral protein
 CC translation or viral replication. Viral mRNA translation is initiated at
 CC the IRES and the LAP peptide prevents translation initiation factors from
 CC binding at the site. The peptide can be used alone or in combination with
 CC an inhibitor RNA (IRNA see A4245200). The LAP peptide is useful as an
 CC antiviral agent, which works through the inhibition of mRNA translation,
 CC especially viral RNA. Examples of viruses which can be inhibited are
 CC picornavirus, flavivirus, coronavirus, hepatitis A B or C viruses,
 CC rhadovirus, adenovirus, and parainfluenza virus, poliovirus, rhinovirus,
 CC coxsackie virus, encephalomyocarditis virus, foot-and-mouth disease
 CC virus, echo virus, hepatitis C virus, infectious bronchitis virus, duck
 CC and human hepatitis B virus, and vesicular stomatitis virus. The peptide
 CC also inhibits replication of the above viruses. The LAP peptide
 CC selectively inhibits viral protein translation, and is therefore not
 CC toxic to the host cell
 CC
 XX
 SQ Sequence 18 AA;
 XX

Query Match 76.0%; Score 76; DB 3; Length 18;
 Best Local Similarity 81.2%; Pred. No. 7e-05;
 Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 LDLPKICEQIEYFGDF 18
 |||||
 DB 3 LEAKICHOIEYFGDF 18

RESULT 4
 ABG72101
 ID ABG72101 standard; peptide; 18 AA.
 XX
 AC ABG72101;
 XX
 DT 28-JAN-2003 (first entry)
 XX
 DE Viral replication inhibiting peptide, LAP.
 XX
 KM Viral replication inhibitor; IRES initiated translation; LAP;

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OM protein - protein search, using sw model

Run on: September 10, 2004, 16:58:20 / Search time 56.3129 Seconds
(without alignments)
90.314 Million cell updates/sec

Title: US-09-836-073-15

Perfect score: 100

Sequence: 1 LDLPKICEQIEYFGDF 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : A_Geneseq_29Jan04:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100	100.0	18	6	ABG72115
2	76	76.0	17	6	ABG72113
3	76	76.0	18	3	AAV52200
4	76	76.0	18	6	ABG72101
5	76	76.0	18	6	ABG72114
6	76	76.0	92	3	AAAG01351
7	76	76.0	408	5	AAAG03716
8	76	76.0	408	5	ABP65252
9	76	76.0	408	7	ADP63991
10	76	76.0	408	7	ADDA6272
11	76	76.0	408	7	ADP63995
12	76	76.0	408	7	ADP62859
13	76	76.0	415	7	ADP63989
14	76	76.0	415	7	ADP63993
15	76	76.0	439	4	ABG08417
16	76	76.0	460	3	AAAB58987
17	76	76.0	460	5	ABP41511
18	76	76.0	460	5	ABG72102
19	72	72.0	18	6	ABG72104
20	70	70.0	18	6	ABG72109
21	68	68.0	18	6	ABG72111
22	68	68.0	18	6	ABG72112
23	67	67.0	18	6	ABG72110
24	65.5	65.5	19	6	ABG72116
25	65	65.0	18	6	ABG72103

26	65	65.0	21	2	AAAR43394	AAAR43394	Ia/SSB ep
27	64	64.0	18	6	ABG72105	ABG72105	Viral rep
28	61	61.0	18	6	ABG72107	ABG72107	Viral rep
29	60	60.0	18	6	ABG72108	ABG72108	Viral rep
30	55	55.0	18	6	ABG72117	ABG72117	Viral rep
31	54	54.0	16	6	ABG72119	ABG72119	Viral rep
32	54	54.0	381	6	ABU19009	ABU19009	Pathogen
33	54	54.0	391	6	ABM72091	ABM72091	Scaphyloc
34	53	53.0	411	6	ABP70526	ABP70526	Histone d
35	51	51.0	377	6	ABU743510	ABU743510	Protein e
36	48	48.0	390	4	ABP65316	ABP65316	Drosophila
37	47	47.0	913	3	AAAG47714	AAAG47714	Arabidops
38	47	47.0	923	3	AAAG47713	AAAG47713	Arabidops
39	47	47.0	993	3	AAAG47712	AAAG47712	Arabidops
40	46.5	46.5	412	5	AAU96342	AAU96342	Der HMW-m
41	46.5	46.5	462	5	AAU96341	AAU96341	Der HMW-m
42	46	46.0	491	5	ABP43683	ABP43683	FLJ11196
43	46	46.0	492	3	ABAB43110	ABAB43110	Human ORF
44	46	46.0	706	6	ABU18600	ABU18600	Protein e
45	45.0	45.0	18	6	ABG72106	ABG72106	Viral rep

ALIGNMENTS

RESULT 1	ABG72115	standard; peptide; 18 AA.
AC	ABG72115	
AC	ABG72115	
DT	28-JAN-2003	(first entry)
XX		
DE	Viral replication inhibiting peptide, XENOPUS.	
XX		
KW	Viral replication inhibitor; IRBS initiated translation; LAP;	
KW	internal ribosome entry site initiated translation; La antigen protein;	
KW	viral life cycle; antiviral therapy; pharmaceutical; veterinary;	
KW	agricultural; horticultural; viticulture; xenopus.	
XX		
OS	Xenopus sp.	
XX		
PN	WO200283858-A2.	
XX		
PD	24-OCT-2002.	
XX		
PF	12-APR-2002; 2002WO-US011589.	
XX		
PR	16-APR-2001; 2001US-00836073.	
XX		
PA	(UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.	
XX		
PI	Dasgupta A, Das S, Baidya N;	
XX		
DR	WPI; 2003-058634/05.	
XX		
PT	New compound containing acidic and aromatic amino acids, useful as	
PT	antiviral therapy in pharmaceutical, veterinary or	
PT	agricultural/horticultural applications.	
XX		
PS	Claim 1; Page 15; 19pp; English.	
XX		
CC	The present invention relates to peptides and methods of inhibiting the	
CC	replication of viruses that utilize internal ribosome entry site (IRES)	
CC	initiated translation, and/or inhibiting viruses that utilize the La	
CC	antigen protein (LAP) in any phase of their life cycle. The peptides of	
CC	the invention compete with LAP and inhibit the utilisation of various	
CC	biochemical and physiological functions of LAP required for a productive	
CC	life cycle. The methods and compositions are useful as antiviral therapy	
CC	in pharmaceutical, veterinary or agricultural/horticultural applications.	
CC	ABG72101-ABG72119 represent peptides useful as antiviral agents	
XX		
SO	Sequence 18 AA;	

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Mon Sep 13 09:36:11 2004

us-09-836-073-14.rapb

Page 5

Search completed: September 10, 2004, 18:11:55
Job time : 40.424 secs

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FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-10

Query Match          90.9%; Score 90; DB 9; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.8e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AALEAKICHQIEYYFGDF 18
Db      1 AALEAKICHQIEYYGDF 18

RESULT 12
US-09-836-073-16
; Sequence 16, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 16
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Rat
US-09-836-073-16

Query Match          89.4%; Score 88.5; DB 9; Length 19;
Best Local Similarity 94.7%; Pred. No. 5.1e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy      1 AALEAKICHQI EYYFGDF 18
Db      1 AALEAKICHQIEYYFGDF 19

RESULT 13
US-09-836-073-2
; Sequence 2, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
```

```
US-09-836-073-2

Query Match          87.9%; Score 87; DB 9; Length 18;
Best Local Similarity 88.9%; Pred. No. 8.2e-07;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AALEAKICHQIEYYFGDF 18
Db      1 AALEAKICHQIEYYFGDF 18

RESULT 14
US-09-836-073-3
; Sequence 3, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-3

Query Match          87.9%; Score 87; DB 9; Length 18;
Best Local Similarity 83.3%; Pred. No. 8.2e-07;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 AALEAKICHQIEYYFGDF 18
Db      1 AALQAKICHQIYYFGDF 18

RESULT 15
US-09-836-073-4
; Sequence 4, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-4

Query Match          87.9%; Score 87; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 EAKICHQIEYYFGDF 18
Db      4 EAKICHQIEYYFGDF 18
```

TYPE: PRT
ORGANISM: Homo sapiens
US-10-264-049-2643

Query Match 100.0%; Score 99; DB 15; Length 460;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEAKICHQIEYFGDF 18
| | | | | | | | | | | | | | | | | | | | | |
DB 63 ALEAKICHQIEYFGDF 80

RESULT 7

US-09-836-073-13
Sequence 13, Application US/09836073
Patent No. US20020173475A1
GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Balidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 17
TYPE: PRT
ORGANISM: Mouse
US-09-836-073-13

Query Match 96.0%; Score 95; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ALEAKICHQIEYFGDF 18
| | | | | | | | | | | | | | | | | | | | | |
DB 1 ALEAKICHQIEYFGDF 17

RESULT 8

US-09-836-073-9
Sequence 9, Application US/09836073
Patent No. US20020173475A1
GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Balidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 18
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-836-073-9

Query Match 93.9%; Score 93; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.3e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ALEAKICHQIEYFGDF 17
| | | | | | | | | | | | | | | | | | | | | |
DB 1 ALEAKICHQIEYFGDF 17

RESULT 9

US-09-836-073-11
Sequence 11, Application US/09836073
Patent No. US20020173475A1
GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Balidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 18
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-836-073-11

Query Match 91.9%; Score 91; DB 9; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.9e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALEAKICHQIEYFGDF 18
| | | | | | | | | | | | | | | | | | | | | |
DB 1 ALEAKICHQIEYFGDF 18

RESULT 10

US-09-836-073-12
Sequence 12, Application US/09836073
Patent No. US20020173475A1
GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Balidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 18
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-836-073-12

Query Match 91.9%; Score 91; DB 9; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.9e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALEAKICHQIEYFGDF 18
| | | | | | | | | | | | | | | | | | | | | |
DB 1 ALEAKICHQIEYFGDF 18

RESULT 11

US-09-836-073-10
Sequence 10, Application US/09836073
Patent No. US20020173475A1
GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Balidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION

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; APPLICANT: Bajda, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Bovine
US-09-836-073-14

Query Match          100.0%; Score 99; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 1,1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AALEAKICHQIEYFGDF 18
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Db      1 AALEAKICHQIEYFGDF 18

RESULT 3
US-10-170-385-477
; Sequence 477, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Bingley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingman, Susan Mary
; APPLICANT: Kirge, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 477
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-477

Query Match          100.0%; Score 99; DB 12; Length 408;
Best Local Similarity 100.0%; Pred. No. 2,5e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AALEAKICHQIEYFGDF 18
      |||
Db      11 AALEAKICHQIEYFGDF 28

RESULT 4
US-09-925-298-695
; Sequence 695, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103
; CURRENT APPLICATION NUMBER: US/09/925,298
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; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 695
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-298-695

Query Match          100.0%; Score 99; DB 12; Length 460;
Best Local Similarity 100.0%; Pred. No. 2,8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AALEAKICHQIEYFGDF 18
      |||
Db      63 AALEAKICHQIEYFGDF 80

RESULT 5
US-10-102-806-695
; Sequence 695, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 695
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-102-806-695

Query Match          100.0%; Score 99; DB 14; Length 460;
Best Local Similarity 100.0%; Pred. No. 2,8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AALEAKICHQIEYFGDF 18
      |||
Db      63 AALEAKICHQIEYFGDF 80

RESULT 6
US-10-264-049-2643
; Sequence 2643, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2643
; LENGTH: 460
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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:52:06; Search time 40.324 Seconds

(without alignments)
143.151 Million cell updates/sec

Title: US-09-836-073-14

Perfect score: 99

Sequence: 1 AALEAKICHOIEYFGDF 18

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Maximum Match 100%

Listing first 45 summaries

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17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	99	100.0	18	US-09-836-073-1	Sequence 1, Appli
2	99	100.0	18	US-09-836-073-14	Sequence 14, Appli
3	99	100.0	408	US-10-170-385-477	Sequence 477, App
4	99	100.0	460	US-09-925-298-695	Sequence 695, App
5	99	100.0	460	US-10-102-806-695	Sequence 695, App
6	99	100.0	460	US-10-264-049-2643	Sequence 2643, Ap
7	95	96.0	17	US-09-836-073-13	Sequence 13, Appli
8	93	96.0	18	US-09-836-073-9	Sequence 9, Appli
9	91	91.9	18	US-09-836-073-11	Sequence 11, Appli
10	91	91.9	18	US-09-836-073-12	Sequence 12, Appli
11	90	90.9	18	US-09-836-073-10	Sequence 10, Appli
12	88.5	89.4	19	US-09-836-073-16	Sequence 16, Appli
13	87	87.9	18	US-09-836-073-2	Sequence 2, Appli
14	87	87.9	18	US-09-836-073-3	Sequence 3, Appli
15	87	87.9	18	US-09-836-073-4	Sequence 4, Appli

16	84.8	84.8	18	US-09-836-073-7	Sequence 7, Appli
17	83	83.8	18	US-09-836-073-8	Sequence 8, Appli
18	76	76.8	18	US-09-836-073-15	Sequence 15, Appli
19	75	75.8	18	US-09-836-073-5	Sequence 5, Appli
20	73	73.7	21	US-10-376-121A-20	Sequence 20, Appli
21	68	68.7	18	US-09-836-073-6	Sequence 6, Appli
22	68	68.7	18	US-10-325-810-214	Sequence 214, App
23	59	59.6	38	US-09-843-676-25	Sequence 25, Appli
24	59	59.6	38	US-09-766-253-25	Sequence 25, Appli
25	59	59.6	38	US-09-438-486-25	Sequence 25, Appli
26	59	59.6	38	US-10-325-810-215	Sequence 215, App
27	59	59.6	38	US-10-053-758-25	Sequence 25, Appli
28	59	59.6	38	US-10-054-295-25	Sequence 25, Appli
29	59	59.6	38	US-10-054-611-25	Sequence 25, Appli
30	58.5	59.1	37	US-09-843-676-24	Sequence 24, Appli
31	58.5	59.1	37	US-09-766-253-24	Sequence 24, Appli
32	58.5	59.1	37	US-09-438-486-24	Sequence 24, Appli
33	58.5	59.1	37	US-10-053-758-24	Sequence 24, Appli
34	58.5	59.1	37	US-10-054-295-24	Sequence 24, Appli
35	58.5	59.1	37	US-10-054-611-24	Sequence 24, Appli
36	57	57.6	16	US-09-836-073-19	Sequence 19, Appli
37	53	53.5	922	US-10-437-963-125036	Sequence 125036, Sequence 128072,
38	52	52.5	420	US-10-437-963-128072	Sequence 254661,
39	50	50.5	143	US-10-424-559-254661	Sequence 254664,
40	50	50.5	395	US-10-424-559-254664	Sequence 8, Appli
41	50	50.5	411	US-10-177-478-8	Sequence 26, Appli
42	48	48.5	39	US-09-843-676-26	Sequence 26, Appli
43	48	48.5	39	US-09-766-253-26	Sequence 26, Appli
44	48	48.5	39	US-09-438-486-26	Sequence 26, Appli
45	48	48.5	39	US-10-325-810-216	Sequence 216, App

ALIGNMENTS

RESULT 1
US-09-836-073-1
; Sequence 1, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-1

Query Match 100.0%; Score 99; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AALEAKICHOIEYFGDF 18
DB 1 AALEAKICHOIEYFGDF 18

RESULT 2
US-09-836-073-14
; Sequence 14, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-854-050-24

Query Match 59.1%; Score 58.5; DB 3; Length 37;
Best Local Similarity 91.7%; Pred. No. 0.0075;
Matches 11; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 7 ICHQIEYFGDF 18
Db 1 ICHQ-EYFGDF 11

RESULT 15
US-09-430-323-24
Sequence 24, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Langner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: NO. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-430-323-24

Query Match 59.1%; Score 58.5; DB 4; Length 37;
Best Local Similarity 91.7%; Pred. No. 0.0075;
Matches 11; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 7 ICHQIEYFGDF 18
Db 1 ICHQ-EYFGDF 11

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FILED DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 215:
US-09-721-456-215

Query Match 59.6%; Score 59; DB 4; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.0064; 1;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ICHQIEYFGD 17
DB 1 ICEQIEYFGD 11

RESULT 13
US-08-851-843A-24
Sequence 24, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017

FILED DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-851-843A-24

Query Match 59.1%; Score 58.5; DB 3; Length 37;
Best Local Similarity 91.7%; Pred. No. 0.0075; 1;
Matches 11; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 7 ICHQIEYFGD 18
DB 1 ICHQ-EYFGDF 11

RESULT 14
US-08-854-050-24
Sequence 24, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536

FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-430-323-25

Query Match 59.6%; Score 59; DB 4; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.0064;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ICHOIEYFFGD 17
Db 1 ICEQIEYFFGD 11

RESULT 11
US-09-402-181B-215
Sequence 215, Application US/09402181B
Patent No. 6610839
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhub, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 215:
US-09-402-181B-215

Query Match 59.6%; Score 59; DB 4; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.0064;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ICHOIEYFFGD 17
Db 1 ICEQIEYFFGD 11

RESULT 12
US-09-721-456-215
Sequence 215, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017

FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-215

Query Match 59.6%; Score 59; DB 3; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.0064;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ICHQIEYYFGD 17
DB 1 ICEQIEYYFGD 11

RESULT 9
US-08-854-050-25
Sequence 25, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-854-050-25

Query Match 59.6%; Score 59; DB 3; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.0064;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ICHQIEYYFGD 17
DB 1 ICEQIEYYFGD 11

RESULT 10
US-09-430-323-25
Sequence 25, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843

FILED DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-721-456-214

Query Match 68.7%; Score 68; DB 4; Length 38;
Best Local Similarity 91.7%; Pred. No. 0.00022;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ICHQIEYFFGDF 18
Db 1 ICHQIEYFFGDF 12

RESULT 7
US-08-851-843A-25
Sequence 25, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Hatley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-851-843A-25

Query Match 59.6%; Score 59; DB 3; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.0064;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ICHQIEYFFGDF 17
Db 1 ICHQIEYFFGDF 11

RESULT 8
US-08-974-549A-215
Sequence 215, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Hatley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050

APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-214

Query Match 68.7%; Score 68; DB 3; Length 38;
Best Local Similarity 91.7%; Pred. No. 0.00022;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ICHQIEYYFGDF 18
||| |||||
Db 1 ICHQIEYYFGDF 12

RESULT 5
US-09-402-181B-214
Sequence 214, Application US/09402181B
Patent No. 6610839
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Auserhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-402-181B-214

Query Match 68.7%; Score 68; DB 4; Length 38;
Best Local Similarity 91.7%; Pred. No. 0.00022;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ICHQIEYYFGDF 18
||| |||||
Db 1 ICHQIEYYFGDF 12

RESULT 6
US-09-721-456-214
Sequence 214, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-NOV-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312

PRIOR FILING DATE: 1997-10-06
PRIOR APPLICATION NUMBER: 08/321,427
PRIOR FILING DATE: 1994-10-11
PRIOR APPLICATION NUMBER: 60/086,527
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 4
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: B-LAP
US-09-316-630-4

Query Match 100.0%; Score 99; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.5e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AALEAKICHQIEYFGDF 18
DB 1 AALEAKICHQIEYFGDF 18

RESULT 3
US-08-475-955-20
Sequence 20, Application US/08475955
Patent No. 6641813
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patricia L. Pabst
STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,955
FILING DATE: June 7, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patricia L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF14CIP(2) DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Binding-site
LOCATION: 8..15
US-08-475-955-20

Query Match 73.7%; Score 73; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 ICHOIEYFGDF 18
DB 1 ICHOIEYFGDF 12

RESULT 4
US-08-974-549A-214
Sequence 214, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:

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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:43:01; Search time 15.8883 Seconds

(without alignments)
58.488 Million cell updates/sec

Title: US-09-836-073-14

Perfect score: 99

Sequence: 1 AALEAKICHOIEYFGDF 18

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	99	100.0	18	3	US-09-316-630-3	Sequence 3, Appl1
2	99	100.0	18	3	US-09-316-630-4	Sequence 4, Appl1
3	73	73.7	21	4	US-08-475-955-20	Sequence 20, Appl1
4	68	68.7	38	3	US-08-974-549A-214	Sequence 214, App
5	68	68.7	38	4	US-09-402-181B-214	Sequence 214, App
6	68	68.7	38	4	US-09-721-456-214	Sequence 214, App
7	59	59.6	38	3	US-08-851-843A-25	Sequence 25, Appl
8	59	59.6	38	3	US-08-974-549A-215	Sequence 215, Appl
9	59	59.6	38	3	US-08-854-050-25	Sequence 25, Appl
10	59	59.6	38	4	US-09-430-323-25	Sequence 25, Appl
11	59	59.6	38	4	US-09-402-181B-215	Sequence 215, App
12	59	59.6	38	4	US-09-721-456-215	Sequence 215, App
13	58.5	59.1	37	3	US-08-851-843A-24	Sequence 24, Appl
14	58.5	59.1	37	3	US-08-854-050-24	Sequence 24, Appl
15	58.5	59.1	37	4	US-09-430-323-24	Sequence 24, Appl
16	48	48.5	39	3	US-08-851-843A-26	Sequence 26, Appl
17	48	48.5	39	3	US-08-974-549A-216	Sequence 216, App
18	48	48.5	39	3	US-08-854-050-26	Sequence 26, Appl
19	48	48.5	39	4	US-09-430-323-26	Sequence 26, Appl
20	48	48.5	39	4	US-09-402-181B-216	Sequence 216, App
21	48	48.5	39	4	US-09-721-456-216	Sequence 216, App
22	42	42.4	456	1	US-08-205-719-4	Sequence 4, Appl1
23	42	42.4	456	3	US-08-431-517F-6	Sequence 6, Appl1
24	42	42.4	482	3	US-08-431-517F-5	Sequence 5, Appl1
25	42	42.4	482	6	5245013-2	Patent No. 5245013
26	41.5	41.9	124	4	US-09-489-039A-9103	Sequence 9103, Ap
27	41	41.4	483	3	US-09-027-166-7	Sequence 7, Appl1

28	41	41.4	497	4	US-09-489-039A-8926	Sequence 8926, Ap
29	41	41.4	1220	2	US-08-680-326-38	Sequence 38, Appl
30	41	41.4	431	1	US-08-311-023-2	Sequence 2, Appl1
31	40	40.4	593	4	US-09-252-991A-23340	Sequence 23340, A
32	40	40.4	868	4	US-09-800-729-106	Sequence 106, App
33	40	40.4	921	4	US-09-800-729-199	Sequence 199, App
34	39	39.4	69	4	US-09-621-976-7385	Sequence 7385, Ap
35	39	39.4	582	4	US-09-976-594-733	Sequence 733, App
36	39	39.4	754	2	US-08-941-262-1	Sequence 1, Appl1
37	39	39.4	755	2	US-08-941-262-3	Sequence 3, Appl1
38	39	39.4	811	4	US-09-199-617A-93	Sequence 93, Appl
39	39	39.4	812	1	US-08-248-628A-1	Sequence 1, Appl1
40	39	39.4	812	1	US-08-451-932-1	Sequence 1, Appl1
41	39	39.4	812	1	US-08-452-260-1	Sequence 1, Appl1
42	39	39.4	812	1	US-08-326-785-1	Sequence 1, Appl1
43	39	39.4	812	2	US-08-612-788-1	Sequence 1, Appl1
44	39	39.4	812	2	US-08-605-598B-1	Sequence 1, Appl1
45	39	39.4	812	2	US-08-423-743-1	Sequence 1, Appl1

ALIGNMENTS

```
RESULT 1
US-09-316-630-3
; Sequence 3, Application US/09316630
; Patent No. 6291637
; GENERAL INFORMATION:
; APPLICANT: Das, Saumitra
; TITLE OF INVENTION: INTERFERENCE WITH VIRAL IRES-MEDIATED TRANSLATION BY A
; FILE REFERENCE: 22000-20548-21
; CURRENT APPLICATION NUMBER: US/09/316,630
; PRIOR FILING DATE: 1997-05-21
; PRIOR APPLICATION NUMBER: 08/817,953
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 08/321,427
; PRIOR FILING DATE: 1994-10-11
; PRIOR APPLICATION NUMBER: 60/086,527
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LAP
US-09-316-630-3
Query Match          100.0%; Score 99; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.5e-10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB          1 AALEAKICHOIEYFGDF 18
          1 AALEAKICHOIEYFGDF 18
RESULT 2
US-09-316-630-4
; Sequence 4, Application US/09316630
; Patent No. 6291637
; GENERAL INFORMATION:
; APPLICANT: Das, Saumitra
; TITLE OF INVENTION: INTERFERENCE WITH VIRAL IRES-MEDIATED TRANSLATION BY A
; FILE REFERENCE: 22000-20548-21
; CURRENT APPLICATION NUMBER: US/09/316,630
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 08/817,953
```

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KM		multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW		cardiovascular disorder; wound healing; neurological disease.
XX		
OS	Homo sapiens.	
XX		
FN	WO20055173-A1.	
XX		
PD	21-SEP-2000.	
XX		
PF	08-MAR-2000; 2000WO-US005881.	
XX		
PR	12-MAR-1999; 99US-0124270P.	
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
PI	Rosen CA, Ruben SM;	
XX		
DR	WPI; 2000-611515/58.	
XX	N-PsDB; AAF21890.	
PT	New human breast and ovarian cancer associated gene sequences and the	
PT	polypeptides encoded by these genes, useful in the prevention, treatment	
PT	and diagnosis of cancer, immune disorders, cardiovascular disorders and	
PT	neurological diseases.	
XX		
PS	Claim 11; Page 1149-111150; 12999p; English.	
XX		
CC	Sequences AAF1614 - AAF22031 represent DNA sequences encoding human	
CC	proteins AAB5711 - AAB59128. The DNA and protein sequences are	
CC	associated with breast and ovarian cancer. Included in the invention are	
CC	sequences AAF22032 - AAF22040 and AAB59129 which are used in the	
CC	isolation and characterisation of the DNA and protein sequences of the	
CC	invention. The breast and ovarian cancer associated DNA, protein, agonist	
CC	or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic;	
CC	neuroprotective; antiviral; antiallergic; hepatotrophic; antidiabetic;	
CC	antiinflammatory; antiviral; vulnerable; anticonvulsant; antibacterial;	
CC	antifungal; antiparasitic and cardiant activity. The polynucleotide and	
CC	protein sequences are used in the diagnosis of cancer, particularly	
CC	breast and ovarian cancer. The nucleic acid sequences, proteins, agonists	
CC	and agonists may also be used in the diagnosis, prevention and treatment	
CC	of immune disorders e.g. Addison's disease, allergies, autoimmune	
CC	haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's	
CC	disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;	
CC	cardiovascular disorders such as myocardial ischaemia; wound healing;	
CC	neurological diseases such as cerebral anoxia and epilepsy; and	
CC	infectious diseases	
XX		
SQ	Sequence 460 AA;	
	Query Match 100.0%; Score 99; DB 3; Length 460;	
	Best Local Similarity 100.0%; Pred. No. 3.2e-07;	
	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
Qy	1 AALEAKICHQIEYFGDF 18 	
Db	63 AALEAKICHQIEYFGDF 80	
RESULT 15		
ABP41511		
ID	ABP41511 standard; protein; 460 AA.	
AC	ABP41511;	
XX		
DT	22-AUG-2002 (first entry)	
XX		
DE	Human ovarian antigen HVVAF56, SEQ ID NO:2643.	
XX		
KW	Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;	
KW	ovarian cancer; breast cancer; tumour; reproductive system disorder;	
KW	infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;	
KW	PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;	
KW	inflammatory condition; immune disorder; blood disorder;	

KM cardiovascular disorder; respiratory disorder; neurological disorder;
KM gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
XX antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KM antiinflammatory; gynaecological; reproductive.
XX
OS Homo sapiens.
XX
PN WO200200677-A1.
XX
PD 03-JAN-2002.
XX
PF 07-JUN-2001; 2001WO-US018569.
XX
PR 07-JUN-2000; 2000US-0209467P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Birse CE, Rosen CA;
XX
DR WPI; 2002-147878/19..
XX
N-PSTDB; ABQ54588.
XX
PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
PT cancer), immune disorders, cardiovascular disorders and neurological
PT diseases.
XX
XX Claim 11; SEQ ID NO 2643; 2922pp; English.

The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 460 AA;

Query Match	100.0%; Score 99; DB 5; Length 460;
Best Local Similarity	100.0%; Pred. NO. 3.2e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

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QY      1 AALEAKICHQIEYYFGDF 18
        |||EEEE|||
Db      63 AALEAKICHQIEYYFGDF 80

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XX 14-AUG-2002; 2002WO-US025765.
PF 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M,
PI WPI: 2003-268312/26.
XX GENBANK; P38656.
DR
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 415 AA;
SQ
Query Match 100.0%; Score 99; DB 7; Length 415;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AALEAKICHOIEYFGDF 18
DB 11 AALEAKICHOIEYFGDF 28
RESULT 13
ABG08417
ID ABG08417 standard; protein; 439 AA.
XX
XX ABG08417;
AC
XX
XX 13-FEB-2002 (first entry)
DT
XX
XX Novel human diagnostic protein #8408.
DE
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.

XX
PN WO200175067-A2.
XX
XX 11-OCT-2001.
PD
XX
XX 30-MAR-2001; 2001WO-US008631.
PF
XX
XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
PA
XX
XX Drmanac RT, Liu C, Tang YT;
PI WPI: 2001-639362/73.
XX N-PSDB; AAS72604.
DR
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 20; SEQ ID NO 38776; 103pp; English.
PS
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 439 AA;
SQ
Query Match 100.0%; Score 99; DB 4; Length 439;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AALEAKICHOIEYFGDF 18
DB 41 AALEAKICHOIEYFGDF 58
RESULT 14
AAB58987
ID AAB58987 standard; protein; 460 AA.
XX
XX AAB58987;
AC
XX
XX 27-MAR-2001 (first entry)
DT
XX
XX Breast and ovarian cancer associated antigen protein sequence SEQ ID 695.
DE
XX
XX Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW neutropenic; neuroprotective; antiviral; antiallergic; hepatocytic;
KW antidiabetic; antiinflammatory; anticancer; vulnerary; anticonvulsant;
KW antibacterial; antifungal; antiparasitic; cardiac; immune disorder;
KW Addison's disease; allergy; autoimmune haemolytic anaemia;
KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease.

PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI, 2003-268312/26.
DR GENBANK, P05455.
XX
PT New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
PS Claim 1, Page: 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
CC
XX
SQ Sequence 408 AA;
Query Match 100.0%; Score 99; DB 7; Length 408;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AALEAKICHQIEYYFGDF 18
DB 11 AALEAKICHQIEYYFGDF 28
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ADE63989
ID ADE63989 standard; protein; 415 AA.
XX
AC ADE63989;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein P38656, SEQ ID NO 9935.
XX
KM Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
PI WPI, 2003-268312/26.
DR GENBANK, P38656.
XX
PT New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
PS Claim 1, Page: 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
CC
XX
SQ Sequence 415 AA;
Query Match 100.0%; Score 99; DB 7; Length 415;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AALEAKICHQIEYYFGDF 18
DB 11 AALEAKICHQIEYYFGDF 28
RESULT 12
ADE63993
ID ADE63993 standard; protein; 415 AA.
XX
AC ADE63993;
XX
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein P38656, SEQ ID NO 9939.
XX
KM Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
OS Rattus norvegicus.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.

PS Claim 1, Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 408 AA;

Query Match 100.0%; Score 99; DB 7; Length 408;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AALEAKICHOIEYFGDF 18
| | | | | | | | | | | | | | | | | | | | | |
DB 11 AALEAKICHOIEYFGDF 28

RESULT 9
ADE63995
ID ADE63995 standard; protein; 408 AA.

AC ADE63995;

DT 29-JAN-2004 (first entry)

DE Human Protein P05455, SEQ ID NO 9941.

XX Human; pain; neuronal tissue; gene therapy;
KM spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.

OS Homo sapiens.

PN WO2003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

PA (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR

DR GENBANK; P05455.

XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.

PS Claim 1, Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

SO Sequence 408 AA;

Query Match 100.0%; Score 99; DB 7; Length 408;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AALEAKICHOIEYFGDF 18
| | | | | | | | | | | | | | | | | | | | | |
DB 11 AALEAKICHOIEYFGDF 28

RESULT 10
ADE62859
ID ADE62859 standard; protein; 408 AA.

AC ADE62859;

DT 29-JAN-2004 (first entry)

DE Human Protein P05455, SEQ ID NO 8793.

XX Human; pain; neuronal tissue; gene therapy;
KM spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.

OS Homo sapiens.

PN WO2003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

PA (GEHO) GEN HOSPITAL CORP.

PS Claim 35; Page 425; 538pp; English.

XX The present invention relates to methods for identifying genes and
CC proteins that are implicated in a specific disease or physiological
CC condition. The method comprises comparing the transcriptome/proteome of a
CC specialised cell type implicated in a disease or condition with that of a
CC second specialised cell type, under two experimental conditions, and
CC identifying a gene that is differentially regulated in the two
CC specialised cell types under experimental conditions. ABV77873-ABV78116
CC and ABP65061-ABP65257 were identified using the methods of the invention.
CC The coding sequences and proteins are useful for treating a disease in a
CC patient, for manufacture of a medicament for treating hypoxia-regulated
CC conditions, and for regulating tumorigenesis, angiogenesis, apoptosis,
CC biological response to hypoxia conditions, or hypoxic-associated
CC pathology in a patient. The coding sequences and proteins are also useful
CC for monitoring the therapeutic treatment of a disease or physiological
CC condition, such as cancer, ischemic conditions, reperfusion injury,
CC retinopathy, neonatal stress, pre-eclampsia, atherosclerosis, inflammatory
CC conditions, wound healing, inflammation, erythropoiesis or hair loss

XX Sequence 408 AA;

SO

Query Match 100.0%; Score 99; DB 5; Length 408;
Best Local Similarity 100.0%; Pred. No. 2,8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AALEAKICHQIEYFGDF 18
|||
DB 11 AALEAKICHQIEYFGDF 28

RESULT 7
ADE63991
ID ADE63991 standard; protein; 408 AA.
XX
AC ADE63991;
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P05455, SEQ ID NO 9937.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P05455.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also

CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC- which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (SNI), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 408 AA;

SO

Query Match 100.0%; Score 99; DB 7; Length 408;
Best Local Similarity 100.0%; Pred. No. 2,8e-07;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AALEAKICHQIEYFGDF 18
|||
DB 11 AALEAKICHQIEYFGDF 28

RESULT 8
ADD46272
ID ADD46272 standard; protein; 408 AA.
XX
AC ADD46272;
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P05455, SEQ ID NO 11947.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GHEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P05455.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX

KW gene therapy; chromosome mapping.
 XX
 OS Homo sapiens.
 XX
 PN EP1033401-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 21-FEB-2000; 2000EP-00200610.
 XX
 PR 26-FEB-1999; 99US-0122487P.
 XX
 PA (GSEST) GENSEST.
 XX
 PI Dumas Milne Edwards J, Duclert A, Giordano J;
 XX
 DR WPI; 2000-500381/45.
 DR N-PSDB; AAC01357.
 XX
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX
 PS Claim 13; SEQ ID NO 5432; 71bp + Sequence Listing; English.
 XX
 CC The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors
 XX
 SQ Sequence 92 AA;
 XX
 Query Match 100.0%; Score 99; DB 3; Length 92;
 Best Local Similarity 100.0%; Pred. No. 5.8e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 AALEAKICHQIEYFGDF 18
 |||
 11 AALEAKICHQIEYFGDF 28
 DB
 RESULT 5
 AAM03716
 ID AAM03716 standard; protein; 408 AA.
 XX
 AC AAM03716;
 XX
 DT 25-MAR-2003 (revised)
 DT 12-MAR-1997 (first entry)
 XX
 DE Human autoantigen Ia(SS-B).
 XX
 KW Autoimmune disease; Ia autoantigen; Sjogren's syndrome;
 KW systemic lupus erythematosus; diagnosis.
 XX
 OS Homo sapiens.
 OS
 PN USS541291-A.
 XX
 PD 30-JUL-1996.
 PD
 PF 27-MAY-1987; 87US-00054871.
 PF
 PT 31-DEC-1984; 84US-00687908.
 PT
 XX

XX
 PA (UYDU-) UNIV DUKE.
 XX
 PI Keene JD;
 XX
 DR WPI; 1996-362015/36.
 XX
 PT Auto-antigen U2-RNP, associated with severe polymyositis-scleroderma
 PT overlap syndrome - useful for diagnosis and treatment of autoimmune
 PT diseases.
 XX
 PS Disclosure; Col 15-16; 21pp; English.
 XX
 CC The human lupus antigen (Ia) is diagnostic for Sjogren's syndrome, as
 CC well as occurring in systemic lupus erythematosus patients. The Ia protein
 CC is clinically related to the Ro protein that is highly common among
 CC autoimmune patients. Ia and Ro antigens sometimes reside on the same
 CC cellular ribonucleoprotein particle; most Ia patients contain some Ro
 CC antibodies and vice versa. Ia cDNA has been isolated from a human liver
 CC library. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 408 AA;
 XX
 Query Match 100.0%; Score 99; DB 2; Length 408;
 Best Local Similarity 100.0%; Pred. No. 2.8e-07;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 QY 1 AALEAKICHQIEYFGDF 18
 |||
 11 AALEAKICHQIEYFGDF 28
 DB
 RESULT 6
 ABP65252
 ID ABP65252 standard; protein; 408 AA.
 XX
 AC ABP65252;
 XX
 DT 12-NOV-2002 (first entry)
 XX
 DE Hypoxia-regulated protein #126.
 XX
 KW Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy;
 KW antiinflammatory; vulnereary; gynecological; ophthalmological; vaccine;
 KW hypoxia; tumourigenesis; angiogenesis; apoptosis; cancer;
 KW ischaemic condition; reperfusion injury; retinopathy; neonatal stress;
 KW preclapmsia; atherosclerosis; inflammatory condition; wound healing;
 KW inflammation; erythropoiesis; hair loss; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200246465-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 10-DEC-2001; 2001WO-GB005458.
 XX
 PR 08-DEC-2000; 2000GB-00030076.
 PR 08-FEB-2001; 2001GB-00003156.
 PR 25-OCT-2001; 2001GB-00025666.
 XX
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.
 XX
 PI White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;
 PI Rayner WN;
 XX
 DR WPI; 2002-627238/67.
 XX
 PT Identifying a gene involved in disease for treating hypoxia-regulated
 PT conditions, comprises comparing the transcriptome/proteome of two cell
 PT types under different conditions and identifying a differentially
 PT regulated gene.
 XX

CC rhabdovirus, adenovirus, and parainfluenza virus, poliovirus, rhinovirus,
 CC coxsackie virus, encephalomyocarditis virus, foot-and-mouth disease
 CC virus, echo virus, hepatitis C virus, infectious bronchitis virus, duck
 CC and human hepatitis B virus, and vesicular stomatitis virus. The peptide
 CC also inhibits replication of the above viruses. The LAP peptide
 CC selectively inhibits viral protein translation, and is therefore not
 CC toxic to the host cell

XX Sequence 18 AA;

Query Match 100.0%; Score 99; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AALEAKICHQIEYFGDF 18
 Db 1 AALEAKICHQIEYFGDF 18

RESULT 2
 ABG72101
 ID ABG72101 standard; peptide; 18 AA.

XX AC ABG72101;

DT 28-JAN-2003 (first entry)

XX Viral replication inhibiting peptide, LAP.

XX Viral replication inhibitor; IRES initiated translation; LAP;
 KM internal ribosome entry site initiated translation; La antigen protein;
 KM viral life cycle; antiviral therapy; pharmaceutical; veterinary;
 KM agricultural; horticultural; virucide.

XX Unidentified.

XX WO200283858-A2.

XX PD 24-OCT-2002.

XX PF 12-APR-2002; 2002WO-US011589.

XX BR 16-APR-2001; 2001US-00836073.

XX PA (UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.

XX PI Dasgupta A, Das S, Baidya N;

XX WPI; 2003-058634/05.

XX New compound containing acidic and aromatic amino acids, useful as
 PT antiviral therapy in pharmaceutical, veterinary or
 PT agricultural/horticultural applications.

XX Claim 1; Page 15; 19pp; English.

XX The present invention relates to peptides and methods of inhibiting the
 CC replication of viruses that utilise internal ribosome entry site (IRES)
 CC initiated translation, and/or inhibiting viruses that utilise the La
 CC antigen protein (LAP) in any phase of their life cycle. The peptides of
 CC the invention compete with LAP and inhibit the utilisation of various
 CC biochemical and physiological functions of LAP required for a productive
 CC life cycle. The methods and compositions are useful as antiviral therapy
 CC in pharmaceutical, veterinary or agricultural/horticultural applications.
 CC ABG72101-ABG72119 represent peptides useful as antiviral agents

XX Sequence 18 AA;

Query Match 100.0%; Score 99; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AALEAKICHQIEYFGDF 18

Db 1 AALEAKICHQIEYFGDF 18

RESULT 3
 ABG72114
 ID ABG72114 standard; peptide; 18 AA.

XX AC ABG72114;

DT 28-JAN-2003 (first entry)

XX Viral replication inhibiting peptide, BOVINE.

XX Viral replication inhibitor; IRES initiated translation; LAP;
 KM internal ribosome entry site initiated translation; La antigen protein;
 KM viral life cycle; antiviral therapy; pharmaceutical; veterinary;
 KM agricultural; horticultural; virucide; bovine.

XX Bovinae.

XX WO200283858-A2.

XX PD 24-OCT-2002.

XX PF 12-APR-2002; 2002WO-US011589.

XX PR 16-APR-2001; 2001US-00836073.

XX PA (UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.

XX PI Dasgupta A, Das S, Baidya N;

XX WPI; 2003-058634/05.

XX New compound containing acidic and aromatic amino acids, useful as
 PT antiviral therapy in pharmaceutical, veterinary or
 PT agricultural/horticultural applications.

XX Disclosure; Page 6; 19pp; English.

XX The present invention relates to peptides and methods of inhibiting the
 CC replication of viruses that utilise internal ribosome entry site (IRES)
 CC initiated translation, and/or inhibiting viruses that utilise the La
 CC antigen protein (LAP) in any phase of their life cycle. The peptides of
 CC the invention compete with LAP and inhibit the utilisation of various
 CC biochemical and physiological functions of LAP required for a productive
 CC life cycle. The methods and compositions are useful as antiviral therapy
 CC in pharmaceutical, veterinary or agricultural/horticultural applications.
 CC ABG72101-ABG72119 represent peptides useful as antiviral agents

XX Sequence 18 AA;

Query Match 100.0%; Score 99; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AALEAKICHQIEYFGDF 18
 Db 1 AALEAKICHQIEYFGDF 18

RESULT 4
 AAG01351
 ID AAG01351 standard; protein; 92 AA.

XX AC AAG01351;

XX 06-OCT-2000 (first entry)

XX Human secreted protein, SEQ ID NO: 5432.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2004, 16:58:20 ; Search time 56.3129 Seconds
(without alignments)
90.314 Million cell updates/sec

Title: US-09-836-073-14

Perfect score: 99

Sequence: 1 AALFAKICHOIEYFGDF 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	99	100.0	18	3	AAY52200	Aay52200 Human la
2	99	100.0	18	6	ABG72101	Abg72101 Viral rep
3	99	100.0	18	6	ABG72114	Abg72114 Viral rep
4	99	100.0	92	3	AA601351	Aa601351 Human sec
5	99	100.0	408	2	AAW03716	Aaw03716 Human aut
6	99	100.0	408	5	ABP65252	Abp65252 Hypoxia-r
7	99	100.0	408	7	ADBE63991	Adbe63991 Human pro
8	99	100.0	408	7	ADDA6272	Adda6272 Human pro
9	99	100.0	408	7	ADBE63995	Adbe63995 Human pro
10	99	100.0	408	7	ADBE62859	Adbe62859 Human pro
11	99	100.0	415	7	ADBE63989	Adbe63989 Rat Prote
12	99	100.0	415	7	ADBE63993	Adbe63993 Rat Prote
13	99	100.0	439	4	ABG08417	Abg08417 Novel hum
14	99	100.0	460	3	AAB58987	Aab58987 Breast an
15	99	100.0	460	3	ABP41511	Abp41511 Human ova
16	95	96.0	17	6	ABG72113	Abg72113 Viral rep
17	93	93.9	18	6	ABG72109	Abg72109 Viral rep
18	91	91.9	18	6	ABG72111	Abg72111 Viral rep
19	91	91.9	18	6	ABG72112	Abg72112 Viral rep
20	90	90.9	18	6	ABG72110	Abg72110 Viral rep
21	88.5	89.4	19	6	ABG72116	Abg72116 Viral rep
22	87	87.9	18	6	ABG72102	Abg72102 Viral rep
23	87	87.9	18	6	ABG72103	Abg72103 Viral rep
24	87	87.9	18	6	ABG72104	Abg72104 Viral rep
25	84	84.8	18	6	ABG72107	Abg72107 Viral rep

26	83	83.8	18	6	ABG72108	Abg72108 Viral rep
27	76	76.8	18	6	ABG72115	Abg72115 Viral rep
28	75	75.8	18	6	ABG72105	Abg72105 Viral rep
29	73	73.7	21	2	AAR43394	Aar43394 La/SSB ep
30	68	68.7	18	6	ABG72106	Abg72106 Viral rep
31	57	57.6	16	6	ABG72119	Abg72119 Viral rep
32	51	51.5	390	4	ABE65316	Abbe5316 Drosophila
33	50	50.5	411	6	ABP70526	Abp70526 Histone d
34	49	49.5	381	6	ABJ19009	Abj19009 Pathogen
35	49	49.5	391	6	ABM72091	Abm72091 Staphyloc
36	48	48.5	913	3	AA647714	Aa647714 Arabidops
37	48	48.5	923	3	AA647712	Aa647712 Arabidops
38	48	48.5	993	3	AA647712	Aa647712 Arabidops
39	46	46.5	377	6	ABU43510	Abu43510 Protein e
40	44	44.4	18	6	ABG72117	Abg72117 Viral rep
41	44	44.4	135	4	ABG27058	Abg27058 Novel hum
42	44	44.4	224	5	ABR89645	Abbr89645 Human pol
43	44	44.4	224	6	AD55336	Ad55336 Human pro
44	43	43.4	176	4	AAU52458	Aau52458 Propionib
45	43	43.4	176	6	ABM48977	Abm48977 Propionib

ALIGNMENTS

RESULT 1	AA52200	standard; peptide; 18 AA.
ID	AA52200	standard; peptide; 18 AA.
AC	AA52200;	
DT	14-MAR-2000	(first entry)
XX	Human la autoantigen peptide (LAP).	
DE		
XX	La autoantigen; LAP, internal ribosome entry site; IRBS; translation; viral replication; RNA; antiviral agent; picornavirus; flavivirus; coronavirus; hepatitis virus; rhabdovirus; adenovirus; coxsackie virus; foot-and-mouth disease virus; poliovirus; rhinovirus; encephalomyocarditis virus; vesicular stomatitis virus.	
OS	Homo sapiens.	
PN	WO961613-A2.	
PD	02-DEC-1999.	
XX	21-MAY-1999; 99WO-US011281.	
PR	22-MAY-1998; 98US-0086527P.	
PA	(REGC) UNIV CALIFORNIA.	
PI	Das S, Dasgupta A;	
DR	WPI; 2000-062712/05.	
PT	New yeast inhibitory peptide useful for inhibiting viral protein translation and replication.	
PS	Claim 5; Page 57; 81pp; English.	
CC	This sequence is the la autoantigen binding domain (LAP). LAP is a cellular protein which binds to an internal ribosome entry site (IRBS). The peptide is used to inhibit mRNA translation, viral protein translation or viral replication. Viral mRNA translation is initiated at the IRBS and the LAP peptide prevents translation initiation factors from binding at the site. The peptide can be used alone or in combination with an inhibitor RNA (RNA see AA245200). The LAP peptide is useful as an antiviral agent, which works through the inhibition of mRNA translation, especially viral mRNA. Examples of viruses which can be inhibited are picornavirus, flavivirus, coronavirus, hepatitis A B or C viruses,	

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Mon Sep 13 09:36:10 2004

us-09-836-073-12.rapb

Page 5

Search completed: September 10, 2004, 18:11:55
Job time : 40.424 secs

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FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-11
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Query Match      85.6%; Score 83; DB 9; Length 18;
Best Local Similarity 88.9%; Pred. No. 1.9e-06;
Matches 16; Conservative 0; Mismatches 2; Indels 0;
```

```
Qy      1 AALEAKICHQIEYFGDF 18
      |||||
Db      1 AALEAKICHQIEYFGDF 18
```

```
RESULT 12
US-09-836-073-10
; Sequence 10, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-10
```

```
Query Match      84.5%; Score 82; DB 9; Length 18;
Best Local Similarity 88.9%; Pred. No. 2.7e-06;
Matches 16; Conservative 0; Mismatches 2; Indels 0;
```

```
Qy      1 AALEAKICHQIEYFGDF 18
      |||||
Db      1 AALEAKICHQIEYFGDF 18
```

```
RESULT 13
US-09-836-073-16
; Sequence 16, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Rat
```

```
US-09-836-073-16
```

```
Query Match      83.0%; Score 80.5; DB 9; Length 19;
Best Local Similarity 89.5%; Pred. No. 5e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
```

```
Qy      1 AALEAKICHQIEYFGDF 18
      |||||
Db      1 AALEAKICHQIEYFGDF 19
```

```
RESULT 14
US-09-836-073-2
; Sequence 2, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-2
```

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Query Match      81.4%; Score 79; DB 9; Length 18;
Best Local Similarity 83.3%; Pred. No. 8.2e-06;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy      1 AALEAKICHQIEYFGDF 18
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Db      1 AALEAKICHQIEYFGDF 18
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RESULT 15
US-09-836-073-3
; Sequence 3, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-3
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Query Match      81.4%; Score 79; DB 9; Length 18;
Best Local Similarity 77.8%; Pred. No. 8.2e-06;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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Qy      1 AALEAKICHQIEYFGDF 18
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Db      1 AALEAKICHQIEYFGDF 18
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-102-806-695

Query Match
Best Local Similarity 93.8%; Score 91; DB 14; Length 460;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AALEAKICHQIEYFGDF 18
Db 63 AALEAKICHQIEYFGDF 80

RESULT 7
US-10-264-049-2643
; Sequence 2643, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P413P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: Patentin Ver. 3.1
; SEQ ID NO 2643
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-2643

Query Match
Best Local Similarity 93.8%; Score 91; DB 15; Length 460;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AALEAKICHQIEYFGDF 18
Db 63 AALEAKICHQIEYFGDF 80

RESULT 8
US-09-836-073-8
; Sequence 8, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Balidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-836-073-8

Query Match
Best Local Similarity 91.8%; Score 89; DB 9; Length 18;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AALEAKICHQIEYFGDF 18
Db 1 AALEAKICHQIEYFGDF 18
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RESULT 9
US-09-836-073-13
; Sequence 13, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Balidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mouse
US-09-836-073-13

Query Match
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Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AALEAKICHQIEYFGDF 18
Db 1 AALEAKICHQIEYFGDF 17

RESULT 10
US-09-836-073-9
; Sequence 9, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Balidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-836-073-9

Query Match
Best Local Similarity 87.6%; Score 85; DB 9; Length 18;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AALEAKICHQIEYFGDF 17
Db 1 AALEAKICHQIEYFGDF 17

RESULT 11
US-09-836-073-11
; Sequence 11, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Balidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
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; APPLICANT: Baldeva, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-1
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Query Match          93.8%; Score 91; DB 9; Length 18;
Best Local Similarity 94.4%; Pred. No. 9.5e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AALEAKICHQIEYFGDF 18
Db 1 AALEAKICHQIEYFGDF 18

RESULT 3
US-09-836-073-14
; Sequence 14, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baldeva, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 14
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Bovine
US-09-836-073-14
;
Query Match          93.8%; Score 91; DB 9; Length 18;
Best Local Similarity 94.4%; Pred. No. 9.5e-08;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AALEAKICHQIEYFGDF 18
Db 1 AALEAKICHQIEYFGDF 18

RESULT 4
US-10-170-385-477
; Sequence 477, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
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; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 477
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-477
;
Query Match          93.8%; Score 91; DB 12; Length 408;
Best Local Similarity 94.4%; Pred. No. 2.4e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AALEAKICHQIEYFGDF 18
Db 11 AALEAKICHQIEYFGDF 28

RESULT 5
US-09-925-298-695
; Sequence 695, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103
; CURRENT APPLICATION NUMBER: US/09/925,298
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05861
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 695
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-298-695
;
Query Match          93.8%; Score 91; DB 12; Length 460;
Best Local Similarity 94.4%; Pred. No. 2.7e-06;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AALEAKICHQIEYFGDF 18
Db 63 AALEAKICHQIEYFGDF 80

RESULT 6
US-10-102-806-695
; Sequence 695, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05861
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 695
; LENGTH: 460
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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:52:06 ; Search time 40.324 Seconds

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Title: US-09-836-073-12

Sequence: 1 AALEAKICHQIEYFGDF 18

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Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0

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Maximum Match 100%

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Database : Published Applications AA.*

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3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	91	93.8	18	US-09-836-073-1	Sequence 1, Appl
3	91	93.8	18	US-09-836-073-14	Sequence 14, Appl
4	91	93.8	408	US-10-170-385-477	Sequence 477, App
5	91	93.8	460	US-09-925-298-695	Sequence 695, App
6	91	93.8	460	US-10-102-806-695	Sequence 695, App
7	91	93.8	460	US-10-264-049-2643	Sequence 2643, Ap
8	89	91.8	18	US-09-836-073-8	Sequence 8, Appl
9	87	89.7	17	US-09-836-073-13	Sequence 13, Appl
10	85	87.6	18	US-09-836-073-9	Sequence 9, Appl
11	85	85.6	18	US-09-836-073-11	Sequence 11, Appl
12	82	84.5	18	US-09-836-073-10	Sequence 10, Appl
13	80.5	83.0	19	US-09-836-073-16	Sequence 16, Appl
14	79	81.4	18	US-09-836-073-2	Sequence 2, Appl
15	79	81.4	18	US-09-836-073-3	Sequence 3, Appl

15	79	81.4	18	9	US-09-836-073-4	Sequence 4, Appl
17	76	78.4	18	9	US-09-836-073-7	Sequence 7, Appl
18	74	76.3	18	9	US-09-836-073-6	Sequence 6, Appl
19	68	70.1	18	9	US-09-836-073-15	Sequence 15, Appl
20	67	69.1	18	9	US-09-836-073-5	Sequence 5, Appl
21	65	67.0	21	15	US-10-376-121A-20	Sequence 20, Appl
22	60	61.9	38	12	US-10-325-810-214	Sequence 214, App
23	51	52.6	38	9	US-09-843-676-25	Sequence 25, Appl
24	51	52.6	38	9	US-09-766-253-25	Sequence 25, Appl
25	51	52.6	38	10	US-09-438-486-25	Sequence 25, Appl
26	51	52.6	38	12	US-10-325-810-215	Sequence 215, App
27	51	52.6	38	12	US-10-053-758-25	Sequence 25, Appl
28	51	52.6	38	14	US-10-054-293-25	Sequence 25, Appl
29	51	52.6	38	14	US-10-054-611-25	Sequence 25, Appl
30	50.5	52.1	37	9	US-09-843-676-24	Sequence 24, Appl
31	50.5	52.1	37	9	US-09-766-253-24	Sequence 24, Appl
32	50.5	52.1	37	10	US-09-438-486-24	Sequence 24, Appl
33	50.5	52.1	37	14	US-10-053-758-24	Sequence 24, Appl
34	50.5	52.1	37	14	US-10-054-293-24	Sequence 24, Appl
35	50.5	52.1	37	14	US-10-054-611-24	Sequence 24, Appl
36	49	50.5	16	9	US-09-836-073-19	Sequence 19, Appl
37	48	49.5	182	12	US-10-282-132A-49328	Sequence 49328, A
38	48	49.5	696	16	US-10-437-963-200901	Sequence 200901, A
39	48	49.5	1527	16	US-10-437-963-200899	Sequence 200899, A
40	47	48.5	654	15	US-10-094-749-1854	Sequence 1854, Ap
41	47	48.5	658	15	US-10-210-130-66	Sequence 66, Appl
42	47	48.5	691	16	US-10-398-037-6	Sequence 6, Appl
43	46	47.4	343	16	US-10-437-963-111769	Sequence 111769, A
44	45	46.4	161	16	US-10-437-963-201436	Sequence 201436, A
45	45	46.4	224	15	US-10-094-749-2904	Sequence 2904, Ap

ALIGNMENTS

RESULT 1
US-09-836-073-12
; Sequence 12, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Daesupda, Asim
; APPLICANT: Daes, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-12

Query Match 100.0%; Score 97; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e-08; 0;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AALEAKICHQIEYFGDF 18
DB 1 AALEAKICHQIEYFGDF 18

RESULT 2
US-09-836-073-1
; Sequence 1, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Daesupda, Asim
; APPLICANT: Daes, S.

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-854-050-24

Query Match 52.1%; Score 50.5; DB 3; Length 37;
Best Local Similarity 83.3%; Pred. No. 0.065; 1; Indels 1; Gaps 1;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 7 ICHQIEYFGDF 18
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1 ICHQ-EYFQDF 11

Db 1 ICHQ-EYFQDF 11

RESULT 15
US-09-430-323-24
Sequence 24, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-430-323-24

Query Match 52.1%; Score 50.5; DB 4; Length 37;
Best Local Similarity 83.3%; Pred. No. 0.065; 1; Indels 1; Gaps 1;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 7 ICHQIEYFGDF 18
||| |||
1 ICHQ-EYFQDF 11

Db 1 ICHQ-EYFQDF 11

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FILED DATE: 25-APR-1997
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 215:
US-09-721-456-215

Query Match 52.6%; Score 51; DB 4; Length 38;
Best Local Similarity 81.8%; Pred. No. 0.055;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 ICHQIEYFGD 17
DB 1 ICHQIEYFGD 11

RESULT 13
US-08-851-843A-24
Sequence 24, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
CLASSIFICATION: US 08/846,017

FILED DATE: 25-APR-1997
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-851-843A-24

Query Match 52.1%; Score 50.5; DB 3; Length 37;
Best Local Similarity 83.3%; Pred. No. 0.065;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 7 ICHQIEYFGDF 18
DB 1 ICHQIEYFGDF 11

RESULT 14
US-08-854-050-24
Sequence 24, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536

FILED DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-430-323-25

Query Match 52.6%; Score 51; DB 4; Length 38;
Best Local Similarity 81.8%; Pred. No. 0.055; 2; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 2; Indels 0;

Qy 7 ICHQIEYQFGD 17
Db 1 ICEQIEYFGD 11

RESULT 11
US-09-402-181B-215
Sequence 215, Application US/09402181B
Patent No. 6610839
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050

FILED DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhub, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 215:
US-09-402-181B-215

Query Match 52.6%; Score 51; DB 4; Length 38;
Best Local Similarity 81.8%; Pred. No. 0.055; 2; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 2; Indels 0;

Qy 7 ICHQIEYQFGD 17
Db 1 ICEQIEYFGD 11

RESULT 12
US-09-721-456-215
Sequence 215, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-Nov. 6617110-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017

FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17685
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-215

Query Match 52.6%; Score 51; DB 3; Length 38;
Best Local Similarity 81.8%; Pred. No. 0.055;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 ICHQIHYFGD 17
DB 1 ICEQIHYFGD 11

RESULT 9
US-08-854-050-25
Sequence 25, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-854-050-25

Query Match 52.6%; Score 51; DB 3; Length 38;
Best Local Similarity 81.8%; Pred. No. 0.055;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 ICHQIHYFGD 17
DB 1 ICEQIHYFGD 11

RESULT 10
US-09-430-323-25
Sequence 25, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843

FILED DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-721-456-214

Query Match 61.9%; Score 60; DB 4; Length 38;
Best Local Similarity 83.3%; Pred. No. 0.0015;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 ICHOIEYFGDF 18
DB 1 ICHOIEYFGDF 12

RESULT 7
US-08-851-843A-25
Sequence 25, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Hatley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-851-843A-25

Query Match 52.6%; Score 51; DB 3; Length 38;
Best Local Similarity 81.8%; Pred. No. 0.055;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 ICHOIEYFGD 17
DB 1 ICHOIEYFGD 11

RESULT 8
US-08-974-549A-215
Sequence 215, Application US/08974549A
Patent No. 616178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Hatley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050

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1 APPLICATION NUMBER: WO PCT/US97/117885
2 FILING DATE: 01-OCT-1997
3 ATTORNEY/AGENT INFORMATION:
4
5 NAME: Apple, Randolph Ted
6 REGISTRATION NUMBER: 36,429
7 REFERENCE/DOCKET NUMBER: 015389-002610US
8 TELECOMMUNICATION INFORMATION:
9
10 TELEPHONE: (415) 576-0200
11 TELEFAX: (415) 576-0300
12 INFORMATION FOR SEQ ID NO: 214:
13
14 SEQUENCE CHARACTERISTICS:
15
16 LENGTH: 38 amino acids
17
18 TYPE: amino acid
19
20 STRANDEDNESS:
21
22 TOPOLOGY: linear
23
24 MOLECULE TYPE: peptide
25
26 US-08-974-549A-214

```

Query Match	61.9%;	Score 60;	DB 3;	Length 38;
Best Local Similarity	83.3%;	Pred. No. 0.0015;		
Matches 10;	Conservative	0;	Mismatches 2;	Indels 0;
				Gaps 0;

Db	1	2	3	4	5	6	7	8	9	10	11	12
	1	2	3	4	5	6	7	8	9	10	11	12

RESULT 5
 US-09-402-181B-214
 Sequence 214, Application US/09402181B
 Patent No. 6610839
 GENERAL INFORMATION:
 APPLICANT: Cech, Thomas R.
 Lingner, Joachim
 Nakamura, Toru
 Chapman, Karen B.
 Morin, Gregg B.
 Harley, William B.
 Andrews, William H.
 TITLE OF INVENTION: Human Telomerase Catalytic Subunit
 NUMBER OF SEQUENCES: 633
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/402,181B
 FILING DATE: 29-Sep-1997
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,643
 FILING DATE: 01-OCT-1996
 APPLICATION NUMBER: US 08/844,419
 FILING DATE: 18-APR-1997
 APPLICATION NUMBER: US 08/846,017
 FILING DATE: 25-APR-1997
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 06-MAY-1997
 APPLICATION NUMBER: US 08/854,050
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: US 08/911,112
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/912,951
 FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997
 APPLICATION NUMBER: WO PCT/US97/17885
 FILING DATE: 01-OCT-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Auesenius, Scott L.
 REGISTRATION NUMBER: 42,271
 REFERENCE/DOCKET NUMBER: 015389-002620USE
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 214:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 38 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 214:
 US-09-402-181B-214

Query Match	61.9%	Score 60	DB 4	length 38
Best Local Similarity	83.3%	Pred. No.	0.0015	
Matches 10	Conservative	0	Mismatches 2	Indels 0
				Gaps 0

QY	7	ICHQIEYQFGDF	18
Db	1	ICHQXEYFEGDF	12

US-09721456-214
; Sequence 214, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Hartley, Calvin H.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/772,456
; FILING DATE: 22-Nov. 6617110-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-Nov-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-Oct-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-Apr-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-Apr-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-May-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-May-1997
; APPLICATION NUMBER: US 08/911,312

PRIOR FILING DATE: 1997-10-06
PRIOR APPLICATION NUMBER: 08/321,427
PRIOR FILING DATE: 1994-10-11
PRIOR APPLICATION NUMBER: 60/086,527
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO: 4
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: B-LAP
US-09-316-630-4
OTHER INFORMATION: this peptide is bicyclic

Query Match 93.8%; Score 91; DB 3; Length 18;
Best Local Similarity 94.4%; Pred. No. 3.2e-09;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AALEKICHOIEYFGDF 18
Db 1 AALEKICHOIEYFGDF 18

RESULT 3

US-08-475-955-20
Sequence 20, Application US/08475955
Patent No. 6641813
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,955
FILING DATE: June 7, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/667,819
FILING DATE: April 13, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMFI14C1P(2) DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Binding-site
LOCATION: 8..15
US-08-475-955-20

Query Match 67.0%; Score 65; DB 4; Length 21;
Best Local Similarity 91.7%; Pred. No. 0.00011;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ICHOIEYFGDF 18
Db 1 ICHOIEYFGDF 12

RESULT 4

US-08-974-549A-214
Sequence 214, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:43:01; Search time 15.8883 seconds
(without alignments)
58.488 Million cell updates/sec

Title: US-09-836-073-12

Sequence: 1 AALEAKICHQIEYFGDF 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents AA:
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2: /cgnt2_6/prodata/2/iaa/5B_COMB.pep.*
3: /cgnt2_6/prodata/2/iaa/6A_COMB.pep.*
4: /cgnt2_6/prodata/2/iaa/6B_COMB.pep.*
5: /cgnt2_6/prodata/2/iaa/PCTUS_COMB.pep.*
6: /cgnt2_6/prodata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	91	93.8	18	US-09-316-630-3	Sequence 3, Appl1
2	91	93.8	18	US-09-316-630-4	Sequence 4, Appl1
3	65	67.0	21	US-08-475-955-20	Sequence 20, Appl1
4	60	61.9	38	US-08-974-549A-214	Sequence 214, App
5	60	61.9	38	US-09-402-181B-214	Sequence 214, App
6	60	61.9	38	US-09-721-456-214	Sequence 214, App
7	51	52.6	38	US-08-851-843A-25	Sequence 25, Appl
8	51	52.6	38	US-08-974-549A-215	Sequence 215, App
9	51	52.6	38	US-08-854-050-25	Sequence 25, Appl
10	51	52.6	38	US-09-430-323-25	Sequence 25, Appl
11	51	52.6	38	US-09-402-181B-215	Sequence 215, App
12	51	52.6	38	US-09-721-456-215	Sequence 215, App
13	50.5	52.1	37	US-08-851-843A-24	Sequence 24, Appl
14	50.5	52.1	37	US-08-854-050-24	Sequence 24, Appl
15	50.5	52.1	37	US-09-430-323-24	Sequence 24, Appl
16	44.5	45.9	124	US-09-489-039A-9103	Sequence 9103, Ap
17	44	45.4	431	US-08-311-023-2	Sequence 2, Appl1
18	44	45.4	456	US-08-205-719-4	Sequence 4, Appl1
19	42	43.3	456	US-08-431-517F-6	Sequence 6, Appl1
20	42	43.3	482	US-08-431-517F-5	Sequence 5, Appl1
21	42	43.3	482	5245013-2	Patent No. 5245013
22	41	42.3	699	US-09-543-681A-5118	Sequence 5118, Ap
23	40	41.2	39	US-08-851-843A-26	Sequence 26, Appl
24	40	41.2	39	US-08-974-549A-216	Sequence 216, App
25	40	41.2	39	US-08-854-050-26	Sequence 26, Appl
26	40	41.2	39	US-09-430-323-26	Sequence 26, Appl
27	40	41.2	39	US-09-402-181B-216	Sequence 216, App

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29	40	41.2	483	3	US-09-027-166-7	Sequence 7, Appl1
30	40	41.2	658	4	US-09-252-991A-25861	Sequence 25861, A
31	40	41.2	1068	1	US-08-537-210A-2	Sequence 2, Appl1
32	40	41.2	1068	1	US-09-113-825-2	Sequence 2, Appl1
33	40	41.2	2556	1	US-08-185-423-17	Sequence 17, Appl
34	40	41.2	2556	1	US-08-083-590A-20	Sequence 20, Appl
35	40	41.2	2556	3	US-08-532-384-20	Sequence 20, Appl
36	40	41.2	2556	1	US-08-899-232-2	Sequence 2, Appl1
37	39	40.2	158	2	US-08-933-750C-15	Sequence 15, Appl
38	39	40.2	158	3	US-09-234-613-15	Sequence 15, Appl
39	39	40.2	212	4	US-08-937-067-4	Sequence 4, Appl1
40	39	40.2	295	4	US-08-937-067-2	Sequence 2, Appl1
41	39	40.2	295	4	US-09-148-545-179	Sequence 179, App
42	39	40.2	296	4	US-09-148-545-237	Sequence 237, App
43	39	40.2	811	4	US-09-199-637A-93	Sequence 93, Appl
44	39	40.2	812	1	US-08-248-629A-1	Sequence 1, Appl1
45	39	40.2	812	1	US-08-451-932-1	Sequence 1, Appl1

ALIGNMENTS

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RESULT 1
US-09-316-630-3
Sequence 3, Application US/09316630
Patent No. 6291637
GENERAL INFORMATION:
APPLICANT: Das, Saumitra
APPLICANT: Dasgupta, Asim
TITLE OF INVENTION: INTERFERENCE WITH VIRAL IRES-MEDIATED TRANSLATION BY A
TITLE OF INVENTION: SMALL YEAST RNA REVEALS CRITICAL RNA-PROTEIN INTERACTIONS
FILE REFERENCE: 22000-20548-21
CURRENT APPLICATION NUMBER: US/09/316,630
CURRENT FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 08/817,953
PRIOR FILING DATE: 1997-10-06
PRIOR APPLICATION NUMBER: 08/321,427
PRIOR FILING DATE: 1994-10-11
PRIOR APPLICATION NUMBER: 60/086,527
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: LAP
US-09-316-630-3
Query Match 93.8%; Score 91; DB 3; Length 18;
Best Local Similarity 94.4%; Pred. No. 3.2e-09;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CY 1 AALEAKICHQIEYFGDF 18
DB 1 AALEAKICHQIEYFGDF 18
RESULT 2
US-09-316-630-4
Sequence 4, Application US/09316630
Patent No. 6291637
GENERAL INFORMATION:
APPLICANT: Das, Saumitra
APPLICANT: Dasgupta, Asim
TITLE OF INVENTION: INTERFERENCE WITH VIRAL IRES-MEDIATED TRANSLATION BY A
TITLE OF INVENTION: SMALL YEAST RNA REVEALS CRITICAL RNA-PROTEIN INTERACTIONS
FILE REFERENCE: 22000-20548-21
CURRENT APPLICATION NUMBER: US/09/316,630
CURRENT FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 08/817,953

```

DR N-PSDB; AAS72604.
 XX
 XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 PS Claim 20; SEQ ID NO 38776; 103pp; English.
 XX
 XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (II) is useful in gene therapy techniques to restore normal
 CC activity of (I) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 439 AA;

Query Match 93.8%; Score 91; DB 4; Length 439;
 Best Local Similarity 94.4%; Pred. No. 7.3e-07;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AALEAKICHQIEYFGDF 18
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 DB 41 AALEAKICHQIEYFGDF 58

RESULT 15

AAB58987
 ID AAB58987 standard; protein; 460 AA.

AC AAB58987;

DT 27-MAR-2001 (first entry)

DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 695.

XX Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
 KW neurologic; neuroprotective; antiviral; antiallergic; hepatotropic;
 KW antidiabetic; antinflammatory; antitumor; vulnerary; anticonvulsant;
 KW antibacterial; antifungal; antiparasitic; cardiac; immune disorder;
 KW Addison's disease; allergy; autoimmune haemolytic anaemia;
 KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
 KW cardiovascular disorder; wound healing; neurological disease.
 XX

OS Homo sapiens.

PN WO200055173-A1.

PD 21-SEP-2000.

PF 08-MAR-2000; 2000MO-US005881.

PR 12-MAR-1999; 99US-0124270P.

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Rosen CA, Ruben SM;
 XX
 XX WPI, 2000-611515/58.
 DR N-PSDB; AAF21890.
 XX
 XX New human breast and ovarian cancer associated gene sequences and the
 PT polypeptides encoded by these genes, useful in the prevention, treatment
 PT and diagnosis of cancer, immune disorders, cardiovascular disorders and
 PT neurological diseases.
 PS Claim 11; Page 1149-1150; 1299pp; English.
 XX
 XX Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
 CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
 CC associated with breast and ovarian cancer. Included in the invention are
 CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
 CC isolation and characterisation of the DNA and protein sequences of the
 CC invention. The breast and ovarian cancer associated DNA, protein, agonist
 CC or antagonist sequences exhibit cytostatic; immunosuppressive; neurologic;
 CC neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic;
 CC antinflammatory; antitumor; vulnerary; anticonvulsant; antibacterial;
 CC antifungal; antiparasitic and cardiac activity. The polynucleotide and
 CC protein sequences are used in the diagnosis of cancer, particularly
 CC breast and ovarian cancer. The nucleic acid sequences, proteins, agonists
 CC and agonists may also be used in the diagnosis, prevention and treatment
 CC of immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
 CC cardiovascular disorders such as myocardial ischaemias; wound healing;
 CC neurological diseases such as cerebral anoxia and epilepsy; and
 CC infectious diseases
 XX

SQ Sequence 460 AA;

Query Match 93.8%; Score 91; DB 3; Length 460;
 Best Local Similarity 94.4%; Pred. No. 7.7e-07;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AALEAKICHQIEYFGDF 18
 |||||
 DB 63 AALEAKICHQIEYFGDF 80

Search completed: September 10, 2004, 17:51:48
 Job time : 58.4128 secs

XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPD at
CC ftp.wipo.int/pub/published_pct_sequences.

Query Match	93.8%	Score 91	DB 7	Length 415
Best Local Similarity	94.4%	Pred. No. 6.9e-07		
Matches 17	Conservative	0	Mismatches 1	Indels 0
				Gaps 0

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Db	11	AALBAKICHQIEYFFGDF	28

RESULT 13
ADE63993
ID ADE63993 standard; protein; 415 AA.

AC ADE63993;

DT 29-JAN-2004 (first entry)

Rat Protein P38656, SEQ ID NO 9939.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KM chronic constriction injury; CCI; spared nerve injury; SN; Chung.
KM

OS *Rattus norvegicus*.

PN WO2003016475-A2.

PD 27-FEB-2003.

14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 26-NOV-2001; 2001US-0333347P.

PA (GEHO) GEN HOSPITAL CORP.

XX

XX

DR GENBANK; P38656.

PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 25 Claim 1; Page; 1017p; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polynucleotides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at http://wipo.int/publ/published_pct_sequences.

Query Match	93.8%	Score 91;	DB 7;	Length 415;
Best Local Similarity	94.4%	Pred. No. 6.9e-07;		
Matches 17; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

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QY      1 AALEAKICHQIEYQFGDF 18
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Db      11 AALEAKICHQIEYFGDF 28
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RESULT 14
ABG08417
ID ABG08417 standard; protein; 439 AA.

AC ABG08417;

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #8408.

AA Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US008631.

PR 31-MAR-2000; 2000US-00540217.

XX

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099
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XX

100

CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 408 AA;

Query Match 93.8%; Score 91; DB 7; Length 408;
Best Local Similarity 94.4%; Pred. No. 6.7e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 AALEAKICHQIEYFGDF 18
Db 11 AALEAKICHQIEYFGDF 28

RESULT 11

ADE62859 ADE62859 standard; protein; 408 AA.

XX ADE62859;

XX 29-JAN-2004 (first entry)

XX Human Protein P05455, SEQ ID NO 8793.

XX Human; pain; neuronal tissue; gene therapy;

XX spinal segmental nerve injury; chronic constriction injury; CCI;

XX spared nerve injury; SNI; Chung.

XX Homo sapiens.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GEHO) GEN HOSPITAL CORP.

XX (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI, 2003-268312/26.

XX GENBANK, P05455.

XX New composition comprising two or more isolated polypeptides, useful for

XX preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 408 AA;

Query Match 93.8%; Score 91; DB 7; Length 408;
Best Local Similarity 94.4%; Pred. No. 6.7e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 AALEAKICHQIEYFGDF 18
Db 11 AALEAKICHQIEYFGDF 28

RESULT 12

ADE63989 ADE63989 standard; protein; 415 AA.

XX ADE63989;

XX 29-JAN-2004 (first entry)

XX Rat Protein P38656, SEQ ID NO 9935.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;

XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GEHO) GEN HOSPITAL CORP.

XX (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI, 2003-268312/26.

XX GENBANK, P38656.

XX New composition comprising two or more isolated polypeptides, useful for

XX preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from MIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 408 AA;

XX Query Match 93.8%; Score 91; DB 7; Length 408;

XX Best Local Similarity 94.4%; Pred. No. 6.7e-07;

XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 AALEAKICHQIEYFGDF 18
DB 11 AALEAKICHQIEYFGDF 28

RESULT 9
ADD6272
ID ADD6272 standard; protein; 408 AA.

XX ADD6272;

XX 29-JAN-2004 (first entry)

XX Human Protein P05455, SEQ ID NO 11947.

XX Human; pain; neuronal tissue; gene therapy;

XX spinal segmental nerve injury; chronic constriction injury; CCI;

XX spared nerve injury; SNI; Chung.

XX Homo sapiens.

XX MO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-033347P.

XX (GEHO) GEN HOSPITAL CORP.

XX (FARB) BAYER AG.

XX WOOLF C, D'ureo D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

XX GENBANK; P05455.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the

CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from MIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 408 AA;

XX Query Match 93.8%; Score 91; DB 7; Length 408;

XX Best Local Similarity 94.4%; Pred. No. 6.7e-07;

XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 AALEAKICHQIEYFGDF 18
DB 11 AALEAKICHQIEYFGDF 28

RESULT 10
ADE63995
ID ADE63995 standard; protein; 408 AA.

XX ADE63995;

XX 29-JAN-2004 (first entry)

XX Human Protein P05455, SEQ ID NO 9941.

XX Human; pain; neuronal tissue; gene therapy;

XX spinal segmental nerve injury; chronic constriction injury; CCI;

XX spared nerve injury; SNI; Chung.

XX Homo sapiens.

XX MO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-033347P.

XX (GEHO) GEN HOSPITAL CORP.

XX (FARB) BAYER AG.

XX WOOLF C, D'ureo D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

XX GENBANK; P05455.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence

CC is clinically related to the Ro protein that is highly common among
CC autoimmune patients. La and Ro antigens sometimes reside on the same
CC cellular ribonucleoprotein particle; most La patients contain some Ro
CC antibodies and vice versa. La cDNA has been isolated from a human liver
CC library. (Updated on 25-MAR-2003 to correct PF field.)
XX

Sequence 408 AA;

Query Match 93.8%; Score 91; DB 2; Length 408;
Best Local Similarity 94.4%; Pred. No. 6.7e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 AALEAKICHQIEYFGDF 18
|||
DB 11 AALEAKICHQIEYFGDF 28

RESULT 7

ID ABP65252 standard; protein; 408 AA.

XX ABP65252;

DT 12-NOV-2002 (first entry)

XX Hypoxia-regulated protein #126.

XX Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy;
XX antiinflammatory; vulnary; gynecological; ophthalmological; vaccine;
XX hypoxia; tumorigenesis; angiogenesis; apoptosis; cancer;
XX ischaemic condition; reperfusion injury; retinopathy; neonatal stress;
XX preclapmsia; atherosclerosis; inflammatory condition; wound healing;
XX inflammation; erythropoiesis; hair loss; human.

XX Homo sapiens.

XX WO200246465-A2.

XX 13-JUN-2002.

XX 10-DEC-2001; 2001WO-GB005458.

XX 08-DEC-2000; 2000GB-00030076.

XX 08-FEB-2001; 2001GB-00003156.

XX 25-OCT-2001; 2001GB-00025666.

XX (OXFO-) OXFORD BIOMEDICA UK LTD.

XX White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;

XX Rayner WN;

XX WPI; 2002-627238/67.

XX Identifying a gene involved in disease for treating hypoxia-regulated
XX conditions, comprises comparing the transcriptome/proteome of two cell
XX types under different conditions and identifying a differentially
XX regulated gene.

XX Claim 35; Page 425; 538pp; English.

XX The present invention relates to methods for identifying genes and
XX proteins that are implicated in a specific disease or physiological
XX condition. The method comprises comparing the transcriptome/proteome of a
XX specialised cell type implicated in a disease or condition with that of a
XX second specialised cell type, under two experimental conditions, and
XX identifying a gene that is differentially regulated in the two
XX specialised cell types under experimental conditions. ABV7873-ABV7816
XX and AB65061-ABP65257 were identified using the methods of the invention.
XX The coding sequences and proteins are useful for treating a disease in a
XX patient, for manufacture of a medicament for treating hypoxia-regulated
XX conditions, and for regulating tumorigenesis, angiogenesis, apoptosis,
XX biological response to hypoxia conditions, or hypoxic-associated
XX pathology in a patient. The coding sequences and proteins are also useful

CC for monitoring the therapeutic treatment of a disease or physiological
CC condition, such as cancer, ischaemic conditions, reperfusion injury,
CC retinopathy, neonatal stress, preclapmsia, atherosclerosis, inflammatory
CC conditions, wound healing, inflammation, erythropoiesis or hair loss
XX

Sequence 408 AA;

Query Match 93.8%; Score 91; DB 5; Length 408;
Best Local Similarity 94.4%; Pred. No. 6.7e-07;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 AALEAKICHQIEYFGDF 18
|||
DB 11 AALEAKICHQIEYFGDF 28

RESULT 8

ID ADE63991 standard; protein; 408 AA.

XX ADE63991;

DT 29-JAN-2004 (first entry)

XX Human Protein P05455, SEQ ID NO. 9937.

XX Human; pain; neuronal tissue; gene therapy;

XX spinal segmental nerve injury; chronic constriction injury; CCI;

XX spared nerve injury; SNI; Chung.

XX Homo sapiens.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GEHO) GEN HOSPITAL CORP.

XX (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-268312/26.

XX GENBANK; P05455.

XX Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more

KM internal ribosome entry site initiated translation; Ia antigen protein;
 KM viral life cycle; antiviral therapy; pharmaceutical; veterinary;
 KM agricultural; horticultural; virucide; bovine.
 XX Bovinae.
 OS WO200283858-A2.
 XX PM
 XX PD 24-OCT-2002.
 XX PF 12-APR-2002; 2002WO-US011589.
 XX PR 16-APR-2001; 2001US-00836073.
 XX PA (UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.
 XX PI Dasgupta A, Das S, Balda N;
 XX DR WPI; 2003-058634/05.
 XX PT New compound containing acidic and aromatic amino acids, useful as
 PT antiviral therapy in pharmaceutical, veterinary or
 PT agricultural/horticultural applications.
 XX PS Disclosure; Page 6; 19pp; English.
 XX CC The present invention relates to peptides and methods of inhibiting the
 CC replication of viruses that utilise internal ribosome entry site (IRES)
 CC initiated translation, and/or inhibiting viruses that utilise the Ia
 CC antigen protein (IAP) in any phase of their life cycle. The peptides of
 CC the invention compete with IAP and inhibit the utilisation of various
 CC biochemical and physiological functions of IAP required for a productive
 CC life cycle. The methods and compositions are useful as antiviral therapy
 CC in pharmaceutical, veterinary or agricultural/horticultural applications.
 CC ABG72101-ABG72119 represent peptides useful as antiviral agents
 XX SQ
 XX Sequence 18 AA:
 Query Match 93.8%; Score 91; DB 6; Length 18;
 Best Local Similarity 94.4%; Pred. No. 2.2e-08;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AALEAKICHOIEYQFGDF 18
 DB 1 AALEAKICHOIEYFGDF 18
 RESULT 5
 ID AAG01351 standard; protein; 92 AA.
 XX AC
 XX AAG01351;
 XX DT 06-OCT-2000 (first entry)
 XX DE Human secreted protein, SEQ ID NO: 5432.
 XX KM Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KM gene therapy; chromosome mapping.
 XX OS Homo sapiens.
 XX PN BP1033401-A2.
 XX PD 06-SEP-2000.
 XX PF 21-FEB-2000; 2000EP-00200610.
 XX PR 26-FEB-1999; 99US-0122487P.
 XX PA (GEST) GENSET.
 XX PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX MPI; 2000-500381/45.
 DR N-PSDB; AAC01357.
 XX PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX PS Claim 13; SEQ ID NO 5432; 71pp + Sequence listing; English.
 XX CC The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors
 XX SQ
 XX Sequence 92 AA:
 Query Match 93.8%; Score 91; DB 3; Length 92;
 Best Local Similarity 94.4%; Pred. No. 1.3e-07;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AALEAKICHOIEYQFGDF 18
 DB 11 AALEAKICHOIEYFGDF 28
 RESULT 6
 ID AAW03716 standard; protein; 408 AA.
 XX AC
 XX AAW03716;
 XX DT 25-MAR-2003 (revised)
 DT 12-MAR-1997 (first entry)
 XX DE Human autoantigen La(SS-B).
 XX KM Autoimmune disease; Ia autoantigen; Sjogren's syndrome;
 KM systemic lupus erythematosus; diagnosis.
 XX OS Homo sapiens.
 XX PN US5541291-A.
 XX PD 30-JUL-1996.
 XX PF 27-MAY-1987; 87US-00054871.
 XX PR 31-DEC-1984; 84US-00687908.
 XX PA (UYDU-) UNIV DUKE.
 XX PI Keene JD;
 XX DR WPI; 1996-362015/36.
 XX PT Auto-antigen U2-RNP, associated with severe polymyositis-scleroderma
 PT overlap syndrome - useful for diagnosis and treatment of autoimmune
 PT diseases.
 XX PS Disclosure; Col 15-16; 21pp; English.
 XX CC The human lupus antigen (Ia) is diagnostic for Sjogren's syndrome, as
 CC well as occurring in systemic lupus erythematosus patients. The Ia protein

Query Match 100.0%; Score 97; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2.1e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AALEAKICHQIEYFGDF 18
 DB 1 AALEAKICHQIEYFGDF 18

RESULT 2
 ID AAY52200 standard; peptide; 18 AA.

AC AAY52200;
 DT 14-MAR-2000 (first entry)
 DE Human Ia autoantigen peptide (LAP).

KM Ia autoantigen; LAP, internal ribosome entry site, IRES, translation;
 KM viral replication; IRNA, antiviral agent; picornavirus; flavivirus;
 KM coronavirus; hepatitis virus; rhadovirus; adenovirus; coxsackie virus;
 KM parainfluenza virus; poliovirus; rhinovirus; encephalomyocarditis virus;
 KM foot-and-mouth disease virus; echo virus; infectious bronchitis virus;
 KM vesicular stomatitis virus.

OS Homo sapiens.
 PN WO961613-A2.
 PD 02-DEC-1999.
 PF 21-MAY-1999; 99WO-US011281.
 PR 22-MAY-1998; 98US-0086527P.
 PA (REGC) UNIV CALIFORNIA.

PI Das S, Dasgupta A;
 DR WPI, 2000-062712/05.

PT New yeast inhibitory peptide useful for inhibiting viral protein
 translation and replication.

PS Claim 5; Page 57; 81pp; English.

CC This sequence is the Ia autoantigen binding domain (LAP). LAP is a
 CC cellular protein which binds to an internal ribosome entry site (IRES).
 CC The peptide is used to inhibit mRNA translation, viral protein
 CC translation or viral replication. Viral mRNA translation is initiated at
 CC the IRES and the LAP peptide prevents translation initiation factors from
 CC binding at the site. The peptide can be used alone or in combination with
 CC an inhibitor RNA (IRNA see A425200). The LAP peptide is useful as an
 CC antiviral agent, which works through the inhibition of mRNA translation,
 CC especially viral RNA. Examples of viruses which can be inhibited are
 CC picornavirus, flavivirus, coronavirus, hepatitis A B or C viruses,
 CC rhadovirus, adenovirus, and parainfluenza virus, poliovirus, rhinovirus,
 CC coxsackie virus, encephalomyocarditis virus, foot-and-mouth disease
 CC virus, echo virus, hepatitis C virus, infectious bronchitis virus, duck
 CC and human hepatitis B virus, and vesicular stomatitis virus. The peptide
 CC also inhibits replication of the above viruses. The LAP peptide
 CC selectively inhibits viral protein translation, and is therefore not
 CC toxic to the host cell

CC Sequence 18 AA;

Query Match 93.8%; Score 91; DB 3; Length 18;
 Best Local Similarity 94.4%; Pred. No. 2.2e-08;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AALEAKICHQIEYFGDF 18

DB 1 AALEAKICHQIEYFGDF 18

RESULT 3
 ID ABG72101 standard; peptide; 18 AA.

AC ABG72101;
 DT 28-JAN-2003 (first entry)

DE Viral replication inhibiting peptide, LAP.

KM Viral replication inhibitor; IRES initiated translation; LAP;
 KM internal ribosome entry site initiated translation; Ia antigen protein;
 KM viral life cycle; antiviral therapy; pharmaceutical; veterinary;
 KM agricultural; horticultural; virucide.

OS Unidentified.
 PN WO200283858-A2.

PD 24-OCT-2002.
 PF 12-APR-2002; 2002WO-US011589.

PR 16-APR-2001; 2001US-00836073.
 PA (UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.

PI Dasgupta A, Das S, Baidya N;
 DR WPI; 2003-058634/05.

PT New compound containing acidic and aromatic amino acids, useful as
 PT antiviral therapy in pharmaceutical, veterinary or
 PT agricultural/horticultural applications.

PS Claim 1; Page 15; 19pp; English.

CC The present invention relates to peptides and methods of inhibiting the
 CC replication of viruses that utilize internal ribosome entry site (IRES)
 CC initiated translation, and/or inhibiting viruses that utilize the Ia
 CC antigen protein (LAP) in any phase of their life cycle. The peptides of
 CC the invention compete with LAP and inhibit the utilization of various
 CC biochemical and physiological functions of LAP required for a productive
 CC life cycle. The methods and compositions are useful as antiviral therapy
 CC in pharmaceutical, veterinary or agricultural/horticultural applications.
 CC ABG72101-ABG72119 represent peptide useful as antiviral agents

CC Sequence 18 AA;

Query Match 93.8%; Score 91; DB 6; Length 18;
 Best Local Similarity 94.4%; Pred. No. 2.2e-08;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AALEAKICHQIEYFGDF 18
 DB 1 AALEAKICHQIEYFGDF 18

RESULT 4
 ID ABG72114 standard; peptide; 18 AA.

AC ABG72114;

DT 28-JAN-2003 (first entry)
 DE Viral replication inhibiting peptide, BOVINE.

KM Viral replication inhibitor; IRES initiated translation; LAP;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2004, 16:58:20 ; Search time 56.3129 Seconds
(without alignments)
90.314 Million cell updates/sec

Title: US-09-836-073-12

Perfect score: 97

Sequence: 1 AALEAKICHQIEYGFDF 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	18	6	ABG72112
2	91	93.8	18	3	AAI52200
3	91	93.8	18	6	ABG72101
4	91	93.8	18	6	ABG72114
5	91	93.8	92	3	AA601351
6	91	93.8	408	2	AAW03716
7	91	93.8	408	5	ABP65252
8	91	93.8	408	7	ADBE63991
9	91	93.8	408	7	ADDA6272
10	91	93.8	408	7	ADBE63995
11	91	93.8	408	7	ADBE62859
12	91	93.8	415	7	ADBE63989
13	91	93.8	415	7	ADBE63993
14	91	93.8	439	4	ABG08417
15	91	93.8	460	3	AA858987
16	91	93.8	460	5	ABP41511
17	89	91.8	18	6	ABG72108
18	89	91.8	17	6	ABG72113
19	87	87.6	18	6	ABG72109
20	83	85.6	18	6	ABG72111
21	82	84.5	18	6	ABG72110
22	80.5	83.0	19	6	ABG72116
23	79	81.4	18	6	ABG72102
24	79	81.4	18	6	ABG72103
25	79	81.4	18	6	ABG72104

26	76	78.4	18	6	ABG72107
27	74	76.3	18	6	ABG72106
28	68	70.1	18	6	ABG72115
29	67	69.1	18	6	ABG72105
30	65	67.0	21	2	AA843394
31	49	50.5	16	6	ABG72119
32	48	49.5	182	6	ABU21404
33	47	48.5	654	6	ADA54286
34	47	48.5	658	7	ADBA47704
35	47	48.5	691	5	ABP43482
36	46	47.4	517	5	AAU74627
37	46	47.4	519	5	ABP71162
38	46	47.4	519	5	AAU74628
39	45	46.4	135	4	ABG27058
40	45	46.4	224	5	ABB89645
41	45	46.4	224	6	ADA55336
42	44	45.4	129	6	ADA55269
43	44	45.4	160	4	AAW93460
44	44	45.4	203	4	AAW40110
45	44	45.4	204	3	AA859035

ALIGNMENTS

RESULT 1	ABG72112	standard; peptide; 18 AA.
ID	ABG72112	standard; peptide; 18 AA.
XX	ABG72112;	
XX	28-JAN-2003	(first entry)
DE	Viral replication inhibiting peptide, 633.	
XX	Viral replication inhibitor; IRES initiated translation; LAP;	Abg72107 Viral rep
XX	internal ribosome entry site initiated translation; La antigen protein;	Abg72106 Viral rep
KW	viral life cycle; antiviral therapy; pharmaceutical; veterinary;	Abg72115 Viral rep
KW	agricultural; horticultural; virucide.	Abg72105 Viral rep
XX	Unidentified.	AA843394
XX	WO200283858-A2.	ABG72119
XX	24-OCT-2002.	ABU21404
XX	12-APR-2002; 2002WO-US011589.	ADA54286
XX	16-APR-2001; 2001US-00836073.	ADBA47704
PR	(UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.	ABP43482
PA	Dasgupta A, Das S, Baidya N;	AAU74627
PI	Dasgupta A, Das S, Baidya N;	ABP71162
XX	WPI; 2003-058634/05.	AAU74628
DR	New compound containing acidic and aromatic amino acids, useful as	ABG27058 Novel hum
PT	antiviral therapy in pharmaceutical, veterinary or	ABB89645 Human pol
PT	agricultural/horticultural applications.	ADA55336 Human pro
XX	Claim 10; Page 16; 19pp; English.	ADA55269 Human pro
XX	The present invention relates to peptides and methods of inhibiting the	AAW93460 Human pol
CC	replication of viruses that utilize internal ribosome entry site (IRES)	AAW40110 Breast an
CC	initiated translation, and/or inhibiting viruses that utilize the La	Abg72107 Viral rep
CC	antigen protein (LAP) in any phase of their life cycle. The peptides of	Abg72115 Viral rep
CC	the invention compete with LAP and inhibit the utilisation of various	Abg72106 Viral rep
CC	biochemical and physiological functions of LAP required for a productive	Abg72119 Viral rep
CC	life cycle. The methods and compositions are useful as antiviral therapy	Abg72104 Protein e
CC	in pharmaceutical, veterinary or agricultural/horticultural applications.	ADA54286 Human pro
CC	ABG72101-ABG72119 represent peptides useful as antiviral agents	ADBA47704 Human NOV
XX	Sequence 18 AA;	ABP43482 Human sec
SQ		AAU74627 Oestrogen

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Mon Sep 13 09:36:23 2004

us-09-836-073-4.rapb

Search completed: September 10, 2004, 18:11:55
Job time : 40.424 secs

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FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 18
TYPE: prt
ORGANISM: Homo Sapiens
US-09-836-073-11

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Query Match	77.5%	Score 79	DB 9	Length 18
Best Local Similarity	93.3%	Pred. No.	1.9e-05	
Matches 14, Conservative	0	Mismatches 1	Indels 0	Gaps 0

Qy	4	EAKICHQIEYFGDF	18
Db	4	EAKICHQIEQYFGDF	18

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RESULT 12 073-12
US-09-836-073-12
, Sequence 12, Application US/09836073
, Patent No. US20020173475A1
, GENERAL INFORMATION:
, APPLICANT: Dasgupta, Asim
, APPLICANT: Das, S.
, APPLICANT: Balidya, Narayan
, TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
, FILE REFERENCE: 220002054822
, CURRENT APPLICATION NUMBER: US/09/836,073
, CURRENT FILING DATE: 2002-10-24
, PRIOR APPLICATION NUMBER: 09/316,630
, PRIOR FILING DATE: 1999-05-21
, NUMBER OF SEQ ID NOS: 19
, SOFTWARE: Fastseq for Windows Version 4.0
, SEQ ID NO 12
, LENGTH: 16
, TYPE: PRT
, ORGANISM: Homo Sapiens
US-09-836-073-12

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Query Match	77.5%	Score 79	DB 9	Length 18
Local Similarity	93.3%	Pred. No.	1.9e-05	
Matches 14	Conservative	0	Mismatches 1	Indels 0
				Gaps 0

Qy 4 EAKICHQIEYFGDF 18
 |||||
 Db 4 EAKICHQIEYQFGDF 18

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RESULT 13 US-09-836-073-10
: Sequence 10, Application US/09836073
: Patent No. US20020173475A1
: GENERAL INFORMATION:
: APPLICANT: Dasgupta, Asim
: APPLICANT: Das, S.
: APPLICANT: Badhya, Narayan
: TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
: FILE REFERENCE: 22002054822
: CURRENT APPLICATION NUMBER: US/09/836, 073
: CURRENT FILING DATE: 2002-10-24
: PRIOR APPLICATION NUMBER: 09/316, 630
: PRIOR FILING DATE: 1999-05-21
: NUMBER OF SEQ ID NOS: 19
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 10
: LENGTH: 18
: TYPE: PRT
: ORGANISM: Homo Sapiens

```

US-09-836-073-10

Query Match	76.5%;	Score 78;	DB 9;	Length 18;
Best Local Similarity	93.3%;	Pred. No. 2.7e-05;		
Matches 14;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

QY **4** EAKICHQIEYYFGDF 18
 |||||
Db **4** EAKICHQIEYYQGDF 18

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RESULT 14
US-09-836-073-16
; Sequence 16, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Dae, S.
; APPLICANT: Baldaia, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 19
; TYPE: RPT
; ORGANISM: Rat
US-09-836-073-16

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Query Match	75.0%	Score 76.5;	DB 9;	Length 19;
Best Local Similarity	93.8%	Pred. No. 4.8e-05;		
Matches 15; Conservative	0;	Mismatches 0;	Indels 1;	Gaps 1;

QY	4	EAKICHQI-EYFPGDF	18
Db	4	EAKICHQIEEYFPGDF	19

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RESULT 15:03-073-2
US-09-836-073-2
Sequence 2, Application US/09836073
Patent No. US20020173475A1
GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Balidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 18
TYPE: EXT
ORGANISM: Homo Sapiens
US-09-836-073-2

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Query Match	73.5%	Score 75;	DB 9;	Length 18;
Best Local Similarity	86.7%;	Pred. No. 7.9e-05;		
Matches 13;	Conservative 1;	Mismatches 1;	Indels 0;	Gaps 0;

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QY      4 EAKICHQIEYYFGDF 18
         ||:|| ||||| |||
Db      4 EAQICQQIEYYFGDF 18
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US-10-170-385-477

Query Match 85.3%; Score 87; DB 12; Length 408;
Best Local Similarity 100.0%; Pred. No. 2.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EAKICHOIEYFGDF 18
|||||
Db 14 EAKICHOIEYFGDF 28

RESULT 7

US-09-925-298-695
; Sequence 695, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103
; CURRENT APPLICATION NUMBER: US/09/925,298
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 695
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-298-695

Query Match 85.3%; Score 87; DB 12; Length 460;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EAKICHOIEYFGDF 18
|||||
Db 66 EAKICHOIEYFGDF 80

RESULT 8

US-10-102-806-695
; Sequence 695, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103P1C1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 695
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-102-806-695

Query Match 85.3%; Score 87; DB 14; Length 460;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EAKICHOIEYFGDF 18
|||||
Db 66 EAKICHOIEYFGDF 80

RESULT 9

US-10-264-049-2643
; Sequence 2643, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: Patentln Ver. 3.1
; SEQ ID NO 2643
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-2643

Query Match 85.3%; Score 87; DB 15; Length 460;
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EAKICHOIEYFGDF 18
|||||
Db 66 EAKICHOIEYFGDF 80

RESULT 10

US-09-836-073-9
; Sequence 9, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 22002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-9

Query Match 79.4%; Score 81; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 9.1e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EAKICHOIEYFGD 17
|||||
Db 4 EAKICHOIEYFGD 17

RESULT 11

US-09-836-073-11
; Sequence 11, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION


```

; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 22002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-5

Query Match      88.2%; Score 90; DB 9; Length 18;
Best Local Similarity 88.9%; Pred. No. 3,5e-07;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 000EAKICHOIEYFGDF 18
DB 1 000EORQCHOIEYFGDF 18

RESULT 3
US-09-836-073-13
; Sequence 13, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 22002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mouse
US-09-836-073-13

Query Match      85.3%; Score 87; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 9,9e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EAKICHOIEYFGDF 18
DB 3 EAKICHOIEYFGDF 17

RESULT 4
US-09-836-073-1
; Sequence 1, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 22002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 18
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-1

Query Match      85.3%; Score 87; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EAKICHOIEYFGDF 18
DB 4 EAKICHOIEYFGDF 18

RESULT 5
US-09-836-073-14
; Sequence 14, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 22002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Bovine
US-09-836-073-14

Query Match      85.3%; Score 87; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EAKICHOIEYFGDF 18
DB 4 EAKICHOIEYFGDF 18

RESULT 6
US-10-170-385-477
; Sequence 477, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 477
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Homo Sapiens
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SW protein - protein search, using sw model

Run on: September 10, 2004, 17:52:06 ; Search time 40.324 Seconds
(without alignments)
143.151 Million cell updates/sec

Title: US-09-836-073-4

Perfect score: 102
Sequence: 1 QOGEAKICHOIEYFGDF 18

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:*

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- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
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- 5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	102	100.0	18	US-09-836-073-4	Sequence 4, Appl1
2	90	88.2	18	US-09-836-073-5	Sequence 5, Appl1
3	87	85.3	17	US-09-836-073-13	Sequence 13, Appl1
4	87	85.3	18	US-09-836-073-1	Sequence 1, Appl1
5	87	85.3	18	US-09-836-073-14	Sequence 14, Appl1
6	87	85.3	408	US-10-170-385-477	Sequence 477, App
7	87	85.3	460	US-09-925-298-695	Sequence 695, App
8	87	85.3	460	US-10-102-806-695	Sequence 695, App
9	87	85.3	460	US-10-264-049-2643	Sequence 2643, App
10	81	79.4	18	US-09-836-073-9	Sequence 9, Appl1
11	79	77.5	18	US-09-836-073-11	Sequence 11, Appl1
12	79	77.5	18	US-09-836-073-12	Sequence 12, Appl1
13	78	76.5	18	US-09-836-073-10	Sequence 10, Appl1
14	76.5	75.0	19	US-09-836-073-16	Sequence 16, Appl1
15	75	73.5	18	US-09-836-073-2	Sequence 2, Appl1

16	75	73.5	18	US-09-836-073-3	Sequence 3, Appl1
17	73	71.6	21	US-10-376-121A-20	Sequence 20, Appl1
18	72	70.6	18	US-09-836-073-7	Sequence 7, Appl1
19	72	70.6	18	US-09-836-073-15	Sequence 15, Appl1
20	71	69.6	18	US-09-836-073-8	Sequence 8, Appl1
21	68	66.7	38	US-10-325-810-214	Sequence 214, App
22	62	60.8	16	US-09-836-073-19	Sequence 19, Appl1
23	59	57.8	38	US-09-843-676-25	Sequence 25, Appl1
24	59	57.8	38	US-09-766-253-25	Sequence 25, Appl1
25	59	57.8	38	US-09-438-486-25	Sequence 25, App
26	59	57.8	38	US-10-325-810-215	Sequence 215, App
27	59	57.8	38	US-10-053-758-25	Sequence 25, Appl1
28	59	57.8	38	US-10-054-295-25	Sequence 25, Appl1
29	59	57.8	38	US-10-054-611-25	Sequence 25, Appl1
30	58.5	57.4	37	US-09-843-676-24	Sequence 24, Appl1
31	58.5	57.4	37	US-09-766-253-24	Sequence 24, Appl1
32	58.5	57.4	37	US-10-438-486-24	Sequence 24, Appl1
33	58.5	57.4	37	US-10-053-758-24	Sequence 24, Appl1
34	58.5	57.4	37	US-10-054-295-24	Sequence 24, Appl1
35	58.5	57.4	37	US-10-054-611-24	Sequence 24, Appl1
36	56	54.9	18	US-09-836-073-6	Sequence 6, Appl1
37	51	50.0	190	US-10-437-963-184914	Sequence 184914, Sequence 272690,
38	49	48.0	488	US-10-424-559-272690	Sequence 125036,
39	49	48.0	922	US-10-437-963-125036	Sequence 26, Appl1
40	48	47.1	39	US-09-843-676-26	Sequence 26, Appl1
41	48	47.1	39	US-09-766-253-26	Sequence 26, Appl1
42	48	47.1	39	US-09-438-486-26	Sequence 26, Appl1
43	48	47.1	39	US-10-325-810-216	Sequence 216, App
44	48	47.1	39	US-10-053-758-26	Sequence 26, Appl1
45	48	47.1	39	US-10-054-295-26	Sequence 26, Appl1

ALIGNMENTS

RESULT 1
US-09-836-073-4
; Sequence 4, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Balidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836, 073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316, 630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-4

Query Match 100.0%; Score 102; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.7e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 QOGEAKICHOIEYFGDF 18
Db 1 QOGEAKICHOIEYFGDF 18

RESULT 2
US-09-836-073-5
; Sequence 5, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULAR TYPE: peptide
US-08-854-050-24

Query Match 57.4%; Score 58.5; DB 3; Length 37;
Best Local Similarity 91.7%; Pred. No. 0.008; 0; Indels 1; Gaps 1;
Matches 11; Conservative 0; Mismatches 0;

Qy 7 ICHQIEYFGDF 18
Db 1 ICHQ-EYFGDF 11

RESULT 15
US-09-430-323-24
Sequence 24, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULAR TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-430-323-24

Query Match 57.4%; Score 58.5; DB 4; Length 37;
Best Local Similarity 91.7%; Pred. No. 0.008; 0; Indels 1; Gaps 1;
Matches 11; Conservative 0; Mismatches 0;

Qy 7 ICHQIEYFGDF 18
Db 1 ICHQ-EYFGDF 11

Search completed: September 10, 2004, 18:05:08
Job time: 16.8883 secs

FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 215:
US-09-721-456-215

Query Match 57.8%; Score 59; DB 4; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.0069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ICHQIEYFGD 17
DB 1 ICEQIEYFGD 11

RESULT 13
US-08-851-843A-24
Sequence 24, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-851-843A-24

Query Match 57.4%; Score 58.5; DB 3; Length 37;
Best Local Similarity 91.7%; Pred. No. 0.008;
Matches 11; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 7 ICHQIEYFGDF 18
DB 1 ICHQ-EYFGDF 11

RESULT 14
US-08-854-050-24
Sequence 24, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536

FILED DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-430-323-25

Query Match 57.8%; Score 59; DB 4; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.0069; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1;

QY 7 ICHQIEYYFGD 17
DB 1 ICEQIEYYFGD 11

RESULT 11
US-09-402-181B-215
Sequence 215, Application US/09402181B
Patent No. 6610839
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050

FILED DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 215:
US-09-402-181B-215

Query Match 57.8%; Score 59; DB 4; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.0069; 1; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1;

QY 7 ICHQIEYYFGD 17
DB 1 ICEQIEYYFGD 11

RESULT 12
US-09-721-456-215
Sequence 215, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-NOV-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017

FILED DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-721-456-214

Query Match 66.7%; Score 68; DB 4; Length 38;
Best Local Similarity 91.7%; Pred. No. 0.00024;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ICHQIEYFGDF 18
DB 1 ICHQIEYFGDF 12

RESULT 7
US-08-851-843A-25
Sequence 25, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-851-843A-25

Query Match 57.8%; Score 59; DB 3; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.0069;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ICHQIEYFGD 17
DB 1 ICHQIEYFGD 11

RESULT 8
US-08-974-549A-215
Sequence 215, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050

APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-214

Query Match 66.7%; Score 68; DB 3; Length 38;
Best Local Similarity 91.7%; Pred. No. 0.00024;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ICHQIEYFGDF 18
Db 1 ICHQIEYFGDF 12

RESULT 5
US-09-402-181B-214
Sequence 214, Application US/09402181B
Patent No. 6610839
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Auesenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-402-181B-214

Query Match 66.7%; Score 68; DB 4; Length 38;
Best Local Similarity 91.7%; Pred. No. 0.00024;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ICHQIEYFGDF 18
Db 1 ICHQIEYFGDF 12

RESULT 6
US-09-721-456-214
Sequence 214, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312

PRIOR FILING DATE: 1997-10-06
PRIOR APPLICATION NUMBER: 08/321,427
PRIOR FILING DATE: 1994-10-11
PRIOR APPLICATION NUMBER: 60/086,527
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 4
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: B-LAP
US-09-316-630-4

Query Match 85.3%; Score 87; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.7e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EAKICHQIEYFGDF 18
DB 4 EAKICHQIEYFGDF 18

RESULT 3
US-08-475-955-20
Sequence 20, Application US/08475955
Patent No. 6641813
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,955
FILING DATE: June 7, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRP14CIP(2) DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Binding-site
LOCATION: 8.15
US-08-475-955-20

Query Match 71.6%; Score 73; DB 4; Length 21;
Best Local Similarity 100.0%; Pred. No. 1.9e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ICHQIEYFGDF 18
DB 1 ICHQIEYFGDF 12

RESULT 4
US-08-974-549A-214
Sequence 214, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:

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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:43:01 ; Search time 15.8883 Seconds
(without alignments)
58.488 Million cell updates/sec

Title: US-09-836-073-4

Perfect score: 102
Sequence: 1 QQQEAKICHOIEYFGDF 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/2/iaa/PTUS.COMB.pep:*
- 6: /cgn2_6/ptodata/2/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	87	85.3	18	3	US-09-316-630-4
3	73	71.6	21	4	US-08-475-955-20
4	68	66.7	38	3	US-08-974-549A-214
5	68	66.7	38	4	US-09-402-181B-214
6	68	66.7	38	4	US-09-721-456-214
7	59	57.8	38	3	US-08-851-843A-25
8	59	57.8	38	3	US-08-974-549A-215
9	59	57.8	38	3	US-08-854-050-25
10	59	57.8	38	4	US-09-430-323-25
11	59	57.8	38	4	US-09-402-181B-215
12	59	57.8	38	4	US-09-721-456-215
13	58.5	57.4	37	3	US-08-851-843A-24
14	58.5	57.4	37	3	US-08-854-050-24
15	58.5	57.4	37	3	US-09-430-323-24
16	48	47.1	39	3	US-08-851-843A-26
17	48	47.1	39	3	US-08-974-549A-216
18	48	47.1	39	3	US-08-854-050-26
19	48	47.1	39	4	US-09-430-323-26
20	48	47.1	39	4	US-09-402-181B-216
21	48	47.1	39	4	US-09-721-456-216
22	41	40.2	497	4	US-09-489-039A-8926
23	41	40.2	1220	2	US-08-680-326-38
24	40	39.2	69	4	US-09-621-976-7385
25	40	39.2	124	4	US-09-489-039A-9103
26	40	39.2	431	1	US-08-311-023-2
27	40	39.2	582	4	US-09-976-594-733

28	39	38.2	122	4	US-09-732-210-62	Sequence 62, Appl
29	39	38.2	246	4	US-09-104-678A-2	Sequence 2, Appl1
30	39	38.2	247	4	US-09-548-938A-12	Sequence 12, Appl
31	39	38.2	333	4	US-09-252-991A-31345	Sequence 31345, A
32	39	38.2	467	4	US-09-252-991A-24329	Sequence 24329, A
33	39	38.2	483	3	US-09-027-166-7	Sequence 7, Appl1
34	39	38.2	754	2	US-08-941-262-1	Sequence 1, Appl1
35	39	38.2	755	2	US-08-941-262-3	Sequence 1, Appl1
36	39	38.2	817	4	US-09-252-991A-27609	Sequence 27609, A
37	38.5	37.7	412	4	US-09-543-681A-4298	Sequence 4298, Ap
38	38	37.3	141	4	US-09-540-236-2332	Sequence 2332, Ap
39	38	37.3	225	4	US-09-134-000C-4312	Sequence 4312, Ap
40	38	37.3	445	4	US-09-489-039A-13869	Sequence 13869, A
41	38	37.3	456	1	US-08-205-719-4	Sequence 4, Appl1
42	38	37.3	456	3	US-08-431-517F-6	Sequence 6, Appl1
43	38	37.3	482	3	US-08-431-517F-5	Sequence 5, Appl1
44	38	37.3	482	3	US-08-431-517F-5	Sequence 5, Appl1
45	38	37.3	505	4	US-09-627-216A-12	Patent No. 5245013 Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-316-630-3
Sequence 3, Application US/09316630
Patent No. 6291637
GENERAL INFORMATION:
APPLICANT: Das, Saumitra
TITLE OF INVENTION: INTERFERENCE WITH VIRAL IRES-MEDIATED TRANSLATION BY A
TITLE OF INVENTION: SMALL YEAST RNA REVEALS CRITICAL RNA-PROTEIN INTERACTIONS
FILE REFERENCE: 22000-20548-21
CURRENT APPLICATION NUMBER: US/09/316,630
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 08/817,953
PRIOR FILING DATE: 1997-10-06
PRIOR APPLICATION NUMBER: 08/321,427
PRIOR FILING DATE: 1994-10-11
PRIOR APPLICATION NUMBER: 60/086,527
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: LAP
US-09-316-630-3
Query Match 85.3%; Score 87; DB 3; Length 18;
Best local similarity 100.0%; Pred. No. 8.7e-08;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 4 EAKICHOIEYFGDF 18
DB 4 EAKICHOIEYFGDF 18
RESULT 2
US-09-316-630-4
Sequence 4, Application US/09316630
Patent No. 6291637
GENERAL INFORMATION:
APPLICANT: Das, Saumitra
TITLE OF INVENTION: INTERFERENCE WITH VIRAL IRES-MEDIATED TRANSLATION BY A
TITLE OF INVENTION: SMALL YEAST RNA REVEALS CRITICAL RNA-PROTEIN INTERACTIONS
FILE REFERENCE: 22000-20548-21
CURRENT APPLICATION NUMBER: US/09/316,630
CURRENT FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 08/817,953

Query Match 85.3%; Score 87; DB 7; Length 415;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EAKICHQIERYFGDF 18
 |||||
 DB 14 EAKICHQIERYFGDF 28

RESULT 15
 ADE63993
 ID ADE63993 standard; protein; 415 AA.

AC ADE63993;

DT 29-JAN-2004 (first entry)

DE Rat Protein P38656, SEQ ID NO 9939.

KM Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

OS Rattus norvegicus.

PN WO2003016475-A2.

PD 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

PA (GENO) GEN HOSPITAL CORP.

PI (FARB) BAYER AG.

PI Woolf C, D'urso D, Befort K, Costigan M;

DR WPI; 2003-268312/26.

DR GENBANK; P38656.

PT New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.

PS Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 415 AA;

Query Match 85.3%; Score 87; DB 7; Length 415;
 Best Local Similarity 100.0%; Pred. No. 1.1e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EAKICHQIERYFGDF 18
 |||||

DB 14 EAKICHQIERYFGDF 28

Search completed: September 10, 2004, 17:51:46
 Job time : 57.4128 secs

	RESULT 13
ID	ADE62859 standard; protein; 408 AA.
XX	ADE62859
AC	ADE62859 standard; protein; 408 AA.
XX	ADE62859;
DT	29-JAN-2004 (first entry)
XX	
DE	Human Protein P05455, SEQ ID NO 8793.
XX	
KW	Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
OS	Homo sapiens.
PX	WO2003016475-A2.
PN	
XX	
PD	27-FEB-2003.
XX	
PF	14-AUG-2002; 2002MO-US025765.
XX	
PR	14-AUG-2001; 2001US-0312147P. PR 01-NOV-2001; 2001US-0346382P. PR 26-NOV-2001; 2001US-0333347P.
XX	
PA	(GHEO) GEN HOSPITAL CORP. (FARB) BAYER AG.
PI	
XX	
PI	Woolf C, D'urso D, Befort K, Costigan M; MPI: 2003-268312/26. DR GENBANK; P05455.
PT	New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
PS	Claim 1; Page: 1017pp; English.
XX	
CC	The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/publ/published_pct_sequences .
XX	
SQ	Sequence 408 AA:
Query Match	85.3%; Score 87; DB 7; Length 408;
Best Local Similarity	100.0%; Pred No. 1.1e-05;
Matches 15; Conservative	0; Mismatches 0; Indels 0; Gaps 0

OY 4 EAKICHOIEVYFGDF 18
 |||||
 Db 14 EAKICHOIEVYFGDF 28
 |||||
 RESULT 14
 ADE63989
 ID ADE63989 standard; protein; 415 AA.
 AC ADE63989;
 DT 29-JAN-2004 (first entry)
 DE Rat Protein P38656, SEQ ID NO 9935.
 KM Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 XX chronic constriction injury; CCI, spared nerve injury; SNI; Chung.
 OS Rattus norvegicus.
 PN WO2003016475-A2.
 XX
 XX 27-FEB-2003.
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GENO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 PI Woolf C, D'urso D, Befort K, Costigan M;
 DR WPI; 2003-268312/26.
 DX GENEANK; P38656.
 PT New composition comprising two or more isolated polypeptides, useful for
 PP preparing a medicament for treating pain in an animal.
 PS Claim 1; Page; 1017pp; English.
 XX
 XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (shown in Table 2 of
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 415 AA;
 SO

CC the invention compete with LAP and inhibit the utilisation of various
 CC biochemical and physiological functions of LAP required for a productive
 CC life cycle. The methods and compositions are useful as antiviral therapy
 CC in pharmaceutical, veterinary or agricultural/horticultural applications.
 CC ABG72101-ABG72119 represent peptides useful as antiviral agents
 CC XX

SO Sequence 18 AA;

Query Match 85.3%; Score 87; DB 6; Length 18;

Best Local Similarity 100.0%; Pred.No. 3.9e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EAKICHQIEYFGDF 18
 |||||
 Db 4 EAKICHQIEYFGDF 18

RESULT 7

AA01351

ID AAG01351 standard; protein; 92 AA.

XX AAG01351;

XX 06-OCT-2000 (first entry)

XX Human secreted protein, SEQ ID NO: 5432.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.

XX Homo sapiens.

XX EPI033401-A2.

XX 06-SEP-2000.

XX 21-FEB-2000; 2000EP-00200610.

XX 26-FEB-1999; 99US-0122487P.

XX (GEST) GENSET.

XX Dumas Mline Edwards J, Duclert A, Giordano J;

XX WPI; 2000-500381/45.

XX N-PSDB; AAC01357.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX Claim 13; SEQ ID NO 5432; 71pp + Sequence Listing; English.

XX The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors

SO Sequence 92 AA;

Query Match 85.3%; Score 87; DB 3; Length 92;

Best Local Similarity 100.0%; Pred.No. 2.2e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EAKICHQIEYFGDF 18
 |||||
 Db 14 EAKICHQIEYFGDF 28

RESULT 8

AA03716

ID AAM03716 standard; protein; 408 AA.

XX AAM03716;

XX 25-MAR-2003 (revised)

XX 12-MAR-1997 (first entry)

XX Human autoantigen La(SS-B).

XX Autoimmune disease; Ia autoantigen; Sjogren's syndrome;
 KW systemic lupus erythematosus; diagnosis.

XX Homo sapiens.

XX US5541291-A.

XX 30-JUL-1996.

XX 27-MAY-1987; 87US-00054871.

XX 31-DEC-1984; 84US-00687908.

XX (UYDU-) UNIV DUKE.

XX Keene JD;

XX WPI; 1996-362015/36.

XX Auto-antigen U2-RNP, associated with severe polymyositis-scleroderma
 PT overlap syndrome - useful for diagnosis and treatment of autoimmune
 PT diseases.

XX Disclosure; Col 15-16; 21pp; English.

XX The human lupus antigen (La) is diagnostic for Sjogren's syndrome, as
 CC well as occurring in systemic lupus erythematosus patients. The La protein
 CC is clinically related to the Ro protein that is highly common among
 CC autoimmune patients. La and Ro antigens sometimes reside on the same
 CC cellular ribonucleoprotein particle; most La patients contain some Ro
 CC antibodies and vice versa. La cDNA has been isolated from a human liver
 CC library. (Updated on 25-MAR-2003 to correct PF field.)

SO Sequence 408 AA;

Query Match 85.3%; Score 87; DB 2; Length 408;

Best Local Similarity 100.0%; Pred.No. 1.1e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EAKICHQIEYFGDF 18
 |||||
 Db 14 EAKICHQIEYFGDF 28

RESULT 9

ABP65252

ID ABP65252 standard; protein; 408 AA.

XX ABP65252;

XX 12-NOV-2002 (first entry)

XX Hypoxia-regulated protein #126.

XX Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy;
 KW antiinflammatory; vulnery; gynecological; ophthalmological; vaccine;
 KW hypoxia; tumourigenesis; angiogenesis; apoptosis; cancer;

XX 02-DEC-1999.
 PD 21-MAY-1999; 99WO-US011281.
 PF 22-MAY-1998; 98US-0086527P.
 PR (REBC) UNIV CALIFORNIA.
 PA Das S, Dasgupta A;
 PI WPI; 2000-062712/05.
 DR New yeast inhibitory peptide useful for inhibiting viral protein
 XX translation and replication.
 PT Claim 5; Page 57; 81pp; English.
 PS This sequence is the Ia autoantigen binding domain (LAP). LAP is a
 CC cellular protein which binds to an internal ribosome entry site (IRES).
 CC The peptide is used to inhibit mRNA translation, viral protein
 CC translation or viral replication. Viral mRNA translation is initiated at
 CC the IRES and the LAP peptide prevents translation initiation factors from
 CC binding at the site. The peptide can be used alone or in combination with
 CC an inhibitor RNA (IRNA see AAZ45200). The LAP peptide is useful as an
 CC antiviral agent, which works through the inhibition of mRNA translation,
 CC especially viral mRNA. Examples of viruses which can be inhibited are
 CC picornavirus, flavivirus, coronavirus, hepatitis A B or C viruses,
 CC rhadovirus, adenovirus, and parainfluenza virus, poliovirus, rhinovirus,
 CC coxsackie virus, encephalomyocarditis virus, foot-and-mouth disease
 CC virus, echo virus, hepatitis C virus, infectious bronchitis virus, duck
 CC and human hepatitis B virus, and vesicular stomatitis virus. The peptide
 CC also inhibits replication of the above viruses. The LAP peptide
 CC selectively inhibits viral protein translation, and is therefore not
 CC toxic to the host cell
 XX
 SQ Sequence 18 AA;
 Query Match 85.3%; Score 87; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.9e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 EAKICHOIEYFGDF 18
 DB 4 EAKICHOIEYFGDF 18
 RESULT 5
 ABG72101
 ID ABG72101 standard; peptide; 18 AA.
 AC ABG72101;
 XX
 DT 28-JAN-2003 (first entry)
 DE Viral replication inhibiting peptide, LAP.
 XX
 XX Viral replication inhibitor; IRES initiated translation; LAP;
 KM internal ribosome entry site initiated translation; Ia antigen protein;
 KW viral life cycle; antiviral therapy; pharmaceutical; veterinary;
 KM agricultural; horticultural; virucide.
 XX
 XX Unidentified.
 OS
 XX WO200283858-A2.
 PN
 PD 24-OCT-2002.
 XX
 XX 12-APR-2002; 2002WO-US011589.
 PF
 XX 16-APR-2001; 2001US-00836073.
 PR
 XX (UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.
 PA

XX Dasgupta A, Das S, Baidya N;
 PI WPI; 2003-058634/05.
 DR New compound containing acidic and aromatic amino acids, useful as
 XX antiviral therapy in pharmaceutical, veterinary or
 PT agricultural/horticultural applications.
 PT Claim 1; Page 15; 19pp; English.
 PS The present invention relates to peptides and methods of inhibiting the
 CC replication of viruses that utilise internal ribosome entry site (IRES)
 CC initiated translation, and/or inhibiting viruses that utilise the Ia
 CC antigen protein (LAP) in any phase of their life cycle. The peptides of
 CC the invention compete with LAP and inhibit the utilisation of various
 CC biochemical and physiological functions of LAP required for a productive
 CC life cycle. The methods and compositions are useful as antiviral therapy
 CC in pharmaceutical, veterinary or agricultural/horticultural applications.
 CC ABG72101-ABG72119 represent peptides useful as antiviral agents
 XX
 SQ Sequence 18 AA;
 Query Match 85.3%; Score 87; DB 6; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.9e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 EAKICHOIEYFGDF 18
 DB 4 EAKICHOIEYFGDF 18
 RESULT 6
 ABG72114
 ID ABG72114 standard; peptide; 18 AA.
 AC ABG72114;
 XX
 DT 28-JAN-2003 (first entry)
 DE Viral replication inhibiting peptide, BOVINE.
 XX
 XX Viral replication inhibitor; IRES initiated translation; LAP;
 KM internal ribosome entry site initiated translation; Ia antigen protein;
 KW viral life cycle; antiviral therapy; pharmaceutical; veterinary;
 KM agricultural; horticultural; virucide; bovine.
 XX
 XX Bovinae.
 OS
 XX WO200283858-A2.
 PN
 PD 24-OCT-2002.
 XX
 XX 12-APR-2002; 2002WO-US011589.
 PF
 XX 16-APR-2001; 2001US-00836073.
 PR
 XX (UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.
 PA Dasgupta A, Das S, Baidya N;
 PI WPI; 2003-058634/05.
 DR New compound containing acidic and aromatic amino acids, useful as
 XX antiviral therapy in pharmaceutical, veterinary or
 PT agricultural/horticultural applications.
 PT Disclosure; Page 6; 19pp; English.
 PS The present invention relates to peptides and methods of inhibiting the
 CC replication of viruses that utilise internal ribosome entry site (IRES)
 CC initiated translation, and/or inhibiting viruses that utilise the Ia
 CC antigen protein (LAP) in any phase of their life cycle. The peptides of

12-APR-2002; 2002WO-US011589.
16-APR-2001; 2001US-00836073.
(UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.
Dasgupta A, Das S, Baidya N;
WPI: 2003-058634/05.
New compound containing acidic and aromatic amino acids, useful as
antiviral therapy in pharmaceutical, veterinary or
agricultural/horticultural applications.
Example 3; Page 14; 19pp; English.
The present invention relates to peptides and methods of inhibiting the
replication of viruses that utilize internal ribosome entry site (IRES)
initiated translation, and/or inhibiting viruses that utilize the IAP
antigen protein (IAP) in any phase of their life cycle. The peptides of
the invention compete with IAP and inhibit the utilisation of various
biochemical and physiological functions of IAP required for a productive
life cycle. The methods and compositions are useful as antiviral therapy
in pharmaceutical, veterinary or agricultural/horticultural applications
AB672101-AB672119 represent peptides useful as antiviral agents

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XX 28-JAN-2003 (first entry)
XX
XX
XX Viral replication inhibiting peptide, MOUSE.
XX
XX Viral replication inhibitor; IRES initiated translation; LAP;
XX internal ribosome entry site initiated translation; Ia antigen protein,
XX viral life cycle; antiviral therapy; pharmaceutical; veterinary;
XX agricultural; horticultural; virocidic; mouse.
XX
XX Mus sp.
XX
XX WO200283858-A2.
XX
XX 24-OCT-2002.
XX
XX 12-APR-2002; 2002WO-US011589.
XX
XX 16-APR-2001; 2001US-00836073.
XX
XX (UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.
XX
XX Daesupta A, Das S, Baidya N;
XX
XX WPI; 2003-058634/05.
XX
XX New compound containing acidic and aromatic amino acids, useful as
XX antiviral therapy in pharmaceutical, veterinary or
XX agricultural/horticultural applications.
XX
XX Claim 1; Page 15; 19pp; English.
XX
XX The present invention relates to peptides and methods of inhibiting the
XX replication of viruses that utilise internal ribosome entry site (IRES)
XX initiated translation, and/or inhibiting viruses that utilise the Ia
XX antigen protein (LAP) in any phase of their life cycle. The peptides of
XX the invention compete with LAP and inhibit the utilisation of various
XX biochemical and physiological functions of LAP required for a productive
XX life cycle. The methods and compositions are useful as antiviral therapy
XX in pharmaceutical, veterinary or agricultural/horticultural applications.
XX AB672101-AB672119 represent peptides useful as antiviral agents
XX
XX Sequence 17 AA;
XX
XX Query Match 85.3%; Score 87; DB 6; Length 17;
XX Best Local Similarity 100.0%; Pred. No. 3.6e-07;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4 EAKICHQIEYFFGDF 18
XX |||||||
XX 3 EAKICHQIEYFFGDF 17
XX
XX RESULT 4
XX ID AAY52200 standard; peptide; 18 AA.
XX
XX AAY52200;
XX
XX 14-MAR-2000 (first entry)
XX
XX Human Ia autoantigen peptide (LAP).
XX
XX La autoantigen; LAP; internal ribosome entry site; IRES; translation;
XX viral replication; IRNA; antiviral agent; picornavirus; flavivirus;
XX coronavirus; hepatitis virus; rabdovirus; adenovirus; coxsackie virus;
XX parainfluenza virus; poliovirus; rhinovirus; encephalomyocarditis virus;
XX foot-and-mouth disease virus; echo virus; infectious bronchitis virus;
XX vesicular stomatitis virus.
XX
XX Homo sapiens.
XX
XX WO9961613-A2

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OM protein - protein search, using sw model

Run on: September 10, 2004, 16:58:20 ; Search time 56.3129 Seconds
(without alignments)
90.314 Million cell updates/sec

Title: US-09-836-073-4

Perfect score: 102
Sequence: 1 QOOEAKICHIQIEYFGDF 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	102	100.0	18	6	ABG72104 Viral rep
2	90	88.2	18	6	ABG72105 Viral rep
3	87	85.3	17	6	ABG72113 Viral rep
4	87	85.3	18	3	AAV52200 Human Ia
5	87	85.3	18	6	ABG72101 Viral rep
6	87	85.3	18	6	ABG72114 Viral rep
7	87	85.3	92	3	AAAG01351 Human sec
8	87	85.3	408	2	AAW03716 Human aut
9	87	85.3	408	5	ABP65252 Hypoxia-r
10	87	85.3	408	5	ABP65252 Human pro
11	87	85.3	408	7	ADDE63991 Human pro
12	87	85.3	408	7	ADDE63995 Human pro
13	87	85.3	408	7	ADDE63995 Human pro
14	87	85.3	415	7	ADDE63989 Rat prote
15	87	85.3	415	7	ADDE63993 Rat prote
16	87	85.3	439	4	ABG08417 Novel hum
17	87	85.3	460	3	AAAS8987 Breast an
18	87	85.3	460	5	ABP41511 Human ova
19	81	79.4	18	6	ABG72109 Viral rep
20	79	77.5	18	6	ABG72111 Viral rep
21	79	77.5	18	6	ABG72112 Viral rep
22	78	76.5	18	6	ABG72110 Viral rep
23	76.5	75.0	19	6	ABG72116 Viral rep
24	75	73.5	18	6	ABG72102 Viral rep
25	75	73.5	18	6	ABG72103 Viral rep

26	73	71.6	21	2	AA43394 Ia/ISB ep
27	72	70.6	18	6	ABG72115 Viral rep
28	72	70.6	18	6	ABG72107 Viral rep
29	71	69.6	18	6	ABG72108 Viral rep
30	62	60.8	16	6	ABG72119 Viral rep
31	57	55.9	390	4	ABBS5316 Drosophi1
32	56	54.9	18	6	ABG72106 Viral rep
33	52	51.0	381	6	ABJ19009 Patchogen
34	52	51.0	391	6	ABM72091 Stephyloc
35	48	47.1	913	3	AA47714 Arabidops
36	48	47.1	923	3	AA47713 Arabidops
37	48	47.1	993	3	AA47712 Arabidops
38	47	46.1	411	6	ABP70526 Histone d
39	46	45.1	33	7	ABO23427 Amino aci
40	46	45.1	377	6	ABU43510 Protein e
41	45	44.1	1900	4	ABBS59107 Drosophi1
42	44	43.1	18	6	ABG72117 Viral rep
43	44	43.1	135	4	ABG27058 Novel hum
44	44	43.1	224	5	ABBS9645 Human pol
45	44	43.1	224	6	ADA55336 Human pro

ALIGNMENTS

RESULT 1
ID ABG72104 standard; peptide; 18 AA.
XX
AC ABG72104;
XX
DT 28-JAN-2003 (first entry)
XX
DE Viral replication inhibiting peptide, 761.
XX
KW Viral replication inhibitor; IRIS initiated translation; LAP;
KW internal ribosome entry site initiated translation; Ia antigen protein;
KW viral life cycle; antiviral therapy; pharmaceutical; veterinary;
KW agricultural; horticultural; virucide.
XX
OS Unidentified.
XX
PN WO200283858-A2.
XX
PD 24-OCT-2002.
XX
PF 12-APR-2002; 2002WO-US011589.
XX
PR 16-APR-2001; 2001US-00836073.
XX
PA (UYCA-) UNIV CALIFORNIA OFFICE PRESIDENT.
XX
PI Dasgupta A, Das S, Baidya N;
XX
XX WPI; 2003-058634/05.
XX
PT New compound containing acidic and aromatic amino acids, useful as
PT antiviral therapy in pharmaceutical, veterinary or
PT agricultural/horticultural applications.
XX
PS Claim 10; Page 16; 19pp; English.
XX
CC The present invention relates to peptides and methods of inhibiting the
CC replication of viruses that utilize internal ribosome entry site (IRES)
CC initiated translation, and/or inhibiting viruses that utilize the Ia
CC antigen protein (IAP) in any phase of their life cycle. The peptides of
CC the invention compete with IAP and inhibit the utilisation of various
CC biochemical and physiological functions of IAP required for a productive
CC life cycle. The methods and compositions are useful as antiviral therapy
CC in pharmaceutical, veterinary or agricultural/horticultural applications.
XX
XX ABG72101-ABG72119 represent peptides useful as antiviral agents
XX
XX Sequence 18 AA;

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Search completed: September 10, 2004, 18:11:55
Job time : 41.424 secs

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FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 18
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-836-073-12

Query Match      80.6%; Score 79; DB 9; Length 18;
Best Local Similarity 77.8%; Pred. No. 8.3e-06;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AALQAKICHQIQYFGQF 18
DB 1 AALEAKICHQIEYFGDF 18

RESULT 12
US-09-836-073-10
Sequence 10, Application US/09836073
Patent No. US20020173475A1
GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Balidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 18
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-836-073-10

Query Match      79.6%; Score 78; DB 9; Length 18;
Best Local Similarity 77.8%; Pred. No. 1.2e-05;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AALQAKICHQIQYFGQF 18
DB 1 AALEAKICHQIEYFGDF 18

RESULT 13
US-09-836-073-16
Sequence 16, Application US/09836073
Patent No. US20020173475A1
GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Balidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16
LENGTH: 19
TYPE: PRT
ORGANISM: Rat
```

```
US-09-836-073-16

Query Match      78.1%; Score 76.5; DB 9; Length 19;
Best Local Similarity 78.9%; Pred. No. 2.2e-05;
Matches 15; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 AALQAKICHQIQYFGQF 18
DB 1 AALEAKICHQIEYFGDF 19

RESULT 14
US-09-836-073-2
Sequence 2, Application US/09836073
Patent No. US20020173475A1
GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Balidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 18
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-836-073-2

Query Match      76.5%; Score 75; DB 9; Length 18;
Best Local Similarity 72.2%; Pred. No. 3.7e-05;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 AALQAKICHQIQYFGQF 18
DB 1 AALEAKICHQIEYFGDF 18

RESULT 15
US-09-836-073-4
Sequence 4, Application US/09836073
Patent No. US20020173475A1
GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Balidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 18
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-836-073-4

Query Match      76.5%; Score 75; DB 9; Length 18;
Best Local Similarity 80.0%; Pred. No. 3.7e-05;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 QAKICHQIQYFGQF 18
DB 4 EAKICHQIEYFGDF 18
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```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-102-806-695

Query Match      88.8%; Score 87; DB 14; Length 460;
Best Local Similarity 83.3%; Pred. No. 1,1e-05;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 AALQAKICHQIQYFFGQF 18
Db      63 AALEAKICHQIEYFFGDF 80

RESULT 7
US-10-264-049-2643
; Sequence 2643, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2643
; LENGTH: 460
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-2643

Query Match      88.8%; Score 87; DB 15; Length 460;
Best Local Similarity 83.3%; Pred. No. 1,1e-05;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 AALQAKICHQIQYFFGQF 18
Db      63 AALEAKICHQIEYFFGDF 80

RESULT 8
US-09-836-073-13
; Sequence 13, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Mouse
US-09-836-073-13

Query Match      84.7%; Score 83; DB 9; Length 17;
Best Local Similarity 82.4%; Pred. No. 1,8e-06;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 ALOAKICHQIQYFFGQF 18
Db      1 ALEAKICHQIEYFFGDF 17
```

```

RESULT 9
US-09-836-073-9
; Sequence 9, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-9

Query Match      82.7%; Score 81; DB 9; Length 18;
Best Local Similarity 87.5%; Pred. No. 3,9e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 AALQAKICHQIQYFFG 16
Db      1 AALEAKICHQIEYFFG 16
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RESULT 10
US-09-836-073-11
; Sequence 11, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-11

Query Match      80.6%; Score 79; DB 9; Length 18;
Best Local Similarity 77.8%; Pred. No. 8,3e-06;
Matches 14; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 AALQAKICHQIQYFFGQF 18
Db      1 AALEAKICHQIEYFFGDF 18

RESULT 11
US-09-836-073-12
; Sequence 12, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
```

```
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 18
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-836-073-1
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```
Query Match      88.8%; Score 87; DB 9; Length 18;
Best Local Similarity 83.3%; Pred. No. 4.3e-07;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY      1 AALQAKICHQIQYFGQF 18
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DB      1 AALEAKICHQIEYFGDF 18
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```
RESULT 3
US-09-836-073-14
Sequence 14, Application US/09836073
Patent No. US20020173475A1
GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Baidya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 18
TYPE: PRT
ORGANISM: Bovine
US-09-836-073-14
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```
Query Match      88.8%; Score 87; DB 9; Length 18;
Best Local Similarity 83.3%; Pred. No. 4.3e-07;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1 AALQAKICHQIQYFGQF 18
      |||:|||||:|||||
DB      1 AALEAKICHQIEYFGDF 18
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```
RESULT 4
US-10-170-385-477
Sequence 477, Application US/10170385
Publication No. US2003020372A1
GENERAL INFORMATION:
APPLICANT: Ward, Neil Raymond
APPLICANT: Mundy, Christopher Robert
APPLICANT: Kan, On
APPLICANT: Harris, Robert Alan
APPLICANT: White, Jonathan
APPLICANT: Binley, Katie Mary
APPLICANT: Rayner, William Nigel
APPLICANT: Naylor, Stuart
APPLICANT: Kingsman, Susan Mary
APPLICANT: Krige, David
TITLE OF INVENTION: ANALYSIS METHOD
FILE REFERENCE: 532682000100
CURRENT APPLICATION NUMBER: US/10/170,385
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CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: PCT/GB02/01662
PRIOR FILING DATE: 2002-04-08
PRIOR APPLICATION NUMBER: PCT/GB01/05458
PRIOR FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 549
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 477
LENGTH: 408
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-170-385-477
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Query Match      88.8%; Score 87; DB 12; Length 408;
Best Local Similarity 83.3%; Pred. No. 9.7e-06;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1 AALQAKICHQIQYFGQF 18
      |||:|||||:|||||
DB      11 AALEAKICHQIEYFGDF 28
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RESULT 5
US-09-925-298-695
Sequence 695, Application US/09925298
Publication No. US20020039764A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103
CURRENT APPLICATION NUMBER: US/09/925,298
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 695
LENGTH: 460
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-298-695
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Query Match      88.8%; Score 87; DB 12; Length 460;
Best Local Similarity 83.3%; Pred. No. 1.1e-05;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1 AALQAKICHQIQYFGQF 18
      |||:|||||:|||||
DB      63 AALEAKICHQIEYFGDF 80
```

```
RESULT 6
US-10-102-806-695
Sequence 695, Application US/10102806
Publication No. US20030054421A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103P1
CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 695
LENGTH: 460
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SUMMARIES

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2	87	88.8	18	9	US-09-836-073-1	Sequence 1, Appli
3	87	88.8	18	9	US-09-836-073-14	Sequence 14, Appli
4	87	88.8	408	12	US-10-170-385-477	Sequence 477, App
5	87	88.8	460	12	US-09-925-298-695	Sequence 695, App
6	87	88.8	460	14	US-10-102-806-695	Sequence 695, App
7	87	88.8	460	15	US-10-264-049-2643	Sequence 2643, Ap
8	83	84.7	17	9	US-09-836-073-13	Sequence 13, Appli
9	81	82.7	18	9	US-09-836-073-9	Sequence 9, Appli
10	79	80.6	18	9	US-09-836-073-11	Sequence 11, Appli
11	79	80.6	18	9	US-09-836-073-12	Sequence 12, Appli
12	78	79.6	18	9	US-09-836-073-10	Sequence 10, Appli
13	76.5	78.1	19	9	US-09-836-073-16	Sequence 16, Appli
14	75	76.5	18	9	US-09-836-073-2	Sequence 2, Appli
15	75	76.5	18	9	US-09-836-073-4	Sequence 4, Appli

16	72	73.5	18	9	US-09-836-073-7	Sequence 7, Appli
17	71	72.4	18	9	US-09-836-073-8	Sequence 8, Appli
18	65	66.3	18	9	US-09-836-073-15	Sequence 15, Appli
19	64	65.3	21	15	US-10-376-121A-20	Sequence 20, Appli
20	63	64.3	18	9	US-09-836-073-5	Sequence 5, Appli
21	59	60.2	38	12	US-10-325-810-214	Sequence 214, App
22	56	57.1	18	9	US-09-836-073-6	Sequence 6, Appli
23	52	53.1	420	16	US-10-437-963-128072	Sequence 128072,
24	50	51.0	38	9	US-09-843-676-25	Sequence 25, Appli
25	50	51.0	38	9	US-09-766-253-25	Sequence 25, Appli
26	50	51.0	38	10	US-09-438-486-25	Sequence 25, Appli
27	50	51.0	38	12	US-10-325-810-215	Sequence 215, App
28	50	51.0	38	14	US-10-053-758-25	Sequence 25, Appli
29	50	51.0	38	14	US-10-054-295-25	Sequence 25, Appli
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31	49.5	50.5	37	9	US-09-843-676-24	Sequence 24, Appli
32	49.5	50.5	37	9	US-09-766-253-24	Sequence 24, Appli
33	49.5	50.5	37	10	US-09-438-486-24	Sequence 24, Appli
34	49.5	50.5	37	14	US-10-053-758-24	Sequence 24, Appli
35	49.5	50.5	37	14	US-10-054-295-24	Sequence 24, Appli
36	49.5	50.5	37	14	US-10-054-611-24	Sequence 24, Appli
37	49	50.0	862	16	US-10-437-963-130390	Sequence 130390,
38	47	48.0	609	10	US-09-805-455-4	Sequence 4, Appli
39	47	48.0	609	16	US-10-678-140-4	Sequence 4, Appli
40	47	48.0	615	10	US-09-805-455-2	Sequence 2, Appli
41	47	48.0	615	16	US-10-678-140-2	Sequence 2, Appli
42	47	48.0	664	10	US-09-805-455-5	Sequence 5, Appli
43	47	48.0	664	16	US-10-678-140-5	Sequence 5, Appli
44	46	46.9	377	12	US-10-282-122A-71434	Sequence 71434, A
45	46	46.9	608	10	US-09-805-455-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-836-073-3
; Sequence 3, Application US/09836073
; Patient No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Balidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ. ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; TYPE: PRT
; LENGTH: 18
; ORGANISM: Homo Sapiens
US-09-836-073-3

Query Match 100.0%; Score 98; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 7.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AALQAKICHQIQYFGQF 18
|||
Db 1 AALQAKICHQIQYFGQF 18

RESULT 2
US-09-836-073-1
; Sequence 1, Application US/09836073
; Patient No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-854-050-24

Query Match 50.5%; Score 49.5; DB 3; Length 37;
Best Local Similarity 75.0%; Pred. No. 0.2;
Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 7 ICHQIQYFGQF 18
|||:||||
1 ICHQ-EYFGDF 11

Db

RESULT 15
US-09-430-323-24
Sequence 24, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-430-323-24

Query Match 50.5%; Score 49.5; DB 4; Length 37;
Best Local Similarity 75.0%; Pred. No. 0.2;
Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 7 ICHQIQYFGQF 18
|||:||||
1 ICHQ-EYFGDF 11

Db

Search completed: September 10, 2004, 18:05:07
Job time: 15.8883 secs

FILED DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 215:
US-09-721-456-215

Query Match 51.0%; Score 50; DB 4; Length 38;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ICHQIOYFYG 16
Db 1 ICEQIEYFYG 10

RESULT 13
US-08-851-843A-24
Sequence 24, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017

FILED DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-851-843A-24

Query Match 50.5%; Score 49.5; DB 3; Length 37;
Best Local Similarity 75.0%; Pred. No. 0.2;
Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 7 ICHQIOYFYGQF 18
Db 1 ICHQ-EYFGDF 11

RESULT 14
US-08-854-050-24
Sequence 24, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536

FILED DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-430-323-25

Query Match 51.0%; Score 50; DB 4; Length 38;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ICHQIQYFG 16
|||:||||
DB 1 ICEQIEYFG 10

RESULT 11
US-09-402-181B-215
Sequence 215, Application US/09402181B
Patent No. 6610839
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050

FILED DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/117885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 215:
US-09-402-181B-215

Query Match 51.0%; Score 50; DB 4; Length 38;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ICHQIQYFG 16
|||:||||
DB 1 ICEQIEYFG 10

RESULT 12
US-09-721-456-215
Sequence 215, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-NOV-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017

FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17865
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-215

Query Match 51.0%; Score 50; DB 3; Length 38;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 7 ICHQIOYFYFG 16
Db 1 ICRQIEYFYFG 10

RESULT 9
US-08-854-050-25
Sequence 25, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-854-050-25

Query Match 51.0%; Score 50; DB 3; Length 38;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 7 ICHQIOYFYFG 16
Db 1 ICRQIEYFYFG 10

RESULT 10
US-09-430-323-25
Sequence 25, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843

FILED DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-721-456-214

Query Match 60.2%; Score 59; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 0.0059;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 ICHQIOYFGQF 18
DB 1 ICHQXEYFGDF 12

RESULT 7
US-08-851-843A-25
Sequence 25, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-851-843A-25

Query Match 51.0%; Score 50; DB 3; Length 38;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ICHQIOYFYG 16
DB 1 ICEQIETFYFG 10

RESULT 8
US-08-974-549A-215
Sequence 215, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050

APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-00261005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-214

Query Match 60.2%; Score 59; DB 3; Length 38;
Best Local Similarity 75.0%; Pred. No. 0.0059;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 ICHQIQYFGQF 18
Db 1 ICHQXEYFGDF 12

RESULT 5
US-09-402-181B-214
Sequence 214, Application US/09402181B
Patent No. 6610839
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESSES:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausubus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-00262005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-402-181B-214

Query Match 60.2%; Score 59; DB 4; Length 38;
Best Local Similarity 75.0%; Pred. No. 0.0059;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 ICHQIQYFGQF 18
Db 1 ICHQXEYFGDF 12

RESULT 6
US-09-721-456-214
Sequence 214, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESSES:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-NOV-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312

PRIOR FILING DATE: 1997-10-06
PRIOR APPLICATION NUMBER: 08/321,427
PRIOR FILING DATE: 1994-10-11
PRIOR APPLICATION NUMBER: 60/086,527
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO: 4
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: B-LAP
US-09-316-630-4

Query Match 88.8%; Score 87; DB 3; Length 18;
Best Local Similarity 83.3%; Pred. No. 7, 5e-08;
Matches 15; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AALAKICHQIQYFGQF 18
Db 1 AALAKICHQIQYFGDF 18

RESULT 3
US-08-475-955-20
Sequence 20, Application US/08475955
Patent No. 6641813
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESS:
ADDRESSER: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,955
FILING DATE: June 7, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMR114CIP(2) DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Binding-site
LOCATION: 8..15
US-08-475-955-20

Query Match 65.3%; Score 64; DB 4; Length 21;
Best Local Similarity 83.3%; Pred. No. 0.00049;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ICHQIQYFGQF 18
Db 1 ICHQIQYFGDF 12

RESULT 4
US-08-974-549A-214
Sequence 214, Application US/08974549A
Patent No. 616178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:

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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:43:01 ; Search time 15.8883 Seconds
(without alignments)
58.488 Million cell updates/sec

Title: US-09-836-073-3

Sequence: 1 AALQAKICHQIOYFGQF 18

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Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	64	65.3	21	4	US-08-475-955-20
4	59	60.2	38	3	US-08-974-549A-214
5	59	60.2	38	4	US-08-402-181B-214
6	59	60.2	38	4	US-09-721-456-214
7	50	51.0	38	3	US-08-851-843A-25
8	50	51.0	38	3	US-08-974-549A-215
9	50	51.0	38	3	US-08-854-050-25
10	50	51.0	38	4	US-09-430-323-25
11	50	51.0	38	4	US-09-402-181B-215
12	50	51.0	38	4	US-09-721-456-215
13	49.5	50.5	37	3	US-08-851-843A-24
14	49.5	50.5	37	3	US-08-854-050-24
15	49.5	50.5	37	4	US-09-430-323-24
16	42	42.9	1220	2	US-08-680-326-38
17	42	42.9	2644	4	US-09-028-047C-2
18	42	42.9	292	4	US-09-134-001C-3515
19	40	40.8	111	4	US-09-257-179-61
20	40	40.8	198	4	US-09-328-352-6436
21	40	40.8	554	4	US-09-540-236-3778
22	40	40.8	616	3	US-09-298-367B-11
23	39	39.8	39	3	US-08-851-843A-26
24	39	39.8	39	3	US-08-974-549A-216
25	39	39.8	39	3	US-08-854-050-26
26	39	39.8	39	4	US-09-430-323-26
27	39	39.8	39	4	US-09-402-181B-216

28	39	39.8	39	4	US-09-721-456-216	Sequence 216, App
29	39	39.8	502	4	US-09-328-352-5891	Sequence 5891, App
30	39	39.8	1336	4	US-09-883-134-4	Sequence 4, Appl1
31	39	39.8	2954	4	US-09-150-867-1	Sequence 1, Appl1
32	38.5	39.3	740	4	US-09-323-872A-23	Sequence 23, Appl1
33	38.5	39.3	740	4	US-09-072-433-15	Sequence 15, Appl1
34	38.5	39.3	864	4	US-09-323-872A-28	Sequence 28, Appl1
35	38.5	39.3	864	4	US-09-072-433-16	Sequence 16, Appl1
36	38	38.8	185	4	US-09-107-532A-6934	Sequence 6934, App
37	38	38.8	289	4	US-09-328-352-6229	Sequence 6229, App
38	38	38.8	305	1	US-08-420-235B-25	Sequence 25, Appl1
39	38	38.8	305	5	PCT-US95-10194-25	Sequence 25, Appl1
40	38	38.8	305	5	US-09-543-681A-6745	Sequence 6745, App
41	38	38.8	463	4	US-09-252-991A-30245	Sequence 30245, A
42	38	38.8	576	4	US-09-287-354-2	Sequence 2, Appl1
43	38	38.8	984	4	US-09-287-354-3	Sequence 3, Appl1
44	38	38.8	1189	4	US-09-287-354-4	Sequence 4, Appl1
45	38	38.8	1189	4	US-09-287-354-4	Sequence 4, Appl1

ALIGNMENTS

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RESULT 1
US-09-316-630-3
; Sequence 3, Application US/09316630
; Patent No. 6291637
; GENERAL INFORMATION:
; APPLICANT: Dae, Saumitra
; TITLE OF INVENTION: INTERFERENCE WITH VIRAL IRES-MEDIATED TRANSLATION BY A
; FILE REFERENCE: SMALL YEAST RNA REVEALS CRITICAL RNA-PROTEIN INTERACTIONS
; CURRENT APPLICATION NUMBER: US/09/316,630
; CURRENT FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 08/817,953
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 08/321,427
; PRIOR FILING DATE: 1994-10-11
; PRIOR APPLICATION NUMBER: 60/086,527
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: IAP
US-09-316-630-3
Query Match      88.8%; Score 87; DB 3; Length 18;
Best Local Similarity 83.3%; Pred. No. 7.5e-08;
Matches 15; Conservative 2; Mismatches 1; Indels 0;
Gaps 0;

Oy      1 AALQAKICHQIOYFGQF 18
Db      1 AALQAKICHQIOYFGQF 18

RESULT 2
US-09-316-630-4
; Sequence 4, Application US/09316630
; Patent No. 6291637
; GENERAL INFORMATION:
; APPLICANT: Dae, Saumitra
; TITLE OF INVENTION: INTERFERENCE WITH VIRAL IRES-MEDIATED TRANSLATION BY A
; FILE REFERENCE: SMALL YEAST RNA REVEALS CRITICAL RNA-PROTEIN INTERACTIONS
; CURRENT APPLICATION NUMBER: US/09/316,630
; CURRENT FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 08/817,953

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Mon Sep 13 09:36:20 2004

us-09-836-073-2.rapb

Page 5

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FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-12

Query Match      82.3%; Score 79; DB 9; Length 18;
Best Local Similarity 83.3%; Pred. No. 1e-05;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 AALEAQCQIQIEYFGDF 18
        |||||:|||||
Db      1 AALEAKICHOIEYFGDF 18

RESULT 12
US-09-836-073-10
; Sequence 10, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-10

Query Match      81.2%; Score 78; DB 9; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.5e-05;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 AALEAQCQIQIEYFGDF 18
        |||||:|||||
Db      1 AALEAKICHOIEYFGDF 18

RESULT 13
US-09-836-073-16
; Sequence 16, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Rat
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US-09-836-073-16

Query Match      79.7%; Score 76.5; DB 9; Length 19;
Best Local Similarity 84.2%; Pred. No. 2.7e-05;
Matches 16; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY      1 AALEAQCQIQI-EYFGDF 18
        |||||:|||||
Db      1 AALEAKICHOIEYFGDF 19

RESULT 14
US-09-836-073-3
; Sequence 3, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-3

Query Match      78.1%; Score 75; DB 9; Length 18;
Best Local Similarity 72.2%; Pred. No. 4.4e-05;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 AALEAQCQIQIEYFGDF 18
        |||||:|||||
Db      1 AALQAKICHOIQYFGDF 18

RESULT 15
US-09-836-073-4
; Sequence 4, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 220002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-836-073-4

Query Match      78.1%; Score 75; DB 9; Length 18;
Best Local Similarity 86.7%; Pred. No. 4.4e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 EAQICQIQIEYFGDF 18
        |||||:|||||
Db      4 EAKICHOIEYFGDF 18
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TYPE: PRT
ORGANISM: Homo sapiens
US-10-102-806-695

Query Match 90.6%; Score 87; DB 14; Length 460;
Best Local Similarity 88.9%; Pred. No. 1.6e-05;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALEAQCQIQIEYFGDF 18
||||:|||||
Db 63 ALEAKICHQIEYFGDF 80

RESULT 7
US-10-264-049-2643
Sequence 2643, Application US/10264049
Publication No. US20040005579A1
GENERAL INFORMATION:
APPLICANT: Birsse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P133P1
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: US 60/209,467
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: PatentIn Ver. 3.1
SEQ ID NO 2643
LENGTH: 460
TYPE: PRT
ORGANISM: Homo sapiens
US-10-264-049-2643

Query Match 90.6%; Score 87; DB 15; Length 460;
Best Local Similarity 88.9%; Pred. No. 1.6e-05;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALEAQCQIQIEYFGDF 18
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Db 63 ALEAKICHQIEYFGDF 80

RESULT 8
US-09-836-073-13
Sequence 13, Application US/09836073
Patent No. US20020173475A1
GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Balaya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 17
TYPE: PRT
ORGANISM: Mouse
US-09-836-073-13

Query Match 86.5%; Score 83; DB 9; Length 17;
Best Local Similarity 88.2%; Pred. No. 2.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ALEAQCQIQIEYFGDF 18
||||:|||||
Db 1 ALEAKICHQIEYFGDF 17

RESULT 9
US-09-836-073-9
Sequence 9, Application US/09836073
Patent No. US20020173475A1
GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Balaya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
US-09-836-073-9

Query Match 84.4%; Score 81; DB 9; Length 18;
Best Local Similarity 88.2%; Pred. No. 4.8e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ALEAQCQIQIEYFGDF 17
||||:|||||
Db 1 ALEAKICHQIEYFGDF 17

RESULT 10
US-09-836-073-11
Sequence 11, Application US/09836073
Patent No. US20020173475A1
GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Balaya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 220002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
US-09-836-073-11

Query Match 82.3%; Score 79; DB 9; Length 18;
Best Local Similarity 83.3%; Pred. No. 1e-05;
Matches 15; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ALEAQCQIQIEYFGDF 18
||||:|||||
Db 1 ALEAKICHQIEYFGDF 18

RESULT 11
US-09-836-073-12
Sequence 12, Application US/09836073
Patent No. US20020173475A1
GENERAL INFORMATION:
APPLICANT: Dasgupta, Asim
APPLICANT: Das, S.
APPLICANT: Balaya, Narayan
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION

```

; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 22002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 18
; TYPE: PRF
; ORGANISM: Homo Sapiens
US-09-836-073-1

Query Match          90.6%; Score 87; DB 9; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.3e-07;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AALEAQCQCIIEYFGDF 18
   |||||:|||||
DB 1 AALEAKICHIIEYFGDF 18

RESULT 3
US-09-836-073-14
; Sequence 14, Application US/09836073
; Patent No. US20020173475A1
; GENERAL INFORMATION:
; APPLICANT: Dasgupta, Asim
; APPLICANT: Das, S.
; APPLICANT: Baidya, Narayan
; TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
; FILE REFERENCE: 22002054822
; CURRENT APPLICATION NUMBER: US/09/836,073
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 09/316,630
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 14
; LENGTH: 18
; TYPE: PRF
; ORGANISM: Bovine
US-09-836-073-14

Query Match          90.6%; Score 87; DB 9; Length 18;
Best Local Similarity 88.9%; Pred. No. 5.3e-07;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AALEAQCQCIIEYFGDF 18
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DB 1 AALEAKICHIIEYFGDF 18

RESULT 4
US-10-170-385-477
; Sequence 477, Application US/10170385
; Publication No. US20030203372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On
; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 53268200100
; CURRENT APPLICATION NUMBER: US/10/170,385
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; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: PCT/GB02/01662
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 477
; LENGTH: 408
; TYPE: PRF
; ORGANISM: Homo Sapiens
US-10-170-385-477

Query Match          90.6%; Score 87; DB 12; Length 408;
Best Local Similarity 88.9%; Pred. No. 1.4e-05;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AALEAQCQCIIEYFGDF 18
   |||||:|||||
DB 11 AALEAKICHIIEYFGDF 28

RESULT 5
US-09-925-298-695
; Sequence 695, Application US/09925298
; Publication No. US20020039764A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103
; CURRENT APPLICATION NUMBER: US/09/925,298
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 695
; LENGTH: 460
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-925-298-695

Query Match          90.6%; Score 87; DB 12; Length 460;
Best Local Similarity 88.9%; Pred. No. 1.6e-05;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AALEAQCQCIIEYFGDF 18
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DB 63 AALEAKICHIIEYFGDF 80

RESULT 6
US-10-102-806-695
; Sequence 695, Application US/10102806
; Publication No. US20030054421A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA103P1
; CURRENT APPLICATION NUMBER: US/10/102,806
; CURRENT FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: 09/925,298
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05881
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 846
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 695
; LENGTH: 460
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GenCore version 5.1.6
Copyright: (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2004, 17:55:06 : Search time 40.324 Seconds
(without alignments)
143.151 Million cell updates/sec

Title: US-09-836-073-2

Perfect score: 96
Sequence: 1 AALAEQICQIEYFGDF 18

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
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- 13: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubppaa/US10C_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	87	90.6	18	US-09-836-073-1	Sequence 1, Appli
3	87	90.6	18	US-09-836-073-14	Sequence 14, Appli
4	87	90.6	408	US-10-170-385-477	Sequence 477, App
5	87	90.6	460	US-09-925-298-695	Sequence 695, App
6	87	90.6	460	US-10-102-806-695	Sequence 695, App
7	87	90.6	460	US-10-264-049-2643	Sequence 2643, App
8	83	86.5	17	US-09-836-073-13	Sequence 13, Appli
9	81	84.4	18	US-09-836-073-9	Sequence 9, Appli
10	79	82.3	18	US-09-836-073-11	Sequence 11, Appli
11	79	82.3	18	US-09-836-073-12	Sequence 12, Appli
12	78	81.2	18	US-09-836-073-10	Sequence 10, Appli
13	76.5	79.7	19	US-09-836-073-16	Sequence 16, Appli
14	75	78.1	18	US-09-836-073-3	Sequence 3, Appli
15	75	78.1	18	US-09-836-073-4	Sequence 4, Appli

16	74	77.1	18	US-09-836-073-15	Sequence 15, Appli
17	72	75.0	18	US-09-836-073-7	Sequence 7, Appli
18	71	74.0	18	US-09-836-073-8	Sequence 8, Appli
19	65	67.7	21	US-10-376-121A-20	Sequence 20, Appli
20	63	65.6	18	US-09-836-073-5	Sequence 5, Appli
21	61	63.5	18	US-09-836-073-25	Sequence 25, Appli
22	61	63.5	38	US-09-766-253-25	Sequence 25, Appli
23	61	63.5	38	US-09-438-486-25	Sequence 25, Appli
24	61	63.5	38	US-10-325-810-215	Sequence 25, App
25	61	63.5	38	US-10-053-758-25	Sequence 25, Appli
26	61	63.5	38	US-10-054-611-25	Sequence 25, Appli
27	61	63.5	38	US-10-054-611-25	Sequence 25, Appli
28	60	62.5	38	US-10-325-810-214	Sequence 214, App
29	58	60.4	16	US-09-836-073-19	Sequence 19, Appli
30	56	58.3	18	US-09-836-073-6	Sequence 6, Appli
31	55	57.3	420	US-10-437-963-125036	Sequence 125036
32	50.5	52.6	37	US-09-843-676-24	Sequence 24, Appli
33	50.5	52.6	37	US-09-766-253-24	Sequence 24, Appli
34	50.5	52.6	37	US-09-438-486-24	Sequence 24, Appli
35	50.5	52.6	37	US-10-053-758-24	Sequence 24, Appli
36	50.5	52.6	37	US-10-054-295-24	Sequence 24, Appli
37	50.5	52.6	37	US-10-054-611-24	Sequence 24, Appli
38	50	52.1	922	US-10-437-963-125036	Sequence 125036
39	49	51.0	39	US-09-843-676-26	Sequence 26, Appli
40	49	51.0	39	US-09-766-253-26	Sequence 26, Appli
41	49	51.0	39	US-09-438-486-26	Sequence 26, Appli
42	49	51.0	39	US-10-325-810-216	Sequence 216, App
43	49	51.0	39	US-10-053-758-26	Sequence 26, Appli
44	49	51.0	39	US-10-054-295-26	Sequence 26, Appli
45	49	51.0	39	US-10-054-611-26	Sequence 26, Appli

ALIGNMENTS

RESULT 1
US-09-836-073-2
Sequence 2, Application US/09836073
Patent No. US20020173475A1
GENERAL INFORMATION:
APPLICANT: Daesup, Asim
APPLICANT: Daesup, Asim
TITLE OF INVENTION: METHODS TO INHIBIT VIRAL REPLICATION
FILE REFERENCE: 22002054822
CURRENT APPLICATION NUMBER: US/09/836,073
CURRENT FILING DATE: 2002-10-24
PRIOR APPLICATION NUMBER: 09/316,630
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 18
TYPE: PRT
ORGANISM: Homo Sapiens
US-09-836-073-2

Query Match 100.0%; Score 96; DB 9; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.9e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 AALAEQICQIEYFGDF 18
Db 1 AALAEQICQIEYFGDF 18

RESULT 2
US-09-836-073-1
Sequence 1, Application US/09836073
Patent No. US20020173475A1
GENERAL INFORMATION:
APPLICANT: Daesup, Asim
APPLICANT: Daesup, S.

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-854-050-24

Query Match 52.6%; Score 50.5; DB 3; Length 37;
Best Local Similarity 83.3%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 7 ICQLEIYYFGDF 18
Db 1 ICHQ-EYYFGDF 11

RESULT 15
US-09-430-323-24
Sequence 24, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-430-323-24

Query Match 52.6%; Score 50.5; DB 4; Length 37;
Best Local Similarity 83.3%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 7 ICQLEIYYFGDF 18
Db 1 ICHQ-EYYFGDF 11

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FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-721-456-214

Query Match 62.5%; Score 60; DB 4; Length 38;
Best Local Similarity 83.3%; Pred. No. 0.0029;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 ICQOIEYFGDF 18
Db 1 ICHQXYFGDF 12

RESULT 13
US-08-851-843A-24
Sequence 24, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-09-851-843A-24

Query Match 52.6%; Score 50.5; DB 3; Length 37;
Best Local Similarity 83.3%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 7 ICQOIEYFGDF 18
Db 1 ICHQ-XYFGDF 11

RESULT 14
US-08-854-050-24
Sequence 24, Application US/08854050
Patent No. 6261836
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 536

APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17685
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-214

Query Match 62.5%; Score 60; DB 3; Length 38;
Best Local Similarity 83.3%; Pred. No. 0.0029;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 ICGQIEYFGDF 18
DB 1 ICHQXEYFGDF 12

RESULT 11
US-09-402-181B-214
Sequence 214, Application US/09402181B
Patent No. 6610839
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17685
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausenius, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-09-402-181B-214

Query Match 62.5%; Score 60; DB 4; Length 38;
Best Local Similarity 83.3%; Pred. No. 0.0029;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 ICGQIEYFGDF 18
DB 1 ICHQXEYFGDF 12

RESULT 12
US-09-721-456-214
Sequence 214, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-NOV-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017

STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 215:
US-09-402-181B-215

Query Match 63.5%; Score 61; DB 4; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.002;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 ICQOIEYFGD 17
Db 1 ICQOIEYFGD 11

RESULT 9
US-09-721-456-215
Sequence 215, Application US/09721456
Patent No. 6617110

GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-NOV-1997
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US/08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US/08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US/08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US/08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US/08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 215:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 215:
US-09-721-456-215

Query Match 63.5%; Score 61; DB 4; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.002;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 ICQOIEYFGD 17
Db 1 ICQOIEYFGD 11

RESULT 10
US-08-974-549A-214
Sequence 214, Application US/08974549A
Patent No. 6166178

GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
APPLICATION NUMBER: US/08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US/08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US/08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US/08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US/08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US/08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:

TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-854-050-25

Query Match 63.5%; Score 61; DB 3; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.002;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 ICQIIEYFGD 17
Db 1 ICEQIEYFGD 11

RESULT 7
US-09-430-323-25
; Sequence 25, Application US/09430323
; Patent No. 6309867
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. 6309867el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,323
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant

MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-430-323-25

Query Match 63.5%; Score 61; DB 4; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.002;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 ICQIIEYFGD 17
Db 1 ICEQIEYFGD 11

RESULT 8
US-09-402-181B-215
; Sequence 215, Application US/09402181B
; Patent No. 6610839
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 633
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/402,181B
; FILING DATE: 29-Sep-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Auehnus, Scott L.
; REGISTRATION NUMBER: 42,271
; REFERENCE/DOCKET NUMBER: 015389-002620US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 215:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid

Query Match 63.5%; Score 61; DB 3; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.002;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 ICGQIEYFGD 17
||:|||||
Db 1 ICGQIEYFGD 11

RESULT 5
US-08-974-549A-215

; Sequence 215, Application US/08974549A

; Patent No. 6166178

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; APPLICANT: Lingner, Joachim

; APPLICANT: Nakamura, Toru

; APPLICANT: Chapman, Karen B.

; APPLICANT: Morin, Gregg B.

; APPLICANT: Harley, Calvin B.

; APPLICANT: Andrews, William H.

; TITLE OF INVENTION: Human telomerase Catalytic Subunit

; NUMBER OF SEQUENCES: 727

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/974,549A

; FILING DATE: 19-NOV-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/854,050

; FILING DATE: 09-MAY-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/911,312

; FILING DATE: 14-AUG-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/912,951

; FILING DATE: 14-AUG-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/915,503

; FILING DATE: 14-AUG-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US97/17618

; FILING DATE: 01-OCT-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US97/17885

; FILING DATE: 01-OCT-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Apple, Randolph Ted

; REGISTRATION NUMBER: 36,429

; REFERENCE/DOCKET NUMBER: 015389-002610US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 215:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-974-549A-215

Query Match 63.5%; Score 61; DB 3; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.002;
Matches 10; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 ICGQIEYFGD 17
||:|||||
Db 1 ICGQIEYFGD 11

RESULT 6
US-08-854-050-25

; Sequence 25, Application US/08854050

; Patent No. 6261836

; GENERAL INFORMATION:

; APPLICANT: Cech, Thomas R.

; APPLICANT: Lingner, Joachim

; APPLICANT: Nakamura, Toru

; APPLICANT: Chapman, Karen B.

; APPLICANT: Morin, Gregg B.

; APPLICANT: Harley, Calvin

; APPLICANT: Andrews, William H.

; TITLE OF INVENTION: No. 6261836el Telomerase

; NUMBER OF SEQUENCES: 225

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: United States of America

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/854,050

; FILING DATE: 09-MAY-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/851,843

; FILING DATE: 06-MAY-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/846,017

; FILING DATE: 25-APR-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/844,419

; FILING DATE: 18-APR-1997

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/724,643

; FILING DATE: 01-OCT-1996

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Apple, Randolph T.

; REGISTRATION NUMBER: 36,429

; REFERENCE/DOCKET NUMBER: 015389-002930US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

PRIOR FILING DATE: 1997-10-06
PRIOR APPLICATION NUMBER: 08/321,427
PRIOR FILING DATE: 1994-10-11
PRIOR APPLICATION NUMBER: 60/086,527
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO: 4
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: B-LAP
US-09-316-630-4

Query Match 90.6%; Score 87; DB 3; Length 18;
Best Local Similarity 88.9%; Pred. No. 4.1e-08;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AALEAQICQOIEYFGDF 18
DB 1 AALEAKICQOIEYFGDF 18

RESULT 3
US-08-475-955-20
Sequence 20, Application US/08475955
Patent No. 6641813
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESS:
ADDRESSER: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,955
FILING DATE: June 7, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRP14CIP(2) DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Binding-site
LOCATION: 8..15
US-08-475-955-20

Query Match 67.7%; Score 65; DB 4; Length 21;
Best Local Similarity 91.7%; Pred. No. 0.00022;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ICQOIEYFGDF 18
DB 1 ICQOIEYFGDF 12

RESULT 4
US-08-851-843A-25
Sequence 25, Application US/08851843A
Patent No. 6093809
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809e1 Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A
FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-851-843A-25

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OM protein - protein search, using sw model

Run on: September 10, 2004, 17:43:01 ; Search time 15.8883 Seconds
(without alignments)
58,488 Million cell updates/sec

Title: US-09-836-073-2

Perfect score: 96
Sequence: 1 AALEAKICQIEYFGDF 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/2/iaa/5B.COMB.pep.*
3: /cgn2_6/prodata/2/iaa/6A.COMB.pep.*
4: /cgn2_6/prodata/2/iaa/6B.COMB.pep.*
5: /cgn2_6/prodata/2/iaa/6CTUS.COMB.pep.*
6: /cgn2_6/prodata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	90.6	18	US-09-316-630-3	Sequence 3, Appli
2	87	90.6	18	US-09-316-630-4	Sequence 4, Appli
3	65	67.7	21	US-08-475-955-20	Sequence 20, Appli
4	61	63.5	38	US-08-851-843A-25	Sequence 25, Appli
5	61	63.5	38	US-08-974-549A-215	Sequence 215, App
6	61	63.5	38	US-08-854-050-25	Sequence 25, Appli
7	61	63.5	38	US-09-430-323-25	Sequence 25, Appli
8	61	63.5	38	US-09-402-181B-215	Sequence 215, App
9	61	63.5	38	US-09-721-456-215	Sequence 215, App
10	60	62.5	38	US-08-974-549A-214	Sequence 214, App
11	60	62.5	38	US-09-402-181B-214	Sequence 214, App
12	60	62.5	38	US-09-721-456-214	Sequence 214, App
13	50.5	52.6	37	US-08-851-843A-24	Sequence 24, Appli
14	50.5	52.6	37	US-08-854-050-24	Sequence 24, Appli
15	50.5	52.6	37	US-09-430-323-24	Sequence 24, Appli
16	49	51.0	39	US-08-851-843A-26	Sequence 26, Appli
17	49	51.0	39	US-08-974-549A-216	Sequence 216, App
18	49	51.0	39	US-08-854-050-26	Sequence 26, Appli
19	49	51.0	39	US-09-430-323-26	Sequence 26, Appli
20	49	51.0	39	US-09-402-181B-216	Sequence 216, App
21	49	51.0	39	US-09-721-456-216	Sequence 216, App
22	44	45.8	392	US-08-451-777A-33	Sequence 33, Appli
23	44	45.8	392	US-08-451-777A-33	Sequence 33, Appli
24	44	45.8	392	US-08-998-208-33	Sequence 33, Appli
25	43	44.8	167	US-09-1134-000C-4435	Sequence 3435, App
26	42	43.8	69	US-09-621-976-7385	Sequence 7385, App
27	42	43.8	582	US-09-976-594-733	Sequence 733, App

28	41	42.7	29	1	US-08-451-777A-3	Sequence 3, Appli
29	41	42.7	29	2	US-08-451-778A-3	Sequence 3, Appli
30	41	42.7	29	2	US-08-998-208-3	Sequence 3, Appli
31	41	42.7	29	5	PCT-US94-10825-3	Sequence 3, Appli
32	41	42.7	29	5	PCT-US95-06743-3	Sequence 3, Appli
33	40	41.7	141	4	US-09-540-236-2332	Sequence 2332, App
34	40	41.7	258	4	US-09-489-039A-11751	Sequence 11751, A
35	40	41.7	505	4	US-09-627-216A-12	Sequence 12, Appli
36	40	41.7	505	4	US-09-126-420A-22	Sequence 22, Appli
37	40	41.7	505	4	US-09-765-873A-12	Sequence 12, Appli
38	40	41.7	754	2	US-08-941-262-1	Sequence 1, Appli
39	40	41.7	755	2	US-08-941-262-3	Sequence 3, Appli
40	40	41.7	957	4	US-09-252-991A-21567	Sequence 21567, A
41	40	41.7	1180	3	US-09-224-024-28	Sequence 28, Appli
42	40	41.7	1180	5	PCT-US94-07902-28	Sequence 28, Appli
43	39	40.6	456	1	US-09-585-858-53	Sequence 53, Appli
44	39	40.6	456	1	US-08-205-719-4	Sequence 4, Appli
45	39	40.6	456	3	US-08-431-517F-6	Sequence 6, Appli

ALIGNMENTS

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RESULT 1
US-09-316-630-3
; Sequence 3, Application US/09316630
; Patent No. 6291637
; GENERAL INFORMATION:
; APPLICANT: Das, Saumitra
; APPLICANT: Das, Saumitra
; TITLE OF INVENTION: INTERFERENCE WITH VIRAL IRES-MEDIATED TRANSLATION BY A
; FILE REFERENCE: 22000-20548-21
; CURRENT APPLICATION NUMBER: US/09/316, 630
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 08/817, 953
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: 08/321, 427
; PRIOR FILING DATE: 1994-10-11
; PRIOR APPLICATION NUMBER: 60/086, 527
; PRIOR FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: LAF
US-09-316-630-3
Query Match 90.6%; Score 87; DB 3; Length 18;
Best Local Similarity 88.9%; Pred. No. 4,1e-08;
Matches 16; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Cy 1 AALEAKICQIEYFGDF 18
Db 1 AALEAKICQIEYFGDF 18
RESULT 2
US-09-316-630-4
; Sequence 4, Application US/09316630
; Patent No. 6291637
; GENERAL INFORMATION:
; APPLICANT: Das, Saumitra
; APPLICANT: Das, Saumitra
; TITLE OF INVENTION: INTERFERENCE WITH VIRAL IRES-MEDIATED TRANSLATION BY A
; FILE REFERENCE: 22000-20548-21
; CURRENT APPLICATION NUMBER: US/09/316, 630
; PRIOR FILING DATE: 1999-05-21
; PRIOR APPLICATION NUMBER: 08/817, 953

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McGarry, Sean

To: STIC-Biotech/ChemLib
Subject: SEQ SEARCH 09/836,073

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Please search a. a. SEQ ID NOS: 2-4, 12, and 14-19.

Thank You